

METHOD FOR THE DETECTION OF GENE TRANSCRIPTS IN BLOOD AND USES THEREOF

RELATED APPLICATION(S)

This application is a continuation-in-part of Application No. 10/268,730 filed on
5 October 9, 2002, which is a continuation of U.S. Application No. 09/477,148 filed January 4,
2000, now abandoned, which claims the benefit of U.S. Provisional Application No.
60/115,125 filed on January 6, 1999.

TABLES

This application includes a compact disc in duplicate (2 compact discs: Tables copy 1
10 and Tables copy 2), which are hereby incorporated by reference in their entirety. Each
compact disc contains the following files (corresponding to Tables 2 – 4) :

FILES NAMES	SIZE	DATE OF CREATION
TABLE 2	1,991,680	6/11/2003
15 TABLE 3A (GeneListFigure8.hyperten)	223,744	6/18/2003
TABLE 3B (GeneListFigure9.obesity)	240,640	6/18/2003
TABLE 3C (GeneListFigure10.allergies)	165,376	6/18/2003
TABLE 3D (GeneListFigure11.syst.ster)	161,792	6/18/2003
TABLE 3E (GeneListFigure12.hyper)	483,328	6/18/2003
20 TABLE 3F (GeneListFigure13.obesity)	291,328	6/18/2003
TABLE 3G (GeneListFigure14.diabetes)	238,080	6/18/2003
TABLE 3H (GeneListFigure15.hyperlipidemia)	267,264	6/18/2003
TABLE 3I (GeneListFigure16.lung)	160,768	6/18/2003
TABLE 3J (GeneListFigure17.bladder)	1,511,424	6/18/2003
25 TABLE 3K (GeneListFigure18.bladder)	1,262,592	6/18/2003

	TABLE 3L (GeneListFigure19.cad)	348,160	6/18/2003
	TABLE 3M (GeneListFigure20).ra	513,024	6/18/2003
	TABLE 3N (GeneListFigure21.depression)	248,320	6/18/2003
	Table 3O (GeneListFigure22).ra	95,232	6/18/2003
5	Table 4	276,480	6/19/2003

SEQUENCE LISTING

The application includes a sequence listing submitted on compact disc in triplicate (3 compact discs: SEQ LIST COPY 1, SEQ LIST COPY 2 and SEQ LIST COPY 3 (Computer readable form), the contents of which are hereby incorporated by reference in its entirety.

10 Each compact disc contains the following file:

FILE NAME	SIZE	DATE OF CREATION
Sequence listing (CDS 1516)	117,888	6/16/2003

BACKGROUND

The blood is a vital part of the human circulatory system for the human body.

15 Numerous cell types make up the blood tissue including monocytes, leukocytes, lymphocytes and erythrocytes. Although many blood cell types have been described, there are likely many as yet undiscovered cell types in the human blood. Some of these undiscovered cells may exist transiently, such as those derived from tissues and organs that are constantly interacting with the circulating blood in health and disease. Thus, the blood

20 can provide an immediate picture of what is happening in the human body at any given time.

The turnover of cells in the hematopoietic system is enormous. It was reported that over one trillion cells, including 200 billion erythrocytes and 70 billion neutrophilic leukocytes, turn over each day in the human body (Ogawa 1993). As a consequence of

25 continuous interactions between the blood and the body, genetic changes that occur within the cells or tissues of the body will trigger specific changes in gene expression within blood. It is the goal of the present invention that these genetic alterations be harnessed for

diagnostic and prognostic purposes, which may lead to the development of therapeutics for ameliorating disease.

For example, isoformic myosin heavy chain genes are known to be generally expressed in cardiac muscle tissue. In the rodent, the (MyHC gene is only highly expressed in the fetus and in diseased states such as overt cardiac hypertrophy, heart failure and diabetes; the (MyHC gene is highly expressed shortly after birth and continues to be expressed in the adult heart. In the human, however, (MyHC is highly expressed in the ventricles from the fetal stage through adulthood. This highly expressed (MyHC, which harbours several mutations, has been demonstrated to be involved in familial hypertrophic cardiomyopathy (Geisterfer-Lowrance *et al.* 1990). It was reported that mutations of (MyHC can be detected by PCR using blood lymphocyte DNA (Ferrie *et al.*, 1992). Most recently, it was also demonstrated that mutations of the myosin-binding protein C in familial hypertrophic cardiomyopathy can be detected in the DNA extracted from lymphocytes (Niimura *et al.*, 1998).

Similarly, APP and APC, which are known to be tissue specific and predominantly expressed in the brain and intestinal tract, are also detectable in the transcripts of blood. These cell- or tissue-specific transcripts are not detectable by Northern blot analysis. However, the low number of transcript copies can be detected by RT-PCR analysis. These findings strongly demonstrate that genes preferentially expressed in specific tissues can be detected by a highly sensitive RT-PCR assay. In recent years, evidence has been obtained to indicate that expression of cell or tissue-restricted genes can be detected in the certain peripheral nucleated blood cells of patients with metastatic transitional cell carcinoma (Yuasa *et al.* 1998) and patients with prostate cancer (Gala *et al.* 1998).

In the prior art, there is a need for large samples and/or costly and time-consuming separation of cell types within the blood (Kimoto (1998) and Chelly *et al.* (1989; 1988)). The prior art, however, is deficient in non-invasive methods of screening for tissue-specific diseases. The present invention fulfills this long-standing need and desire in the art.

SUMMARY OF THE INVENTION

The present invention relates generally to the molecular biology of human diseases. More specifically, the present invention relates to a process using the genetic information contained in human peripheral whole blood for the diagnosis, prognosis and monitoring of
5 genetic and infectious disease in the human body.

This present invention discloses a process of using the genetic information contained in human peripheral whole blood in the diagnosis, prognosis and monitoring of genetic and infectious disease in the human body. The process described herein requires a simple blood sample and is, therefore, non-invasive compared to conventional practices used to detect
10 tissue specific disease, such as biopsies.

The invention is based on the discovery that gene expression in the blood is reflective of body state and, as such, the resultant disruption of homeostasis under conditions of disease can be detected through analysis of transcripts differentially expressed in the blood alone. Thus, the identification of several key transcripts or genetic markers in
15 blood will provide information about the genetic state of the cells, tissues, organ systems of the human body in health and disease

The present invention demonstrates that a simple drop of blood may be used to determine the quantitative expression of various mRNAs that reflect the health/disease state of the subject through the use of RT-PCR analysis. This entire process takes about three
20 hours or less. The single drop of blood may also be used for multiple RT-PCR analyses. It is believed that the present finding can potentially revolutionize the way that diseases are detected, diagnosed and monitored because it provides a non-invasive, simple, highly sensitive and quick screening for tissue-specific transcripts. The transcripts detected in whole blood have potential as prognostic or diagnostic markers of disease, as they reflect
25 disturbances in homeostasis in the human body. Delineation of the sequences and/or quantitation of the expression levels of these marker genes by RT-PCR will allow for an immediate and accurate diagnostic/prognostic test for disease or to assess the efficacy and monitor a particular therapeutic.

One object of the present invention is to provide a non-invasive method for the diagnosis, prognosis and monitoring of genetic and infectious disease in humans and animals.

5 In one embodiment of the present invention, there is provided a method for detecting expression of a gene in blood from a subject, comprising the steps of: a) quantifying RNA from a subject blood sample; and b) detecting expression of the gene in the quantified RNA, wherein the expression of the gene in quantified RNA indicates the expression of the gene in the subject blood. An example of the quantifying method is by mass spectrometry.

10 In another embodiment of the present invention, there is provided a method for detecting expression of one or more genes in blood from a subject, comprising the steps of: a) obtaining a subject blood sample; b) extracting RNA from the blood sample; c) amplifying the RNA; d) generating expressed sequence tags (ESTs) from the amplified RNA product; and e) detecting expression of the genes in the ESTs, wherein the expression of the genes in the ESTs indicates the expression of the genes in the subject blood.
15 Preferably, the subject is a fetus, an embryo, a child, an adult or a non-human animal. The genes are non-cancer-associated and tissue-specific genes. Still preferably, the amplification is performed by RT-PCR using random sequence primers or gene-specific primers.

20 In still another embodiment of the present invention, there is provided a method for detecting expression of one or more genes in blood from a subject, comprising the steps of: a) obtaining a subject blood sample; b) extracting DNA fragments from the blood sample; c) amplifying the DNA fragments; and d) detecting expression of the genes in the amplified DNA product, wherein the expression of the genes in the amplified DNA product indicates the expression of the genes in the subject blood.

25 In yet another embodiment of the present invention, there is provided a method for monitoring a course of a therapeutic treatment in an individual, comprising the steps of: a) obtaining a blood sample from the individual; b) extracting RNA from the blood sample; c) amplifying the RNA; d) generating expressed sequence tags (ESTs) from the amplified RNA product; e) detecting expression of genes in the ESTs, wherein the expression of the

genes is associated with the effect of the therapeutic treatment; and f) repeating steps a)-e), wherein the course of the therapeutic treatment is monitored by detecting the change of expression of the genes in the ESTs. Such a method may also be used for monitoring the onset of overt symptoms of a disease, wherein the expression of the genes is associated with the onset of the symptoms. Preferably, the amplification is performed by RT-PCR, and the change of the expression of the genes in the ESTs is monitored by sequencing the ESTs and comparing the resulting sequences at various time points; or by performing single nucleotide polymorphism analysis and detecting the variation of a single nucleotide in the ESTs at various time points.

In still yet another embodiment of the present invention, there is provided a method for diagnosing a disease in a test subject, comprising the steps of: a) generating a cDNA library for the disease from a whole blood sample from a normal subject; b) generating expressed sequence tag (EST) profile from the normal subject cDNA library; c) generating a cDNA library for the disease from a whole blood sample from a test subject; d) generating EST profile from the test subject cDNA library; and e) comparing the test subject EST profile to the normal subject EST profile, wherein if the test subject EST profile differs from the normal subject EST profile, the test subject might be diagnosed with the disease.

In still yet another embodiment of the present invention, there is provided a kit for diagnosing, prognosing or predicting a disease, comprising: a) gene-specific primers; wherein the primers are designed in such a way that their sequences contain the opposing ends of two adjacent exons for the specific gene with the intron sequence excluded; and b) a carrier, wherein the carrier immobilizes the primer(s). Preferably, the gene-specific primers are selected from the group consisting of insulin-specific primers, atrial natriuretic factor-specific primers, zinc finger protein gene-specific primers, beta-myosin heavy chain gene-specific primers, amyloid precursor protein gene-specific primers, and adenomatous polyposis-coli protein gene-specific primers. Further preferably, the gene-specific primers are selected from the group consisting of SEQ ID Nos. 1 and 2; and SEQ ID Nos. 5 and 6. Such a kit may be applied to a test subject whole blood sample to diagnose, prognose or predict a disease by detecting the quantitative expression levels of specific genes associated with the disease in the test subject and then comparing to the levels of same genes expressed

in a normal subject. Such a kit may also be used for monitoring a course of therapeutic treatment or monitoring the onset of overt symptoms of a disease.

In yet another embodiment of the present invention, there is provided a kit for diagnosing, prognosing or predicting a disease, comprising: a) probes derived from a whole blood sample for a specific disease; and b) a carrier, wherein the carrier immobilizes the probes. Such a kit may be applied to a test subject whole blood sample to diagnose, prognose or predict a disease by detecting the quantitative expression levels of specific genes associated with the disease in the test subject and then comparing to the levels of same genes expressed in a normal subject. Such a kit may also be used for monitoring a course of therapeutic treatment or monitoring the onset of overt symptoms of a disease.

Furthermore, the present invention provides a cDNA library specific for a disease, wherein the cDNA library is generated from whole blood samples.

Other and further aspects, features, and advantages of the present invention will be apparent from the following description of the presently preferred embodiments of the invention. These embodiments are given for the purpose of disclosure.

BRIEF DESCRIPTION OF THE DRAWINGS

The above-recited features, advantages and objects of the invention, as well as others which will become clear, are attained and can be understood in detail, more particular descriptions of the invention briefly summarized above may be had by reference to certain embodiments thereof which are illustrated in the appended drawings. These drawings form a part of the specification. It is to be noted, however, that the appended drawings illustrate preferred embodiments of the invention and therefore are not to be considered limiting in their scope not be considered to limit the scope of the invention.

Figure 1 shows the following RNA samples prepared from human blood; Figure 1A: Lane 1, Molecular weight marker; Lane 2, RT-PCR on APP gene; Lane 3, PCR on APP gene; Lane 4, RT-PCR on APC gene; Lane 5, PCR on APC gene; Figure 1B: Lanes 1 and 2, RT-PCR and PCR of (MyHC, respectively; Lanes 3 and 4, RT-PCR of (MyHC from RNA prepared from human fetal and human adult heart, respectively; Lane 5, Molecular weight marker.

Figure 2 shows quantitative RT-PCR analysis performed on RNA samples extracted from a drop of blood. Forward primer (5'-GCCCTCTGGGGACCTGAC-3', SEQ ID No. 1) of exon 1 and reverse primer (5'-CCCACCTGCAGGTCCTCT-3'', SEQ ID No. 2) of exons 1 and 2 of insulin gene. Blood samples of 4 normal subjects were assayed. Lanes 1, 3, 5 and 7 represent overnight "fasting" blood sample and lanes 2, 4, 6 and 8 represent "non-fasting" samples.

Figure 3 shows quantitative RT-PCR analysis performed on RNA samples extracted from a drop of blood. Lanes 1 and 2 represent normal healthy person and lane 3 represents late-onset diabetes (Type II) and lane 4 represents asymptomatic diabetes.

Figure 4 shows multiple RT-PCR assay in a drop of blood. Primers were derived from insulin gene (INS), zinc-finger protein gene (ZFP) and house-keeping gene (GADH). Lane 1 represents normal person. Lane 2 represents late-onset diabetes and lane 3 represents asymptomatic diabetes.

Figure 5 shows standardized levels of insulin gene (Figure 5A) and ZFP gene (Figure 5B) expressed in a drop of blood. The first three subjects were normal, second two subjects showed normal glucose tolerance, and the last subject had late onset diabetes type II. Figure 5C shows standardized levels of insulin gene expressed in each fractionated cell from whole blood.

Figure 6 shows the differential screening of human blood cell cDNA library with different cDNA probes of heart and brain tissue. Figure 6A shows blood cell cDNA probes vs. adult heart cDNA probes. Figure 6B shows blood cell cDNA probes vs. human brain cDNA probes.

Figure 7 graphically shows the 1,800 unique genes in human blood and in the human fetal heart grouped into seven cellular functions.

Figure 8 shows a diagrammatic representation of gene expression profiles of blood samples from individuals having both osteoarthritis and hypertension as compared with gene expression profiles from normal individuals.

Figure 9 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having both osteoarthritis and who were obese as described herein as compared with gene expression profiles from normal individuals

5 Figure 10 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having both osteoarthritis and allergies as described herein as compared with gene expression profiles from normal individuals.

Figure 11 shows a diagrammatic representation of gene expression profiles of blood samples from individuals having osteoarthritis and who were subject to systemic steroids as described herein as compared with gene expression profiles from normal individuals.

10 Figure 12 shows a diagrammatic representation of gene expression profiles of blood samples from individuals having hypertension as compared with gene expression profiles from samples of both non-hypertensive and normal individuals.

Figure 13 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as obese as described herein as compared
15 with gene expression profiles from normal and non-obese individuals

Figure 14 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having type 2 diabetes as described herein as compared with gene expression profiles from normal and non-type 2 diabetes individuals.

Figure 15 shows a diagrammatic representation of gene expression profiles of blood
20 samples from individuals who were identified as having hyperlipidemia as described herein as compared with gene expression profiles from normal and non-hyperlipidemia patients.

Figure 16 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having lung disease as described herein as compared with gene expression profiles from normal and non lung disease individuals.

25 Figure 17 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having bladder cancer as described herein as compared with gene expression profiles from non bladder cancer individuals.

Figure 18 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having advanced stage bladder cancer or early stage bladder cancer as described herein as compared with gene expression profiles from non bladder cancer individuals

- 5 Figure 19 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having coronary artery disease (CAD) as described herein as compared with gene expression profiles from non-coronary artery disease individuals

- 10 Figure 20 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having rheumatoid arthritis as described herein as compared with gene expression profiles from non-rheumatoid arthritis individuals.

Figure 21 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having depression as described herein as compared with gene expression profiles from non-depression individuals.

- 15 Figure 22 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having various stages of osteoarthritis as described herein as compared with gene expression profiles from normal individuals.

Figure 23 shows RT-PCR of overexpressed genes in CAD peripheral blood cells identified using microarray experiments, including PBP, PF4 and F13A.

- 20 Figure 24 shows the the "Blood Chip", a cDNA microarray slide with 10,368 PCR products derived from peripheral blood cell cDNA libraries. Colors represent hybridization to probes labeled mth Cy3 (green) or Cy5 (red) . Yellow spots indicate common hybri dization between both probes. In slide A, normal bl ood cell RNA samples were labeled with Cy3 and CAD blood cell RNA samples were labeled with Cy5. In slide B, Cy3 and Cy5 were switched to
25 label the RNA samples. (Cluster analysis revealed distinct gene expression profiles for normal and CAD samples.)

DETAILED DESCRIPTION

In accordance with the present invention, there may be employed conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, e.g., Sambrook, Fritsch & Maniatis, "Molecular Cloning: A Laboratory Manual (1982); "DNA Cloning: A Practical Approach," Volumes I and II (D.N. Glover ed. 1985); "Oligonucleotide Synthesis" (M.J. Gait ed. 1984); "Nucleic Acid Hybridization" [B.D. Hames & S.J. Higgins eds. (1985)]; "Transcription and Translation" [B.D. Hames & S.J. Higgins eds. (1984)]; "Animal Cell Culture" [R.I. Freshney, ed. (1986)]; "Immobilized Cells And Enzymes" [IRL Press, (1986)]; B. Perbal, "A Practical Guide To Molecular Cloning" (1984). Therefore, if appearing herein, the following terms shall have the definitions set out below.

A "cDNA" is defined as copy-DNA or complementary-DNA, and is a product of a reverse transcription reaction from an mRNA transcript. "RT-PCR" refers to reverse transcription polymerase chain reaction and results in production of cDNAs that are complementary to the mRNA template(s).

In addition to RT-PCR, other methods of amplifying may also be used for the purpose of measuring/quantitating tissue-specific transcripts in human blood. For example, mass spectrometry may be used to quantify the transcripts (Koster et al., 1996; Fu et al., 1998). The application of presently disclosed method for detecting tissue-specific transcripts in blood does not restrict to subjects undergoing course of therapy or treatment, it may also be used for monitoring a patient for the onset of overt symptoms of a disease. Furthermore, the present method may be used for detecting any gene transcripts in blood. A kit for diagnosing, prognosing or even predicting a disease may be designed using gene-specific primers or probes derived from a whole blood sample for a specific disease and applied directly to a drop of blood. A cDNA library specific for a disease may be generated from whole blood samples and used for diagnosis, prognosis or even predicting a disease.

The term "oligonucleotide" is defined as a molecule comprised of two or more deoxyribonucleotides and/ or ribonucleotides, preferably more than three. Its exact size will depend upon many factors which, in turn, depend upon the ultimate function and use of the

oligonucleotide. The upper limit may be 15, 20, 25, 30, 40 or 50 nucleotides in length. The term "primer" as used herein refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product, which is complementary to a nucleic acid strand, is induced, i.e., in the presence of nucleotides and an inducing agent such as a DNA polymerase and at a suitable temperature and pH. The primer may be either single-stranded or double-stranded and must be sufficiently long to prime the synthesis of the desired extension product in the presence of the inducing agent. The exact length of the primer will depend upon many factors, including temperature, source of primer and the method used. For example, for diagnostic applications, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 15-25 or more nucleotides, although it may contain fewer nucleotides. The factors involved in determining the appropriate length of primer are readily known to one of ordinary skill in the art.

As used herein, random sequence primers refer to a composition of primers of random sequence, i.e. not directed towards a specific sequence. These sequences possess sufficient complementarity to hybridize with a polynucleotide and the primer sequence need not reflect the exact sequence of the template.

"Restriction fragment length polymorphism" refers to variations in DNA sequence detected by variations in the length of DNA fragments generated by restriction endonuclease digestion.

A standard Northern blot assay can be used to ascertain the relative amounts of mRNA in a cell or tissue obtained from plant or other tissue, in accordance with conventional Northern hybridization techniques known to those persons of ordinary skill in the art. The Northern blot uses a hybridization probe, e.g. radiolabelled cDNA, either containing the full-length, single stranded DNA or a fragment of that DNA sequence at least 20 (preferably at least 30, more preferably at least 50, and most preferably at least 100 consecutive nucleotides in length). The DNA hybridization probe can be labelled by any of the many different methods known to those skilled in this art. The labels most commonly employed for these studies are radioactive elements, enzymes, chemicals which fluoresce

when exposed to ultraviolet light, and others. A number of fluorescent materials are known and can be utilized as labels. These include, for example, fluorescein, rhodamine, auramine, Texas Red, AMCA blue and Lucifer Yellow. A particular detecting material is anti-rabbit antibody prepared in goats and conjugated with fluorescein through an isothiocyanate.

5 Proteins can also be labeled with a radioactive element or with an enzyme. The radioactive label can be detected by any of the currently available counting procedures. The preferred isotope may be selected from ^3H , ^{14}C , ^{32}P , ^{35}S , ^{36}Cl , ^{51}Cr , ^{57}Co , ^{58}Co , ^{59}Fe , ^{90}Y , ^{125}I , ^{131}I , and ^{186}Re . Enzyme labels are likewise useful, and can be detected by any of the presently utilized colorimetric, spectrophotometric, fluorospectrophotometric, amperometric or

10 gasometric techniques. The enzyme is conjugated to the selected particle by reaction with bridging molecules such as carbodiimides, diisocyanates, glutaraldehyde and the like. Many enzymes which can be used in these procedures are known and can be utilized. The preferred are peroxidase, (-glucuronidase, (-D-glucosidase, (-D-galactosidase, urease, glucose oxidase plus peroxidase and alkaline phosphatase. U.S. Patent Nos. 3,654,090,

15 3,850,752, and 4,016,043 are referred to by way of example for their disclosure of alternate labeling material and methods.

As used herein, "individual" refers to human subjects as well as non-human subjects. The examples herein are not meant to limit the methodology of the present invention to human subjects only, as the instant methodology is useful in the fields of veterinary

20 medicine, animal sciences and such.

As used herein, "detecting" refers to determining the presence of a gene expression product, for example cDNA, RNA or EST, by any method known to those of skill in the art or taught in numerous texts and laboratory manuals (see for example, Ausubel et al. Short Protocols in Molecular Biology (1995) 3rd Ed. John Wiley & Sons, Inc.). For example,

25 methods of detection include but are not limited to, RNA fingerprinting, Northern blotting, polymerase chain reaction, ligase chain reaction, Qbeta replicase, isothermal amplification method, strand displacement amplification, transcription based amplification systems, nuclease protection (SI nuclease or RNase protection assays) as well as methods disclosed in WO 88/10315, Wo 89/ 06700PCT/US87/00880, PCT/ US89/01025.

As used herein, a disease of the invention includes, but is not limited to, blood disorder, blood lipid disease, autoimmune disease, arthritis (including osteoarthritis, rheumatoid arthritis, lupus, allergies, juvenile rheumatoid arthritis and the like), bone or joint disorder, a cardiovascular disorder, obesity, respiratory disease, lung diseases, hyperlipidemias, endocrine disorder, immune disorder, infectious disease, muscle wasting and whole body wasting disorder, neurological disorders including neurodegenerative and/or neuropsychiatric diseases, mood disorders, skin disorder, kidney disease, scleroderma, stroke, hereditary hemorrhage telangiectasia, diabetes, disorders associated with diabetes (e.g., PVD), hypertension, Gaucher's disease, cystic fibrosis, sickle cell anemia, liver disease, pancreatic disease, eye, ear, nose and/or throat disease, diseases affecting the reproductive organs, gastrointestinal diseases (including diseases of the colon, diseases of the spleen, appendix, gall bladder, and others) and the like. For further discussion of human diseases, see Mendelian Inheritance in Man: A Catalog of Human Genes and Genetic Disorders by Victor A. McKusick (12th Edition (3 volume set) June 1998, Johns Hopkins University Press, ISBN: 0801857422) and Harrison's Principles of Internal Medicine by Braunwald, Fauci, Kasper, Hauser, Longo, & Jameson (15th Edition 2001), the entirety of which is incorporated herein.

In another embodiment of the invention, a disease refers to an immune disorder, such as those associated with overexpression of a gene or expression of a mutant gene (e.g., autoimmune diseases, such as diabetes mellitus, arthritis (including rheumatoid arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic arthritis), multiple sclerosis, encephalomyelitis, myasthenia gravis, systemic lupus erythematosus, autoimmune thyroiditis, dermatitis (including atopic dermatitis and eczematous dermatitis), psoriasis, Sjogren's Syndrome, Crohn's disease, aphthous ulcer, iritis, conjunctivitis, keratoconjunctivitis, ulcerative colitis, asthma, allergic asthma, cutaneous lupus erythematosus, scleroderma, vaginitis, proctitis, drug eruptions, leprosy reversal reactions, erythema nodosum leprosum, autoimmune uveitis, allergic encephalomyelitis, acute necrotizing hemorrhagic encephalopathy, idiopathic bilateral progressive sensorineural hearing loss, aplastic anemia, pure red cell anemia, idiopathic thrombocytopenia, polychondritis, Wegener's granulomatosis, chronic active hepatitis, Stevens-Johnson syndrome, idiopathic sprue, lichen planus, Graves' disease, sarcoidosis, primary biliary

cirrhosis, uveitis posterior, and interstitial lung fibrosis), graft-versus-host disease, cases of transplantation, and allergy.

In another embodiment, a disease of the invention is a cellular proliferative and/or differentiative disorder that includes, but is not limited to, cancer, e.g., carcinoma, sarcoma or other metastatic disorders and the like. As used herein, the term "cancer" refers to cells having the capacity for autonomous growth, i.e., an abnormal state of condition characterized by rapidly proliferating cell growth. "Cancer" is meant to include all types of cancerous growths or oncogenic processes, metastatic tissues or malignantly transformed cells, tissues, or organs, irrespective of histopathologic type or stage of invasiveness.

10 Examples of cancers include but are not limited to solid tumours and leukaemias, including: apudoma, choristoma, branchioma, malignant carcinoid syndrome, carcinoid heart disease, carcinoma (e.g., Walker, basal cell, basosquamous, Brown-Pearce, ductal, Ehrlich tumour, in situ, Krebs 2, Merkel cell, mucinous, non-small cell lung, oat cell, papillary, scirrhous, bronchiolar, bronchogenic, squamous cell, and transitional cell), histiocytic disorders,

15 leukaemia (e.g., B cell, mixed cell, null cell, T cell, T-cell chronic, HTLV-II-associated, lymphocytic acute, lymphocytic chronic, mast cell, and myeloid), histiocytosis malignant, Hodgkin disease, immunoproliferative small, non-Hodgkin lymphoma, plasmacytoma, reticuloendotheliosis, melanoma, chondroblastoma, chondroma, chondrosarcoma, fibroma, fibrosarcoma, giant cell tumours, histiocytoma, lipoma, liposarcoma, mesothelioma,

20 myxoma, myxosarcoma, osteoma, osteosarcoma, Ewing sarcoma, synovioma, adenofibroma, adenolymphoma, carcinosarcoma, chordoma, craniopharyngioma, dysgerminoma, hamartoma, mesenchymoma, mesonephroma, myosarcoma, ameloblastoma, cementoma, odontoma, teratoma, thymoma, trophoblastic tumour, adeno-carcinoma, adenoma, cholangioma, cholesteatoma, cylindroma, cystadenocarcinoma, cystadenoma,

25 granulosa cell tumour, gynandroblastoma, hepatoma, hidradenoma, islet cell tumour, Leydig cell tumour, papilloma, Sertoli cell tumour, theca cell tumour, leiomyoma, leiomyosarcoma, myoblastoma, myoma, myosarcoma, rhabdomyoma, rhabdomyosarcoma, ependymoma, ganglioneuroma, glioma, medulloblastoma, meningioma, neurilemmoma, neuroblastoma, neuroepithelioma, neurofibroma, neuroma, paraganglioma, paraganglioma nonchromaffin,

30 angiokeratoma, angiolymphoid hyperplasia with eosinophilia, angioma sclerosing, angiomatosis, glomangioma, hemangioendothelioma, hemangioma, hemangiopericytoma,

hemangiosarcoma, lymphangioma, lymphangiomyoma, lymphangiosarcoma, pinealoma, carcinosarcoma, chondrosarcoma, cystosarcoma, phyllodes, fibrosarcoma, hemangiosarcoma, leiomyosarcoma, leukosarcoma, liposarcoma, lymphangiosarcoma, myosarcoma, myxosarcoma, ovarian carcinoma, rhabdomyosarcoma, sarcoma (e.g., Ewing, 5 experimental, Kaposi, and mast cell), neoplasms (e.g., bone, breast, digestive system, colorectal, liver, pancreatic, pituitary, testicular, orbital, head and neck, central nervous system, acoustic, pelvic respiratory tract, and urogenital), neurofibromatosis, and cervical dysplasia, and other conditions in which cells have become immortalised or transformed.

As used herein, a gene of the invention is a gene that is expressed in blood and is 10 either upregulated, or downregulated and can be used, either solely or in conjunction with other genes, as a marker for disease as defined herein. The term "gene" includes a region that can be transcribed into RNA, as the invention contemplates detection of RNA or equivalents thereof, i.e., cDNA or EST. A gene of the invention includes but is not limited to genes specific for or involved in a particular biological process, such as apoptosis, 15 differentiation, stress response, aging, proliferation, etc.; cellular mechanism genes, e.g. cell-cycle, signal transduction, metabolism of toxic compounds, and the like; disease associated genes, e.g. genes involved in cancer, schizophrenia, diabetes, high blood pressure, atherosclerosis, viral-host interaction and infection and the like.

For example, the gene of the invention can be an oncogene (Hanahan, D. and R.A. 20 Weinberg, *Cell* (2000) 100:57; and Yokota, J., *Carcinogenesis* (2000) 21(3):497-503) whose expression within a cell induces that cell to become converted from a normal cell into a tumor cell. Further examples of genes of the invention include, but are not limited to, cytokine genes (Rubinstein, M., et al., *Cytokine Growth Factor Rev.* (1998) 9(2):175-81); idiotype (Id) protein genes (Benezra, R., et al., *Oncogene* (2001) 20(58):8334-41; Norton, 25 J.D., *J. Cell Sci.* (2000) 113(22):3897-905); prion genes (Prusiner, S.B., et al., *Cell* (1998) 93(3):337-48; Safar, J., and S.B. Prusiner, *Prog. Brain Res.* (1998) 117:421-34); genes that express molecules that induce angiogenesis (Gould, V.E. and B.M. Wagner, *Hum. Pathol.* (2002) 33(11):1061-3); genes encoding adhesion molecules (Chothia, C. and E.Y. Jones, *Annu. Rev. Biochem.* (1997) 66:823-62; Parise, L.V., et al., *Semin. Cancer Biol.* (2000) 30 10(6):407-14); genes encoding cell surface receptors (Deller, M.C., and Y.E. Jones, *Curr.*

Opin. Struct. Biol. (2000) 10(2):213-9); genes of proteins that are involved in metastasizing and/or invasive processes (Boyd, D., Cancer Metastasis Rev. (1996) 15(1):77-89; Yokota, J., Carcinogenesis (2000) 21(3):497-503); genes of proteases as well as of molecules that regulate apoptosis and the cell cycle (Matrisian, L.M., Curr. Biol. (1999) 9(20):R776-8; 5 Krepela, E., Neoplasia (2001) 48(5):332-49; Basbaum and Werb, Curr. Opin. Cell Biol. (1996) 8:731-738; Birkedal-Hansen, et al., Crit. Rev. Oral Biol. Med. (1993) 4:197-250; Mignatti and Rifkin, Physiol. Rev. (1993) 73:161-195; Stetler-Stevenson, et al., Annu. Rev. Cell Biol. (1993) 9:541-573; Brinkerhoff, E., and L.M. Matrisian, Nature Reviews (2002) 3:207-214; Strasser, A., et al., Annu. Rev. Biochem. (2000) 69:217-45; Chao, D.T. and S.J. 10 Korsmeyer, Annu. Rev. Immunol. (1998) 16:395-419; Mullauer, L., et al., Mutat. Res. (2001) 488(3):211-31; Fotedar, R., et al., Prog. Cell Cycle Res. (1996) 2:147-63; Reed, J.C., Am. J. Pathol. (2000) 157(5):1415-30; D'Ari, R., Bioassays (2001) 23(7):563-5); or multi-drug resistance genes, such as MDR1 gene (Childs, S., and V. Ling, Imp. Adv. Oncol. (1994) 21-36). In another embodiment, a gene of the invention contains a sequence found 15 in Tables 2 or 3 or Figures 22 – 36.

Construction of a Microarray

A nucleic acid microarray (RNA, DNA, cDNA, PCR products or ESTs) according to the invention was constructed as follows.

Nucleic acids (RNA, DNA, cDNA, PCR products or ESTs) (~40 ul) are precipitated 20 with 4 ul (1/10 volume) of 3M sodium acetate (pH 5.2) and 100 ul (2.5 volumes) of ethanol and stored overnight at -20°C. They are then centrifuged at 3,300 rpm at 4°C for 1 hour. The obtained pellets were washed with 50 ul ice-cold 70% ethanol and centrifuged again for 30 minutes. The pellets are then air-dried and resuspended well in 50% dimethylsulfoxide (DMSO) or 20ul 3X SSC overnight. The samples are then deposited either singly or in 25 duplicate onto Gamma Amino Propyl Silane (Corning CMT-GAPS or CMT-GAP2, Catalog No. 40003, 40004) or polylysine-coated slides (Sigma Cat. No. P0425) using a robotic GMS 417 or 427 arrayer (Affymetrix, CA). The boundaries of the DNA spots on the microarray are marked with a diamond scribe. The invention provides for arrays where 10-20,000 different DNAs are spotted onto a solid support to prepare an array, and also may include duplicate or 30 triplicate DNAs.

The arrays are rehydrated by suspending the slides over a dish of warm particle free ddH₂O for approximately one minute (the spots will swell slightly but not run into each other) and snap-dried on a 70-80°C inverted heating block for 3 seconds. DNA is then UV crosslinked to the slide (Stratagene, Stratalinker, 65 mJ – set display to “650” which is 650 x 100 uJ) or baked at 80°C for two to four hours. The arrays are placed in a slide rack. An empty slide chamber is prepared and filled with the following solution: 3.0 grams of succinic anhydride (Aldrich) is dissolved in 189 ml of 1-methyl-2-pyrrolidinone (rapid addition of reagent is crucial); immediately after the last flake of succinic anhydride dissolved, 21.0 ml of 0.2 M sodium borate is mixed in and the solution is poured into the slide chamber. The slide rack is plunged rapidly and evenly in the slide chamber and vigorously shaken up and down for a few seconds, making sure the slides never leave the solution, and then mixed on an orbital shaker for 15-20 minutes. The slide rack is then gently plunged in 95°C ddH₂O for 2 minutes, followed by plunging five times in 95% ethanol. The slides are then air dried by allowing excess ethanol to drip onto paper towels. The arrays are then stored in the slide box at room temperature until use.

Microarrays

Nucleic acid Microarrays

Any combination of the nucleic acid sequences generated from nucleotides complimentary to regions of DNA expressed in blood are used for the construction of a microarray. In one embodiment, the microarray is chondrocyte-specific and encompasses genes which are important in the osteoarthritis disease process. A microarray according to the invention preferably comprises between 10, 100, 500, 1000, 5000, 10,000 and 15,000 nucleic acid members, and more preferably comprises at least 5000 nucleic acid members. The nucleic acid members are known or novel nucleic acid sequences described herein, or any combination thereof. A microarray according to the invention is used to assay for differential gene expression profiles of genes in blood samples from healthy patients as compared to patients with a disease.

Microarray according to the invention

GENECHIP®

GeneChip® probe arrays are manufactured through a unique and robust process— a combination of photolithography and combinatorial chemistry— that results in many of the arrays' powerful capabilities. With a calculated minimum number of synthesis steps, 5 GeneChip technology produces arrays with hundreds of thousands of different probes packed at an extremely high density. This feature enables researchers to obtain high quality, genome-wide data using small sample volumes. Manufacture is scalable because the length of the probes, not their number, determines the number of synthesis steps required. This robust and automated production process yields arrays with highly reproducible properties, which 10 reduces user set-up time by eliminating the need for individual labs to produce and test their own arrays.

Using technologies adapted from the semiconductor industry, GeneChip manufacturing begins with a 5-inch square quartz wafer. Initially the quartz is washed to ensure uniform hydroxylation across its surface. Because quartz is naturally hydroxylated, it 15 provides an excellent substrate for the attachment of chemicals, such as linker molecules, that are later used to position the probes on the arrays.

The wafer is placed in a bath of silane, which reacts with the hydroxyl groups of the quartz, and forms a matrix of covalently linked molecules. The distance between these silane molecules determines the probes' packing density, allowing arrays to hold over 500,000 probe 20 locations, or features, within a mere 1.28 square centimeters. Each of these features harbors millions of identical DNA molecules. The silane film provides a uniform hydroxyl density to initiate probe assembly. Linker molecules, attached to the silane matrix, provide a surface that may be spatially activated by light.

Probe synthesis occurs in parallel, resulting in the addition of an A, C, T, or G 25 nucleotide to multiple growing chains simultaneously. To define which oligonucleotide chains will receive a nucleotide in each step, photolithographic masks, carrying 18 to 20 square micron windows that correspond to the dimensions of individual features, are placed over the coated wafer. The windows are distributed over the mask based on the desired sequence of each probe. When ultraviolet light is shone over the mask in the first step of synthesis, the

exposed linkers become deprotected and are available for nucleotide coupling. Critical to this step is the precise alignment of the mask with the wafer before each synthesis step. To ensure that this critical step is accurately completed, chrome marks on the wafer and on the mask are perfectly aligned.

- 5 Once the desired features have been activated, a solution containing a single type of deoxynucleotide with a removable protection group is flushed over the wafer's surface. The nucleotide attaches to the activated linkers, initiating the synthesis process.

10 Although the process is highly efficient, some activated molecules fail to attach the new nucleotide. To prevent these "outliers" from becoming probes with missing nucleotides, a capping step is used to truncate them. In addition, the side chains of the nucleotides are protected to prevent the formation of branched oligonucleotides.

In the following synthesis step, another mask is placed over the wafer to allow the next round of deprotection and coupling. The process is repeated until the probes reach their full length, usually 25 nucleotides.

- 15 Although each position in the sequence of an oligonucleotide can be occupied by 1 of 4 nucleotides, resulting in an apparent need for 25×4 , or 100, different masks per wafer, the synthesis process can be designed to significantly reduce this requirement. Algorithms that help minimize mask usage calculate how to best coordinate probe growth by adjusting synthesis rates of individual probes and identifying situations when the same mask can be
20 used multiple times.

Once the synthesis is complete, the wafers are deprotected, diced, and the resulting individual arrays are packaged in flowcell cartridges. Depending on the number of probe features per array, a single wafer can yield between 49 and 400 arrays.

- 25 The manufacturing process ends with a comprehensive series of quality control tests. Additionally, a sampling of arrays from every wafer is used to test the batch by running control hybridizations. A quantitative test of hybridization is also performed using standardized control probes.

After passing these rigorous tests, GeneChip probe arrays are well prepared to help pursue ambitious goals ranging from the discovery of basic biological mechanisms to the development of new disease therapies.

THE HUMAN GENOME U133 SET

5 The Human Genome U133 (HG-U133) Set, consisting of two GeneChip® arrays, contains almost 45,000 probe sets representing more than 39,000 transcripts derived from approximately 33,000 well-substantiated human genes. This set design uses sequences selected from GenBank®, dbEST, and RefSeq.

10 The sequence clusters were created from the UniGene database (Build 133, April 20, 2001). They were then refined by analysis and comparison with a number of other publicly available databases including the Washington University EST trace repository and the University of California, Santa Cruz Golden Path human genome database (April 2001 release).

15 The HG-U133A Array includes representation of the RefSeq database sequences and probe sets related to sequences previously represented on the Human Genome U95Av2 Array. The HG-U133B Array contains primarily probe sets representing EST clusters.

15 K Chondrochip (Version 2b)

20 The Chondrochip version 2b is chondrocyte-specific microarray chip comprising 15000 novel and known EST sequences of the chondrocyte from chondrocyte-specific cDNA libraries.

Controls on the Chondrochip

25 There are two types of controls used on microarrays. First, positive controls are genes whose expression level is invariant between different stages of investigation and are used to monitor:

- a) target DNA binding to the slide,
- b) quality of the spotting and binding processes of the target DNA onto the slide,
- c) quality of the RNA samples, and
- d) efficiency of the reverse transcription and fluorescent labelling of the probes.

5 Second, negative controls are external controls derived from an organism unrelated to and therefore unlikely to cross-hybridize with the sample of interest. These are used to monitor for:

- a) variation in background fluorescence on the slide, and
- b) non-specific hybridization.

10 There are currently 63 controls spots on the ChondroChip™ consisting of:

<i>Type</i>	<i>No.</i>
Positive Controls:	2
<i>Alien</i> DNA	12
<i>A. thaliana</i> DNA	10
Spotting Buffer	41

Blood Chip

The “Blood chip” is a cDNA microarray slide with 10,368 PCR products derived from peripheral blood cell cDNA libraries as shown in Figure 24.

Target Nucleic acid Preparation and Hybridization

20 *Preparation of Fluorescent DNA Probe from mRNA*

Fluorescently labeled target nucleic acid samples are prepared for analysis with an array of the invention.

2 μ g Oligo-dT primers are annealed to 2 μ g of mRNA isolated from a blood sample of a patient in a total volume of 15 μ l, by heating to 70°C for 10 min, and cooled on ice. The mRNA is reverse transcribed by incubating the sample at 42°C for 1.5-2 hours in a 100 μ l volume containing a final concentration of 50 mM Tris-HCl (pH 8.3), 75 mM KCl, 3 mM MgCl₂, 25 mM DTT, 25 mM unlabeled dNTPs, 400 units of Superscript II (200 U/ μ L, Gibco BRL), and 15 mM of Cy3 or Cy5 (Amersham). RNA is then degraded by addition of 15 μ l of 0.1N NaOH, and incubation at 70°C for 10 min. The reaction mixture is neutralized by addition of 15 μ l of 0.1N HCL, and the volume is brought to 500 μ l with TE (10mM Tris, 1mM EDTA), and 20 μ g of Cot1 human DNA (Gibco-BRL) is added.

10 The labeled target nucleic acid sample is purified by centrifugation in a Centricon-30 micro-concentrator (Amicon). If two different target nucleic acid samples (e.g., two samples derived from a healthy patient vs patient with a disease) are being analyzed and compared by hybridization to the same array, each target nucleic acid sample is labeled with a different fluorescent label (e.g., Cy3 and Cy5) and separately concentrated. The separately
15 concentrated target nucleic acid samples (Cy3 and Cy5 labeled) are combined into a fresh centricon, washed with 500 μ l TE, and concentrated again to a volume of less than 7 μ l. 1 μ L of 10 μ g/ μ l polyA RNA (Sigma, #P9403) and 1 μ l of 10 μ g/ μ l tRNA (Gibco-BRL, #15401-011) is added and the volume is adjusted to 9.5 μ l with distilled water. For final target nucleic acid preparation 2.1 μ l 20XSSC (1.5M NaCl, 150mM NaCitrate (pH8.0)) and 0.35 μ l 10%SDS
20 is added.

Hybridization

Labeled nucleic acid is denatured by heating for 2 min at 100°C, and incubated at 37°C for 20-30 min before being placed on a nucleic acid array under a 22mm x 22mm glass cover slip. Hybridization is carried out at 65°C for 14 to 18 hours in a custom slide chamber
25 with humidity maintained by a small reservoir of 3XSSC. The array is washed by submersion and agitation for 2-5 min in 2X SSC with 0.1%SDS, followed by 1X SSC, and 0.1X SSC. Finally, the array is dried by centrifugation for 2 min in a slide rack in a Beckman GS-6 tabletop centrifuge in Microplus carriers at 650 RPM for 2 min.

Signal Detection And Data Generation

Following hybridization of an array with one or more labeled target nucleic acid samples, arrays are scanned immediately using a GMS Scanner 418 and Scanalyzer software (Michael Eisen, Stanford University), followed by GeneSpring software (Silicon Genetics, CA) analysis. Alternatively, a GMS Scanner 428 and Jaguar software may be used followed by GeneSpring software analysis.

If one target nucleic acid sample is analyzed, the sample is labeled with one fluorescent dye (e.g., Cy3 or Cy5).

After hybridization to a microarray as described herein, fluorescence intensities at the associated nucleic acid members on the microarray are determined from images taken with a custom confocal microscope equipped with laser excitation sources and interference filters appropriate for the Cy3 or Cy5 fluors.

The presence of Cy3 or Cy5 fluorescent dye on the microarray indicates hybridization of a target nucleic acid and a specific nucleic acid member on the microarray. The intensity of Cy3 or Cy5 fluorescence represents the amount of target nucleic acid which is hybridized to the nucleic acid member on the microarray, and is indicative of the expression level of the specific nucleic acid member sequence in the target sample.

After hybridization, fluorescence intensities at the associated nucleic acid members on the microarray are determined from images taken with a custom confocal microscope equipped with laser excitation sources and interference filters appropriate for the Cy3 and Cy5 fluors. Separate scans are taken for each fluor at a resolution of $225\text{ }\mu\text{m}^2$ per pixel and 65,536 gray levels. Normalization between the images is used to adjust for the different efficiencies in labeling and detection with the two different fluors. This is achieved by manual matching of the detection sensitivities to bring a set of internal control genes to nearly equal intensity followed by computational calculation of the residual scalar required for optimal intensity matching for this set of genes.

The presence of Cy3 or Cy5 fluorescent dye on the microarray indicates hybridization of a target nucleic acid and a specific nucleic acid member on the microarray. The intensities

of Cy3 or Cy5 fluorescence represent the amount of target nucleic acid which is hybridized to the nucleic acid member on the microarray, and is indicative of the expression level of the specific nucleic acid member sequence in the target sample. If a nucleic acid member on the array shows no color, it indicates that the gene in that element is not expressed in either sample. If a nucleic acid member on the array shows a single color, it indicates that a labeled gene is expressed only in that cell sample. The appearance of both colors indicates that the gene is expressed in both tissue samples. The ratios of Cy3 and Cy5 fluorescence intensities, after normalization, are indicative of differences of expression levels of the associated nucleic acid member sequence in the two samples for comparison. A ratio of expression not equal to 10 is used as an indication of differential gene expression.

The array is scanned in the Cy 3 and Cy5 channels and stored as separate 16-bit TIFF images. The images are incorporated and analysed using Scanalyzer software which includes a gridding process to capture the hybridization intensity data from each spot on the array. The fluorescence intensity and background-subtracted hybridization intensity of each spot is collected and a ratio of measured mean intensities of Cy5 to Cy3 is calculated. A linear regression approach is used for normalization and assumes that a scatter plot of the measured Cy5 versus Cy3 intensities should have a slope of one. The average of the ratios is calculated and used to rescale the data and adjust the slope to one. A post-normalization cutoff of a ratio not equal to 1.0 is used to identify differentially expressed genes.

When comparing two or more samples for differences, results are reported as statistically significant when there is only a small probability that similar results would have been observed if the tested hypothesis (i.e., the genes are not expressed at different levels) were true. A small probability can be defined as the accepted threshold level at which the results being compared are considered significantly different. The accepted lower threshold is set at, but not limited to, 0.05 (i.e., there is a 5% likelihood that the results would be observed between two or more identical populations) such that any values determined by statistical means at or below this threshold are considered significant.

When comparing two or more samples for similarities, results are reported as statistically significant when there is only a small probability that similar results would have been observed if the tested hypothesis (i.e., the genes are not expressed at different levels)

were true. A small probability can be defined as the accepted threshold level at which the results being compared are considered significantly different. The accepted lower threshold is set at, but not limited to, 0.05 (i.e., there is a 5% likelihood that the results would be observed between two or more identical populations) such that any values determined by statistical means above this threshold are not considered significantly different and thus similar.

Identification of genes differentially expressed in blood samples from patients with disease as compared to healthy patients is determined by statistical analysis of the gene expression profiles from healthy patient compared to patients with a disease using the Wilcoxon Mann Whitney rank sum test.

Data Acquisition and Analysis of differentially expressed EST Sequences

The differentially expressed EST sequences are then searched against available databases, including the "nt", "nr", "est", "gss" and "htg" databases available through NCBI to determine putative identities for ESTs matching to known genes or other ESTs. Functional characterization of ESTs with known gene matches are made according to any known method. Preferably, differentially expressed EST sequences are compared to the non-redundant Genbank/EMBL/DDBJ and dbEST databases using the BLAST algorithm (Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. Basic local alignment search tool. J Mol Biol 1990;215:403-10). A minimum value of $P = 10^{-10}$ and nucleotide sequence identity >95%, where the sequence identity is non-contiguous or scattered, are required for assignments of putative identities for ESTs matching to known genes or to other ESTs. Construction of a non-redundant list of genes represented in the EST set is done with the help of Unigene, Entrez and PubMed at the National Center for Biotechnology Information (NCBI) web site at www.ncbi.nlm.nih.gov.

Genes are identified from ESTs according to known methods. To identify novel genes from an EST sequence, the EST should preferably be at least 100 nucleotides in length, and more preferably 150 nucleotides in length, for annotation. Preferably, the EST exhibits open reading frame characteristics (i.e., can encode a putative polypeptide).

Because of the completion of the Human Genome Project, a specific EST which matches with a genomic sequence can be mapped onto a specific chromosome based on the chromosomal location of the genomic sequence. However, no function may be known for the protein encoded by the sequence and the EST would then be considered "novel" in a functional sense. In one aspect, the invention is used to identify a novel differentially expressed EST, which is part of a larger known sequence for which no function is known, is used to determine the function of a gene comprising the EST. Alternatively, or additionally, the EST can be used to identify an mRNA or polypeptide encoded by the larger sequence as a diagnostic or prognostic marker of a disease.

10 Having identified an EST corresponding to a larger sequence, other portions of the larger sequence which comprises the EST can be used in assays to elucidate gene function, e.g., to isolate polypeptides encoded by the gene, to generate antibodies specifically reactive with these polypeptides, to identify binding partners of the polypeptides (receptors, ligands, agonists, antagonists and the like) and/or to detect the expression of the gene (or lack thereof) 15 in healthy or diseased individuals.

In another aspect, the invention provides for nucleic acid sequences that do not demonstrate a "significant match" to any of the publicly known sequences in sequence databases at the time a query is done. Longer genomic segments comprising these types of novel EST sequences can be identified by probing genomic libraries, while longer expressed 20 sequences can be identified in cDNA libraries and/or by performing polymerase extension reactions (e.g., RACE) using EST sequences to derive primer sequences as is known in the art. Longer fragments can be mapped to particular chromosomes by FISH and other techniques and their sequences compared to known sequences in genomic and/or expressed sequence databases.

25 The amino acid sequences encoded by the ESTs can also be used to search databases, such as GenBank, SWISS-PROT, EMBL database, PIR protein database, Vecbase, or GenPept for the amino acid sequences of the corresponding full-length genes according to procedures well known in the art.

Identified genes can be catalogued according to their putative function. Functional characterization of ESTs with known gene matches is preferably made according to the categories described by Hwang et al Compendium of Cardiovascular Genes. Circulation 1997;96:4146-203. The distribution of genes in each of the subcellular categories will provide
5 important insights into the disease process.

Alternative methods for analyzing ESTs are also available. For example, the ESTs may be assembled into contigs with sequence alignment, editing, and assembly programs such as PHRED and PHRAP (Ewing, et al., 1998, *Genome Res.* 3:175, incorporated herein; and the web site at bozeman.genome.washington.edu). Contig redundancy is reduced by clustering
10 nonoverlapping sequence contigs using the EST clone identification number, which is common for the nonoverlapping 5 and 3 sequence reads for a single EST cDNA clone. In one aspect, the consensus sequence from each cluster is compared to the non-redundant Genbank/EMBL/DDBJ and dbEST databases using the BLAST algorithm with the help of unigene, Entrez and PubMed at the NCBI site.

15 *Known Nucleic acid Sequences or ESTs and Novel Nucleic acid Sequences or ESTs*

An EST that exhibits a significant match (> 65%, and preferably 90% or greater, identity) to at least one existing sequence in an existing nucleic acid sequence database is characterized as a "known" sequence according to the invention. Within this category, some known ESTs match to existing sequences which encode polypeptides with known function(s)
20 and are referred to as a "known sequence with a function". Other "known" ESTs exhibit a significant match to existing sequences which encode polypeptides of unknown function(s) and are referred to as a "known sequence with no known function".

EST sequences which have no significant match (less than 65% identity) to any existing sequence in the above cited available databases are categorized as novel ESTs. To
25 identify a novel gene from an EST sequence, the EST is preferably at least 150 nucleotides in length. More preferably, the EST encodes at least part of an open reading frame, that is, a nucleic acid sequence between a translation initiation codon and a termination codon, which is potentially translated into a polypeptide sequence.

The following references were cited herein:

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Description of Tables:

Table 1: Overlap of Genes Expressed in Blood

(Estimated from limited known genes of about 1,800 as derived from the database of 6,297 ESTs from human blood cell library).

Table 2: Comparison of 1,800 Unique Genes Identified in the Blood Cell cDNA

Library to Genes Previously Identified in Specific Tissues

Column 1: List of unique genes derived from 6,283 known ESTs from blood cells. Column 2: Number of genes found in randomly sequenced ESTs from blood cells. Column 3: Accession number. Column 4: "+" indicates the presence of the unique gene in publicly available cDNA libraries of blood (Bl), brain (Br), heart (H), kidney (K), liver (Li) and lung (Lu).

**Comparison to previously identified tissue-specific genes was determined using the GenBank of the National Centre of Biotechnology Information (NCBI) Database.

Table 3: Genes that are differentially expressed in blood samples from patients with different diseases as compared to blood samples from healthy patients.

Table 3A shows the identity of those genes that are differentially expressed in blood samples from patients with osteoarthritis and hypertension as depicted in Figure 8

Table 3B shows the identity of those genes that are differentially expressed in blood samples from patients with osteoarthritis and obesity as depicted in Figure 9.

Table 3C shows the identity of those genes that are differentially expressed in blood samples from patients with osteoarthritis and allergies as depicted in Figure 10.

Table 3D shows the identity of those genes that are differentially expressed in blood samples from patients with osteoarthritis and subject to systemic steroids as depicted in Figure 11.

Table 3E shows the identity of those genes that are differentially expressed in blood samples from patients with hypertension as depicted in Figure 12.

Table 3F shows the identity of those genes that are differentially expressed in blood samples from patients obesity as depicted in Figure 13.

- 5 Table 3G shows the identity of those genes that are differentially expressed in blood samples from patients with type II diabetes as depicted in Figure 14.

Table 3H shows the identity of those genes that are differentially expressed in blood samples from patients with hyperlipidemia as depicted in Figure 15.

- 10 Table 3I shows the identity of those genes that are differentially expressed in blood samples from patients with lung disease as depicted in Figure 16.

Table 3J shows the identity of those genes that are differentially expressed in blood samples from patients with bladder cancer as depicted in Figure 17.

Table 3K shows the identity of those genes that are differentially expressed in blood samples from patients with bladder cancer as depicted in Figure 18.

- 15 Table 3L shows the identity of those genes that are differentially expressed in blood samples from patients with coronary artery disease (CAD) as depicted in Figure 19.

Table 3M shows the identity of those genes that are differentially expressed in blood samples from patients with rheumatoid arthritis as depicted in Figure 20.

- 20 Table 3N shows the identity of those genes that are differentially expressed in blood samples from patients with depression as depicted in Figure 21.

Table 3O shows the identity of those genes that are differentially expressed in blood samples from patients with various stages of osteoarthritis as depicted in Figure 22.

Table 4 shows 102 EST sequences of Tables 3A-3O with "no-significant match" to known gene sequences.

Table 5 shows a list of genes showing greater than two fold differential expression in CAD peripheral blood cells vs normal blood cells.

The following examples are given for the purpose of illustrating various
5 embodiments of the invention and are not meant to limit the present invention in any fashion.

EXAMPLE 1

Construction of a cDNA library

10 RNA extracted from human tissues (including fetal heart, adult heart, liver, brain, prostate gland and whole blood) were used to construct unidirectional cDNA libraries. The first mammalian heart cDNA library was constructed as early as 1982. Since then, the methodology has been revised and optimal conditions have been developed for construction of human heart and hematopoietic progenitor cDNA libraries (Liew *et al.*, 1984; Liew 1993,
15 Claudio *et al.*, 1998). Most of the novel genes which were identified by sequence annotation can now be obtained as full length transcripts.

EXAMPLE 2

Catalogue of EST database

20 Random partial sequencing of expressed sequence tags (ESTs) of cDNA clones from the blood cell library was carried out to establish an EST database of blood. The known genes as derived from the ESTs were categorized into seven major cellular functions (Hwang, Dempsey *et al.*, 1997). The preparation of the chondrocyte-specific EST database is reported in WO 02/070737, which is hereby incorporated by reference in its entirety.

EXAMPLE 3

Differential screening of cDNA library

cDNA probes generated from transcripts of each tissue were used to hybridize the blood cell cDNA clones or chondrocyte cDNA clones (Liew *et al.*, 1997; WO 02/070737). The “positive” signals which were hybridized with P-labelled cDNA probes were defined as genes which shared identity with blood and respective tissues. The “negative” spots which were not exposed to P-labelled cDNA probes were considered to be blood-cell-enriched or low frequency transcripts.

EXAMPLE 4

Reverse transcriptase-polymerase chain reaction (RT-PCR) assay

RNA extracted from samples of human tissue was used for RT-PCR analysis (Jin *et al.* 1990). Three pairs of forward and reverse primers were designed for human cardiac beta-myosin heavy chain gene ((MyHC), amyloid precursor protein (APP) gene and adenomatous polyposis-coli protein (APC) gene. The PCR products were also subjected to automated DNA sequencing to verify the sequences as derived from the specific transcripts of blood.

EXAMPLE 5

Detection of tissue specific gene expression in human blood using RT-PCR

The beta-myosin heavy chain gene ((MyHC) transcript (mRNA) is known to be highly expressed in ventricles of the human heart. This sarcomeric protein is important for heart muscle contraction and its presence would not be expected in other non-muscle tissues and blood. In 1990, the gene for human cardiac (MyHC) was completely sequenced (Liew *et al.* 1990) and was comprised of 41 exons and 42 introns.

The method of reverse transcription polymerase chain reaction (RT-PCR) was used to determine whether this cardiac specific mRNA is also present in human blood. A pair of primers was designed; the forward primer (SEQ ID No. 3) was on the boundary of exons 21

and 22, and the reverse primer (SEQ ID No. 4) was on the boundary of exons 24 and 25. This region of mRNA is only present in (MyHC and is not found in the alpha-myosin heavy chain gene ((MyHC).

A blood sample was first treated with lysing buffer and then undergone centrifuge.
5 The resulting pellets were further processed with RT-PCR. RT-PCR was performed using the total blood cell RNA as a template. A nested PCR product was generated and used for sequencing. The sequencing results were subjected to BLAST and the identity of exons 21 to 25 was confirmed to be from (MyHC (Figure 1A).

Using the same method just described, two other tissue specific genes - amyloid
10 precursor protein (APP, forward primer, SEQ ID No. 7; reverse primer, SEQ ID No. 8) found in the brain and associated with Alzheimer's disease, and adenomatous polyposis coli protein (APC) found in the colon and rectum and associated with colorectal cancer (Grodén *et al.* 1991; Santoro and Grodén 1997) - were also detected in the RNA extracted from human blood (Figure 1B).

15

EXAMPLE 6

Multiple RT-PCR analysis on a drop of blood from a normal/diseased individual

A drop of blood was extracted to obtain RNA to carry out quantitative RT-PCR analysis. Specific primers for the insulin gene were designed: forward primer (5'-
20 GCCCTCTGGGGACCTGAC-3', SEQ ID No. 1) of exon 1 and reverse primer (5'-CCCACCTGCAGGTCCTCT-3'', SEQ ID No. 2) of exons 1 and 2 of insulin gene. Such reverse primer was obtained by deleting the intron between the exons 1 and 2. Blood samples of 4 normal subjects were assayed. It was found that the insulin gene is expressed in the blood and the quantitative expression of the insulin gene in a drop of blood is
25 influenced by fasting and non-fasting states of normal healthy subjects (Figure 2). This very low level of expression of the insulin gene reflects the phenotypic status of a person and strongly suggests that there is a physiological and pathological role for its expression, contrary to the basal or illegitimate theory of transcription suggested by Chelly *et al.* (1989) and Kimoto (1998).

Same quantitative RT-PCR analysis was performed using insulin specific primers on RNA samples extracted from a drop of blood from a normal healthy person, a person having late-onset diabetes (Type II) and a person having asymptomatic diabetes. It was found that the insulin gene is expressed differentially amongst subjects that are healthy, diagnosed as type II diabetic, and also in an asymptomatic preclinical patient (Figure 3).

Similarly, specific primers for the atrial natriuretic factor (ANF) gene were designed (forward primer, SEQ ID No. 5; reverse primer, SEQ ID No. 6) and RT-PCR analysis was performed on a drop of blood. ANF is known to be highly expressed in heart tissue biopsies and in the plasma of heart failure patients. However, atrial natriuretic factor was observed to be expressed in the blood and the expression of the atrial natriuretic factor gene is significantly higher in the blood of patients with heart failure as compared to the blood of a normal control patient.

Specific primers for the zinc finger protein gene (ZFP, forward primer, SEQ ID No. 9; reverse primer, SEQ ID No. 10) were also designed and RT-PCR analysis was performed on a drop of blood. ZFP is known to be high in heart tissue biopsies of cardiac hypertrophy and heart failure patients. In the present study, the expression of ZFP was observed in the blood as well as differential expression levels of ZFP amongst the normal, diabetic and asymptomatic preclinical subjects (Figure 4); although neither of the non-normal subjects has been specifically diagnosed as suffering from cardiac hypertrophy and/or heart failure, the higher expression levels of the ZFP gene in their blood may indicate that these subjects are headed in that general direction.

It was hypothesized that a housekeeping gene such as glyceraldehyde dehydrogenase (GADH) which is required and highly expressed in all cells would not be differentially expressed in the blood of normal vs. disease subjects. This hypothesis was confirmed by RT-PCR using GADH specific primers (Figure 4). Thus, GADH is useful as an internal control.

Standardized levels of insulin gene or ZFP gene expressed in a drop of blood were estimated using a housekeeping gene as an internal control relative to insulin or ZFP

expressed (Figures 5A & 5B). The levels of insulin gene expressed in each fractionated cell from whole blood were also standardized and shown in Figure 5C.

EXAMPLE 7

Human blood cell cDNA library

5 In order to further substantiate the present invention, differential screening of the human blood cell cDNA library was conducted. cDNA probes derived from human blood, adult heart or brain were respectively hybridized to the human blood cDNA library clones. As shown in Figure 7, more than 95% of the "positively" identified clones are identical between the blood and other tissue samples.

10 DNA sequencing of randomly selected clones from the human whole blood cell cDNA library was also performed. This allowed information regarding the cellular function of blood to be obtained concurrently with gene identification. More than 20,000 expressed sequence tags (ESTs) have been generated and characterized to date, 17.6% of which did not result in a statistically significant match to entries in the GenBank databases and thus
15 were designated as "Novel" ESTs. These results are summarized in Figure 7 together with the seven cellular functions related to percent distribution of known genes in blood and in the fetal heart.

From 20,000 ESTs, 1,800 have been identified as known genes which may not all appear in the hemapoietic system. For example, the insulin gene and the atrial natriuretic
20 factor gene have not been detected in these 20,000 ESTs but their transcripts were detected in a drop of blood, strongly suggesting that all transcripts of the human genome can be detected by performing RT-PCR analysis on a drop of blood.

In addition, approximately 400 novel genes have been identified from the 20,000 ESTs characterized to date, and these will be subjected to full length sequencing and open
25 reading frame alignment to reduce the actual number of novel ESTs prior to screening for disease markers.

Analysis of the approximately 6,283 ESTs which have known matches in the GenBank databases revealed that this dataset represents over 1,800 unique genes. These genes have been catalogued into seven cellular functions. Comparisons of this set of unique genes with ESTs derived from human brain, heart, lung and kidney demonstrated a greater
5 than 50% overlap in expression (Table 1).

TABLE 1

Overlap of Genes Expressed in Blood *

	Tissues	ESTs**	Overlap in Blood
	brain	134,000	60%
10	heart	65,000	59%
	lung	60,200	58%
	kidney	32,300	54%

* Estimated from limited known genes of about 1,800 as derived from the database of 6,297 ESTs from human blood cell library.

15 ** Obtained from the National Centre of Biotechnology Information (NCBI), U.S.A.

EXAMPLE 8

Blood cell ESTs

20 The results from the differential screening clearly indicate that the transcripts expressed in the whole blood are reflective of genes expressed in all cells and tissues of the body. More than 95% of detectable spots were identical from two different tissues. The remaining 5% of spots may represent cell- or tissue-specific transcripts; however, results obtained from partial sequencing to generate ESTs of these clones revealed most of them
25 not to be cell- or tissue-specific transcripts. Therefore, the negative spots are postulated to

be reflective of low abundance transcripts in the tissue from which the cDNA probes were derived.

An alternative approach that was employed to identify transcripts expressed at low levels is the large-scale generation of expressed sequence tags (ESTs). There is substantial evidence regarding the efficiency of this technology to detect previously characterized (known) and uncharacterized (unknown or novel) genes expressed in the cardiovascular system (Hwang & Dempsey *et al.*, 1997). In the present invention, 20,000 ESTs have been produced from a human blood cell cDNA library and resulted in the identification of approximately 1,800 unique known genes (Table 2)

In the most recent GenBank release, analysis of more than 300,000 ESTs in the database (dbESTs) generated more than 48,000 gene clusters which are thought to represent approximately 50% of the genes in the human genome. Only 4,800 of the dbESTs are blood-derived. In the present invention, 20,000 ESTs have been obtained to date from a human blood cDNA library, which provides the world's most informative database with respect to blood cell transcripts. From the limited amount of information generated so far (i.e. 1,800 unique genes), it has already been determined that more than 50% of the transcripts are found in other cells or tissues of the human body (Table 2). Thus, it is expected that by increasing the number of ESTs generated, more genes will be identified that have an overlap in expression between the blood and other tissues. Furthermore, the transcripts for several genes which are known to have tissue-restricted patterns of expression (i.e. (MyHC, APP, APC, ANF, ZFP) have also been demonstrated to be present in blood.

Most recently, a cDNA library of human hematopoietic progenitor stem cells has also been constructed. From the limited set of 1,000 ESTs, there are at least 200 known genes that are shared with other tissue related genes (Claudio *et al.* 1998).

Table 2 demonstrates the expression of known genes of specific tissues in blood cells. Previously, only the presence of "housekeeping" genes would have been expected. Additionally, the presence of at least 25 of the currently known 500 genes corresponding to molecular drug targets was detected. These molecular drug targets are used in the treatment

of a variety of diseases which involve inflammation, renal and cardiovascular function, neoplastic disease, immunomodulation and viral infection (Drews & Ryser, 1997). It is expected that additional novel ESTs will represent future molecular drug targets.

5

EXAMPLE 9

Blood cDNA chip Microarray Data Analysis of gene expression profiles of blood samples from individuals having coronary artery disease as compared with gene expression profiles from normal individuals

A microarray was constructed using cDNA clones from a human peripheral blood cell cDNA library, as described herein. A total of 10,368 polymerase chain reaction (PCR) products of the clones from the human peripheral blood cell cDNA library were arrayed using GNS 417 arrayer (Affymetrix). RNA for microarray analysis was isolated from whole blood samples obtained from three male and one female patients with coronary heart disease (80 – 90% stenosis) receiving vascular extension drugs and awaiting bypass surgery, and three healthy male controls.

A method of high-fidelity mRNA amplification from 1 pg of total RNA sample was used. Cy5- or Cy3-dUTP was incorporated into cDNA probes by reverse transcription of anti-sense RNA, primed by oligo-dT. Labeled probes were purified and concentrated to the desired volume. Pre- hybridization and hybridization were performed following Hegde's protocol (Hegde P et al. A concise guide to cDNA microarray analysis. Biotechniques 2000;29: 548 – 56). After overnight hybridization and washing, hybridization signals were detected with a GMS 418 scanner at 635-nm (Cy5) and 532-nm (Cy3) wave lengths (see Figure 24). Two RNA pools were labeled alternatively with Cy5- and Cy3-dUTP, and each experiment was repeated twice. Cluster analysis using GeneSpring 4.1.5 (Silicon Genetics) revealed two distinct groups consisting of four CAD and three normal control samples. Two images scanned at different wavelengths were super- imposed. Individual spots were identified on a customized grid. Of 10,368 spots, 10,012 (96.6%) were selected after the removal of spots with irregular shapes. Data quality was assessed with values of ChlGTB2 and Ch2GTB2 provided by ScanAlyze. Only spots with ChlGTB2 and Ch2GTB2 over 0.50

were selected. After evaluation of signal intensities, 8750 (84.4%) spots were left. Signal intensities were normalized using a scatter-plot of the signal intensities of the two channels. After normalization, the expression ratios of β -actin were 1.00 ± 0.21 , 1.11 ± 0.22 , 1.14 ± 0.20 and 1.30 ± 0.18 (24 samples of β -actin were spotted on this slide as the positive control) in the four images. Gene differential expression was assessed as the ratio of two wave-length signal intensities. Spots showing a differential expression more than twofold in all four experiments were identified as peripheral blood cell, differentially expressed candidate genes in CAD. 108 genes are differentially expressed in CAD peripheral blood cells, 43 genes are downregulated in CAD blood cells and 65 are upregulated (see Table 5).

Functional characterization of these genes shows that differential expression takes place in every gene functional category, indicating that profound changes occur in CAD blood cells.

The differential expression of three genes, pro-platelet basic protein (PBP), platelet factor 4 (PF4) and coagulation factor XIII A1 (F13A), initially identified in the microarray data analysis, was further examined by reverse transcriptase-PCR (RT-PCR) using the Titan One-tube RT-PCR kit (Boehringer Mannheim). Reaction solution contains 0.2 mM each dNTP, 5 mM DTT, 1.5 mM MgCl₂ 0.1 μ g of total RNA from each sample and 20 pmol each of left and right primers of PBP (5'-GGTGCTGCTGCTTCTGTCAT-3' and 5'-GGCAGATTTT CCTCCCATCC-3'), F13A (5'-AGTCCACCGTGCTAACCATC-3' and 5'-AGGGAGTCACTGCTCATGCT-3') and PF4 (5' GTTGCTGCTCCTGCCACTT 3' and 5' GTGGCTATCAGTTGGGCAGT-3'). RT-PCR steps are as follows: 1. reverse-transcription: 30 min at 60 °C; 2. PCR: 2 min at 94 °C, followed by 30 – 35 cycles (as optimized for each gene) for 30 s at 94 °C, 30 s at optimized annealing temperature and 2 min at 68 °C; 3. final extension: 7 min at 68 °C. PCR products were electrophoresed on 1.5% agarose gels. Human (β -actin primers (5'-GCGAGAAGATGACCCAGATCAT-3' and 5'-GCTCAGGAGGAGCAATGATCTT-3') were used as the internal control. The RT-PCR analysis confirmed that the expression of the three secreted proteins: PBP, PF4 and F13A were all upregulated in CAD blood cells (see Figure 23).

TABLE 5

	Accession number	Fold (average)	Functional category	Protein Accession Number
<i>Upregulated gene in CAD</i>				
REV3-like, catalytic subunit of DNA polymerase zeta	AF035537	2.3	Cell cycle	NP_002903
TGFB1-induced anti-apoptotic factor 1	D86970	2.2	Cell cycle	NP_510880
A disintegrin and metalloproteinase domain 10	AA044656	2.7	Cell signaling	NP_001101
Centaurin, delta 2	AA351412	2	Cell signaling	NP_631920
Chloride intracellular channel 4	AA411940	2.2	Cell signaling	NP_039234
Endothelin receptor typeA	D90348	2.1	Cell signaling	NP_001948
Glutamate receptor, ionotropic	N33821	2.4	Cell signaling	NP_777567
Mitogen-activated protein kinase 7	L38486	3.7	Cell signaling	NP_002395
Mitogen-activated protein kinase kinase kinase 7	AB009356	4.5	Cell signaling	NP_663306
Myristoylated alanine-rich protein kinase C substrate	D10522	2.5	Cell signaling	NP_002347
NIMA-related kinase 7	AA093324	3.5	Cell signaling	NP_598001
PAK2	AA262968	3.5	Cell signaling	Q13177
Phospholipid scramblase 1	AA054476	3.3	Cell signaling	NP_066928
Serum deprivation response	Z30112	4.5	Cell signaling	NP_004648
Adducin 3	AA029158	2.9	Cell structure	NP_063968
Desmin	AF167579	4.4	Cell structure	NP_001918
Fibromodulin	W23613	2.9	Cell structure	NP_002014
Laminin, beta 2	S77512	2.2	Cell structure	NP_002283
Laminin, beta 3	L25541	2.4	Cell structure	NP_000219
Osteonectin	Y00755	3.1	Cell structure	NP_003109
CD59 antigen p18-20	W01111	2.4	Cell/organism defense	NP_000602
Clusterin	M64722	3.5	Cell/organism defense	NP_001822
F13A	M14539	2.1	Cell/organism defense	NP_000120

Defensin, alpha 1	M26602	4.2	Cell/organism defense	NP_004075
PF4	M25897	2.1	Cell/organism defense	NP_002610
PBP	M54995	5.5	Cell/organism defense	NP_002695
E2F transcription factor 3	D38550	2.1	Gene expression	NP_001940
Early growth response 1	M62829	2.7	Gene expression	NP_001955
Eukaryotic translation elongation factor 1 alpha 1	N86030	2.3	Gene expression	NP_001393
Eukaryotic translation initiation factor 4E	M15353	2.1	Gene expression	NP_001959
F-box and WD-40 domain protein 1B	AB014596	2.7	Gene expression	NP_387449
1 Makorin, ring finger protein, 2	AA331966	2.1	Gene expression	NP_054879
Non-canonical ubiquitin-conjugating enzyme 1	N92776	2.5	Gene expression	NP_057420
Nuclear receptor subfamily 1, group I, member 3	Z30425	4.7	Gene expression	NP_005113
Ring finger protein 11	T08927	3	Gene expression	NP_055187
Transducin-like enhancer of split 1	M99435	3.3	Gene expression	NP_005068
Alkaline phosphatase, liver/bone/kidney	AB011406	2.2	Metabolism	NP_000469
Annexin A3	M63310	3.4	Metabolism	NP_005130
Branched chain aminotransferase 1, cytosolic	AA336265	4.8	Metabolism	NP_005495.1
Cytochrome b	AF042500	2.5	Metabolism	
Glutaminase	D30931	2.6	Metabolism	NP_055720
Lysophospholipase I	AF035293	2.8	Metabolism	NP_006321
NADH dehydrogenase 1, subcomplex unknown 1, 6 kDa	AA056111	2.5	Metabolism	NP_002485
Phosphofructokinase	M26066	2.2	Metabolism	NP_000280
Ubiquinol-cytochrome c reductase binding protein	M22348	2.5	Metabolism	NP_006285
CGI-110 protein	AA341061	2.4	Unclassified	NP_057131
Dactylidin	H95397	2.7	Unclassified	NP_112225
Deleted in split-hand/split-foot 1 region	T24503	2.4	Unclassified	NP_006295
Follistatin-like 1	R14219	2.7	Unclassified	NP_009016
FUS-interacting protein 1	W37945	2.8	Unclassified	NP_473357
Hypothetical protein FLJ12619	W47233	7	Unclassified	NP_112201

Hypothetical protein from EUROIMAGE 588495	N68247	2.7	Unclassified	
Hypothetical protein LOC51315	AA251423	2.2	Unclassified	NP_057702
KIAA1705 protein	T80569	2.7	Unclassified	NP_009121.1
Mesoderm induction early response 1	AI650409	2.2	Unclassified	NP_065999
Phosphodiesterase 4D-interacting protein	AA740661	2.5	Unclassified	NP_055459
Preimplantation protein 3	D59087	2.5	Unclassified	NP_056202
Putative nuclear protein ORF1-FL49	W33098	2.8	Unclassified	NP_115788
Similar to rat nuclear ubiquitous casein kinase 2	H09434	2.2	Unclassified	Q9H1E3
Similar to RIKEN	AA297412	2.5	Unclassified	T02670
Spectrin, beta	AI334431	2.5	Unclassified	Q01082
Stromal cell-derived factor receptor 1	H71558	4.1	Unclassified	NP_816929
Thioredoxin-related protein	AA421549	2.8	Unclassified	NP_110437
Transmembrane 4 superfamily member 2	D29808	2.4	Unclassified	NP_004606
Tumor endothelial marker 8	D79964	2.5	Unclassified	NP_444262
<i>Downregulated gene in CAD</i>				
CASP8 and FADD-like apoptosis regulator	AF015450	0.45	Cell cycle	NP_003870
CD81 antigen	M33680	0.41	Cell cycle	NP_004347
Cell division cycle 25B	M81934	0.4	Cell cycle	NP_068660
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 27	AA985699	0.42	Cell cycle	NP_694705
F-box and leucine-rich repeat protein 11	R98291	0.27	Cell cycle	NP_036440
Minichromosome maintenance deficient 3 associated protein	H10286	0.43	Cell cycle	NP_003897
Protein phosphatase 2, regulatory subunit A, alpha isoform	J02902	0.48	Cell cycle	NP_055040
Thyroid autoantigen 70 kDa	J04607	0.25	Cell cycle	NP_001460
A disintegrin and metalloproteinase domain 17	R32760	0.37	Cell signaling	
A kinase anchor protein 13	M90360	0.31	Cell signaling	NP_658913
Calpastatin	AF037194	0.39	Cell signaling	NP_006471

Diacylglycerol kinase, alpha 80 kDa	AF064770	0.44	Cell signaling	NP_001336
gamma-aminobutyric acid B receptor, 1	AJ012187	0.42	Cell signaling	NP_068705
Inositol polyphosphate-5-phosphatase, 145 kDa	U84400	0.41	Cell signaling	NP_005532
Lymphocyte-specific protein tyrosine kinase	X05027	0.45	Cell signaling	NP_005347
RAP1B, member of RAS oncogene family	P09526	0.4	Cell signaling	P09526
Ras association (RalGDS/AF-6) domain family 1	AF061836	0.43	Cell signaling	NP_733835
CDC42-effector protein 3	AF104857	0.28	Cell signaling	NP_006440
Leupaxin	AF062075	0.31	Cell signaling	NP_004802
Annexin A6	D00510	0.45	Cell structure	NP_004024
RAN-binding protein 9	AB008515	0.41	Cell structure	NP_005484
Thymosin, beta 10	M20259	0.26	Cell structure	NP_066926
GranzymeA	M18737	0.17	Cell/organism defense	NP_006135
ThromboxaneA synthase 1	M80646	0.44	Cell/organism defense	NP_112246
Coatamer protein complex, subunit beta	AA357332	0.39	Gene expression	NP_057535
Cold-inducible RNA-binding protein	H39820	0.27	Gene expression	NP_001271
Leucine-rich repeat interacting protein 1	U69609	0.44	Gene expression	NP_004726
Proteasome subunit, alpha type, 3	D00762	0.31	Gene expression	NP_687033
Proteasome subunit, alpha type, 7	AF022815	0.35	Gene expression	NP_689468
Protein phosphatase 1G, gamma isoform	AI417405	0.5	Gene expression	NP_817092
Ribonuclease/angiogenin inhibitor	M36717	0.44	Gene expression	NP_002930
RNA-binding protein-regulatory subunit	AF021819	0.3	Gene expression	NP_009193
Signal transducer and activator of transcription 6	U16031	0.45	Gene expression	NP_003144
Transcription factor A, mitochondrial	M62810	0.41	Gene expression	NP_036383
Ubiquitin-specific protease 4	AF017306	0.31	Gene expression	NP_003354
Dehydrogenase/reductase SDR family member 1	AA100046	0.46	Metabolism	NP_612461
Solute carrier family 25, member 6	J03592	0.3	Metabolism	NP_001627
Amplified in osteosarcoma	U41635	0.45	Unclassified	NP_006803

Expressed in activated T/LAK lymphocytes	C00577	0.45	Unclassified	NP_009198
Integral inner nuclear membrane protein	W00460	0.4	Unclassified	NP_055134
Phosphodiesterase 4D-interacting protein	T95969	0.45	Unclassified	NP_055459
Tumor endothelial marker 7 precursor	N93789	0.45	Unclassified	NP_065138
Wiskott-Aldrich syndrome protein interacting protein	AF031588	0.22	Unclassified	NP_003378

EXAMPLE 10

ChondroChip Microarray Data Analysis of gene expression profiles of blood samples from individuals having osteoarthritis and hypertension as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with osteoarthritis and hypertension on as compared to blood samples taken from healthy patients.

As used herein, the term "hypertension" is defined as high blood pressure or elevated arterial pressure. Patients identified with hypertension herein include persons who have an increased risk of developing a morbid cardiovascular event and/or persons who benefit from medical therapy designed to treat hypertension. Patients identified with hypertension also can include persons having systolic blood pressure of >130 mm Hg or a diastolic blood pressure of >90 mm Hg or a person takes antihypertensive medication.

Osteoarthritis (OA), as used herein also known as "degenerative joint disease", represents failure of a diarthrodial (movable, synovial-lined) joint. It is a condition, which affects joint cartilage, and or subsequently underlying bone and supporting tissues leading to pain, stiffness, movement problems and activity limitations. It most often affects the hip, knee, foot, and hand, but can affect other joints as well.

OA severity can be graded according to the system described by Marshall (Marshall KW. J Rheumatol, 1996:23(4) 582-85). Briefly, each of the six knee articular surfaces was assigned a cartilage grade with points based on the worst lesion seen on each particular

surface. Grade 0 is normal (0 points), Grade I cartilage is soft or swollen but the articular surface is intact (1 point). In Grade II lesions, the cartilage surface is not intact but the lesion does not extend down to subchondral bone (2 points). Grade III damage extends to subchondral bone but the bone is neither eroded nor eburnated (3 points). In Grade IV lesions, there is eburnation of or erosion into bone (4 points). A global OA score is calculated by summing the points from all six cartilage surfaces. If there is any associated pathology, such as meniscus tear, an extra point will be added to the global score. Based on the total score, each patient is then categorized into one of four OA groups: mild (1-6), moderate (7-12), marked (13-18), and severe (>18). As used herein, patients identified with OA may be categorized in any of the four OA groupings as described above.

Blood samples were taken from patients who were diagnosed with osteoarthritis and hypertension as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of osteoarthritis and hypertension was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a 15K ChondroGene Microarray Chip (Chondrochip) as described herein. Identification of genes differentially expressed in blood samples from patients with disease as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 8 shows a diagrammatic representation of gene expression profiles of blood samples from individuals having hypertension as compared with gene expression profiles from normal individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. In this example, hypertensive patients also presented with OA, as described herein. Normal individuals have no known medical conditions and were not taking any known medication. Hybridizations to create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are

clustered and marked as representing patients who are hypertensive or normal. The “*” indicates those patients who abnormally clustered as either hypertensive, or normal despite presenting with the reverse. The number of hybridizations profiles determined for either hypertensive patients or normal individuals are shown. 861 differentially expressed genes were identified as being differentially expressed with a p value of < 0.05 as between the hypertensive patients and normal individuals. The identity of the differentially expressed genes is shown in Table 3A.

EXAMPLE 11

ChondroChip Microarray Data Analysis of gene expression profiles of blood samples from individuals having osteoarthritis and obesity as compared with gene expression profiles from normal individuals.

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with obesity as compared to blood samples taken from healthy patients.

As used herein, “obesity” is defined as an excess of adipose tissue that imparts a health risk. Obesity is assessed in terms of height and weight in the relevance of age. Patients who are considered obese include, but are not limited to, patients having a body mass index or BMI ((defined as body weight in kg divided by (height in meters)²) greater than or equal to 30.0. Patients having obesity as defined herein are those with a BMI of greater than or equal to 30.0.

Blood samples were taken from patients who were diagnosed with osteoarthritis and obesity as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of the disease was corroborated by a skilled Board certified physician. Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a 15K ChondroGene Microarray Chip (ChondroChip) as described herein. Identification of genes differentially expressed in blood samples from patients with disease as compared to healthy patients was determined by statistical analysis

using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 9 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as obese as described herein as compared with gene expression profiles from normal individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. In this example, obese patients also presented with OA, as described herein. Normal individuals have no known medical conditions and were not taking any known medication. Hybridizations to create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who are obese or normal. The "*" indicates those patients who abnormally clustered as either obese or normal despite presenting with the reverse. The number of hybridization profiles determined for obese patients and normal individuals are shown. 913 genes were identified as being differentially expressed with a p value of < 0.05 as between the obese patients and normal individuals is noted. The identity of the differentially expressed genes is shown in Table 3B.

EXAMPLE 12

ChondroChip Microarray Data Analysis of gene expression profiles of blood samples from individuals having osteoarthritis and allergies as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with allergies as compared to blood samples taken from healthy patients.

As used herein, "allergies" encompasses diseases and conditions wherein a patient demonstrates a hypersensitive or allergic reaction to one or more substances or stimuli such as drugs, food stuffs, plants, animals etc. and as a result has an increased immune response. Such immune responses can include anaphylaxis, allergic rhinitis, asthma, skin sensitivity such as urticaria, eczema, and allergic contact dermatitis and ocular allergies such as allergic

conjunctivitis and contact allergy. Patients identified as having allergies includes patients having one or more of the above noted conditions.

Blood samples were taken from patients who were diagnosed with osteoarthritis and allergies as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of osteoarthritis and allergies was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a 15K ChondroGene Microarray Chip (Chondrochip) as described herein. Identification of genes differentially expressed in blood samples from patients with osteoarthritis and allergies as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 10 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having allergies as described herein as compared with gene expression profiles from normal individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. In this example, patients with allergies also presented with OA, as described herein. Normal individuals have no known medical conditions and were not taking any known medication. Hybridizations to create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who are obese or normal. The “*” indicates those patients who abnormally clustered as either having allergies or being normal despite presenting with the reverse. The number of hybridizations profiles determined for patients with allergies and normal individuals are shown. 633 genes were identified as being differentially expressed with a p value of < 0.05 as between patients with allergies and normal individuals is noted. The identity of the differentially expressed genes is shown in Table 3C.

EXAMPLE 13

ChondroChip Microarray Data Analysis of gene expression profiles of blood samples from individuals having osteoarthritis and subject to systemic steroids as compared with gene
5 expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients subject to systemic steroids as compared to blood samples taken from healthy patients.

As used herein, "systemic steroids" indicates a person subjected to artificial levels of
10 steroids as a result of medical intervention. Such systemic steroids include birth control pills, prednisone, and hormones as a result of hormone replacement treatment. A person identified as having systemic steroids is one who is on one or more of the following treatment regimes.

Blood samples were taken from patients who were diagnosed with osteoarthritis and subject to systemic steroids as defined herein. Gene expression profiles were then analyzed
15 and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of osteoarthritis and systemic steroids was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood
20 sample were generated as described above. Each probe was denatured and hybridized to the 15K ChondroGene Microarray Chip (Chondrochip) as described herein. Identification of genes differentially expressed in blood samples from patients with osteoarthritis and subject to systemic steroids as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed.
25 New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 11 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were subject to systemic steroids as described herein as

compared with gene expression profiles from normal individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. In this example, patients taking systemic steroids also presented with OA, as described herein. Normal individuals have no known medical conditions and were not taking any known medication. Hybridizations to create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who are taking systemic steroids or normal. The "*" indicates those patients who abnormally clustered as either systemic steroids or normal despite presenting with the reverse. The number of hybridizations profiles determined for patients with systemic steroids and normal individuals are shown. 605 genes were identified as being differentially expressed with a p value of < 0.05 as between patients with systemic steroids and normal individuals is noted. The identity of the differentially expressed genes is shown in Table 3D.

EXAMPLE 14

ChondroChip Microarray Data Analysis of gene expression profiles of blood samples from individuals having hypertension as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with hypertension but without osteoarthritis as compared to blood samples taken from healthy patients.

As used herein, the term "hypertension" is defined as high blood pressure or elevated arterial pressure. Patients identified with hypertension herein include persons who have an increased risk of developing a morbid cardiovascular event and/or persons who benefit from medical therapy designed to treat hypertension. Patients identified with hypertension also can include persons having systolic blood pressure of >130 mm Hg or a diastolic blood pressure of >90 mm Hg or a person takes antihypertensive medication.

Blood samples were taken from patients who were diagnosed with hypertension as defined herein. Gene expression profiles were then analyzed and compared to profiles from

patients unaffected by any disease. In each case, the diagnosis of hypertension was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a 15K ChondroGene Microarray Chip (ChondroChip) as described herein. Identification of genes differentially expressed in blood samples from patients with hypertension as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Giantz SA, Primer of Biostatistics, 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 12 shows a diagrammatic representation of gene expression profiles of blood samples from individuals having hypertension as compared with gene expression profiles from samples of both non-hypertensive and normal individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Non-hypertensive individuals presented without hypertension, but may have presented with other medical conditions and may be under various treatment regimes. Normal individuals have no known medical conditions and were not taking any known medication. Hybridizations to create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who are hypertensive, normal or non-hypertensive. The “*” indicates those patients who abnormally clustered as either hypertensive, non-hypertensive or normal despite actual presentation. The number of hybridizations profiles determined for hypertensive patients, non-hypertensive patients and normal individuals are shown. 1,993 genes identified as being differentially expressed with a p value of < 0.05 as between the hypertensive patients and the combined normal and non-hypertensive individuals is noted. The identity of the differentially expressed genes are shown in Table 3E.

EXAMPLE 15

Chondrochip Microarray Data Analysis of gene expression profiles of blood samples from individuals having obesity as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with obesity but without osteoarthritis as compared to blood samples taken from healthy patients.

As used herein, "obesity" is defined as an excess of adipose tissue that imparts a health risk. Obesity is assessed in terms of height and weight in the relevance of age. Patients who are considered obese include, but are not limited to, patients having a body mass index or BMI ((defined as body weight in kg divided by (height in meters)²) greater than or equal to 30.0. Patients having obesity as defined herein are those with a BMI of greater than or equal to 30.0.

Blood samples were taken from patients who were diagnosed with hypertension as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of obesity was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a (Chondrochip) as described herein. Identification of genes differentially expressed in blood samples from patients with obesity as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 13 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as obese as described herein as compared with gene expression profiles from normal and non-obese individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Normal individuals

have no known medical conditions and were not taking any known medication. Non-obese individuals presented without obesity, but may have presented with other medical conditions and may be under various treatment regimes. Hybridizations to create said gene expression profiles were done using the ChondroChip (version 2). A dendogram analysis is shown above. Samples are clustered and marked as representing patients who are obese, normal or non-obese. The "*" indicates those patients who abnormally clustered as either obese, normal or non-obese despite actual presentation. The number of hybridizations profiles determined for obese patients, non-obese patients and normal individuals are shown. 1,147 genes were identified as being differentially expressed with a p value of < 0.05 as between the obese patients and the combination of normal and non-obese individuals is noted. The identity of the differentially expressed genes is shown in Table 3F.

EXAMPLE 16

Chondrochip Microarray Data Analysis of gene expression profiles of blood samples from individuals having type 2 diabetes as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with type 2 diabetes but without osteoarthritis as compared to blood samples taken from healthy patients.

As used herein, "diabetes", or "diabetes mellitus" includes both "type 1 diabetes" (insulin-dependent diabetes (IDDM)) and "type 2 diabetes" (insulin-independent diabetes (NIDDM)). Both type 1 and type 2 diabetes characterized in accordance with Harrison's Principles of Internal Medicine 14th edition, as a person having a venous plasma glucose concentration $\geq 140\text{mg/dL}$ on at least two separate occasions after overnight fasting and venous plasma glucose concentration $\geq 200\text{mg/dL}$ at 2 h and on at least one other occasion during the 2-h test following ingestion of 75g of glucose. Patients identified as having type 2 diabetes as described herein are those demonstrating insulin-independent diabetes as determined by the methods described above.

Blood samples were taken from patients who were diagnosed with type II diabetes as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of type II diabetes was corroborated by a skilled Board certified physician.

5 Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a 15K ChondroGene Microarray Chip (Chondrochip) as described herein. Identification of genes differentially expressed in blood samples from patients with type 2 diabetes as
10 compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 14 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having type 2 diabetes as described herein
15 as compared with gene expression profiles from normal and non-type 2 diabetes individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Normal individuals have no known medical conditions and were not taking any known medication. Non-type 2 diabetes individuals presented without type 2 diabetes, but may have presented
20 with other medical conditions and may be under various treatment regimes. Hybridizations to create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who have type 2 diabetes, are normal or do not have type 2 diabetes. The “*” indicates those patients who abnormally clustered despite actual presentation. The number
25 of hybridizations profiles determined for type 2 diabetes, non-type 2 diabetes and normal individuals are shown. 915 were identified as being differentially expressed with a p value of < 0.05 as between the type 2 diabetes patients and the combination of normal and non type 2 diabetes individuals is noted. The identity of the differentially expressed genes is shown in Table 3G.

EXAMPLE 17

Chondrochip Microarray Data Analysis of gene expression profiles of blood samples from individuals having hyperlipidemia as compared with gene expression profiles from normal individuals

5 This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with hyperlipidemia but without osteoarthritis as compared to blood samples taken from healthy patients.

As used herein, "hyperlipidemia" is defined as an elevation of lipid protein profiles and includes the elevation of chylomicrons, very low-density lipoproteins (VLDL),
10 intermediate-density lipoproteins (IDL), low-density lipoproteins (LDL), and/or high-density lipoproteins (HDL) as compared with the general population. Hyperlipidemia includes hypercholesterolemia and/or hypertriglyceridemia. By hypercholesterolemia, it is meant elevated fasting plasma total cholesterol level of >200mg/dL, and/or LDL-cholesterol levels of >130mg/dL. A desirable level of HDL-cholesterol is > 60mg/dL. By
15 hypertriglyceridemia it is meant plasma triglyceride (TG) concentrations of greater than the 90th or 95th percentile for age and sex and can include, for example, TG > 160mg/dL as determined after an overnight fast.

Blood samples were taken from patients who were diagnosed with hyperlipidemia as defined herein. Gene expression profiles were then analyzed and compared to profiles from
20 patients unaffected by any disease. In each case, the diagnosis of hyperlipidemia was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a
25 15K Chondrogene Microarray Chip (Chondrochip) as described herein. Identification of genes differentially expressed in blood samples from patients with hyperlipidemia as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann

Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 15 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having hyperlipidemia as described herein as compared with gene expression profiles from normal and non-hyperlipidemia patients. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Normal individuals have no known medical conditions and were not taking any known medication. Non hyperlipidemia individuals presented without elevated cholesterol or elevated triglycerides but may have presented with other medical conditions and may be under various treatment regimes. Hybridizations to create said gene expression profiles were done using the ChondroChip (version2). A dendogram analysis is shown above. Samples are clustered and marked as representing patients who have elevated lipids and/or cholesterol, are normal or do not have elevated lipids or cholesterol. The "*" indicates those patients who abnormally clustered as having either hyperlipidemia, normal or non-hyperlipidemia despite actual presentation. The number of hybridizations profiles determined for hyperlipidemia patients, non-hyperlipidemia patients and normal individuals are shown. 1,022 genes were identified as being differentially expressed with a p value of < 0.05 as between the patients with hyperlipidemia and the combination of normal and non hyperlipidemia individuals. The identity of the differentially expressed genes is shown in Table 3H.

EXAMPLE 18

Chondrochip Microarray Data Analysis of gene expression profiles of blood samples from individuals having lung disease as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with lung disease but without osteoarthritis as compared to blood samples taken from healthy patients.

As used herein, "lung disease" encompasses any disease that affects the respiratory system and includes bronchitis, chronic obstructive lung disease, emphysema, asthma, lung cancer. Patients identified as having lung disease includes patients having one or more of the above noted conditions.

5 Blood samples were taken from patients who were diagnosed with lung disease as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of lung disease was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was
10 isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a 15K ChondroGene Microarray Chip (Chondrochip) as described herein. Identification of genes differentially expressed in blood samples from patients with lung disease as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney
15 rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 16 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having lung disease as described herein as compared with gene expression profiles from normal and non lung disease individuals.
20 Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Normal individuals have no known medical conditions and were not taking any known medication. Non-lung disease individuals presented without lung disease, but may have presented with other medical conditions and may be under various treatment regimes. Hybridizations to
25 create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who have lung disease, are normal or do not have lung disease. The "*" indicates those patients who abnormally clustered despite actual presentation. The number of hybridizations profiles determined for either the lung disease patients, non-lung disease
30 patients and normal individuals are shown. 596 genes were identified as being differentially

expressed with a p value of < 0.05 as between the lung disease patients and the combination of normal and non lung disease individuals is noted. The identity of the differentially expressed genes is shown in Table 3I.

EXAMPLE 19

- 5 Affymetrix U133A Chip Microarray Data Analysis of gene expression profiles of blood samples from individuals having bladder cancer as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with bladder cancer but without osteoarthritis
10 as compared to blood samples taken from healthy patients.

As used herein, the term "cancer" or "carcinoma" is defined as a disease in which cells behave abnormally and includes; (i) cancers which originate from a single cell proliferating to form a clone of malignant cells, (ii) cancers wherein the growth of the cell is not regulated by normal biological and physical influences of the environment, (iii) anaplastic cancer, wherein
15 the cells lack normal coordinated cell differentiation and (iv) metastasis cancer, wherein the cells have the capacity for discontinuous growth and dissemination to other parts of the body. The diagnosis of cancer can include careful clinical assessment and/or diagnostic investigations including endoscopy, imaging, histopathology, cytology and laboratory studies.

As used herein, "bladder cancer" includes carcinomas that occur in the transitional
20 epithelium lining the urinary tract, starting at the renal pelvis and extending through the ureter, the urinary bladder, and the proximal two-thirds of the urethra. As used herein, patients diagnosed with bladder cancer include patients diagnosed utilizing any of the following methods or a combination thereof: urinary cytologic evaluation, endoscopic evaluation for the presence of malignant cells, CT (computed tomography), MRI (magnetic
25 resonance imaging) for metastasis status.

Blood samples were taken from patients who were diagnosed with bladder cancer as defined herein. Gene expression profiles were then analyzed and compared to profiles from

patients unaffected by any disease. In each case, the diagnosis of bladder cancer was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a Affymetrix U133A Chip as described herein. Identification of genes differentially expressed in blood samples from patients with bladder cancer as compared to healthy patients was determined by statistical analysis using the Wilcox Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 17 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having bladder cancer as described herein as compared with gene expression profiles from non bladder cancer individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Non bladder cancer individuals presented without bladder cancer, but may have presented with other medical conditions and may be under various treatment regimes. Hybridizations to create said gene expression profiles were done using the Affymetrix U1338 chip. A dendogram analysis is shown above. Samples are clustered and marked as representing patients who have bladder cancer, or do not have bladder cancer. The “*” indicates those patients who abnormally clustered as either bladder cancer, or non bladder cancer despite actual presentation. The number of hybridizations profiles determined for patients with bladder cancer and without bladder cancer are shown. 4,228 genes were identified as being differentially expressed with a p value of < 0.05 as between the bladder cancer patients and the non bladder cancer individuals is noted. The identity of the differentially expressed genes is shown in Table 3J.

EXAMPLE 20

Affymetrix U133A Chip Microarray Data Analysis of gene expression profiles of blood samples from individuals having early or advanced bladder cancer as compared with gene expression profiles from normal individuals

5 This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with early or advanced late stage bladder cancer but without osteoarthritis as compared to blood samples taken from healthy patients.

As used herein, "early stage bladder cancer" includes bladder cancer wherein the detection of the anatomic extent of the tumor, both in its primary location and in metastatic
10 sites, as defined by the TNM staging system in accordance with Harrison's Principles of Internal Medicine 14th edition can be considered early stage. More specifically, early stage bladder cancer can include those instances wherein the carcinoma is mainly superficial.

As used herein, "advanced stage bladder cancer" is defined as bladder cancer wherein the detection of the anatomic extent of the tumor, both in its primary location and in
15 metastatic sites, as defined by the TNM staging system in accordance with Harrison's Principles of Internal Medicine 14th edition, can be considered as advanced stage. More specifically, advanced stage carcinomas can involve instances wherein the cancer has infiltrated the muscle and wherein metastasis has occurred.

Blood samples were taken from patients who were diagnosed with early or advanced
20 late stage bladder cancer as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of early or advanced late stage bladder cancer was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was
25 isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a Affymetrix U133A Chip as described herein. Identification of genes differentially expressed in blood samples from patients with early or advanced late stage bladder cancer as compared

to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 18 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having advanced stage bladder cancer or early stage bladder cancer as described herein as compared with gene expression profiles from non bladder cancer individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Non bladder cancer individuals presented without bladder cancer, but may have presented with other medical conditions and may be under various treatment regimes. Hybridizations to create said gene expression profiles were done using the Affymetrix U1338 chip. A dendogram analysis is shown above. Samples are clustered and marked as representing patients who have early stage bladder cancer, advanced stage bladder cancer, or do not have bladder cancer. The “*” indicates those patients who abnormally clustered despite actual presentation. The number of hybridizations profiles determined for either early stage bladder cancer, advanced bladder cancer or non-bladder cancer are shown. 3,518 genes were identified as being differentially expressed with a p value of < 0.05 as between the bladder cancer patients and the non bladder cancer individuals is noted. The identity of the differentially expressed genes is shown in Table 3K.

20

EXAMPLE 21

Affymetrix U133A Chip Microarray Data Analysis of gene expression profiles of blood samples from individuals having coronary artery disease as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with coronary artery disease but without osteoarthritis as compared to blood samples taken from healthy patients

As used herein, “Coronary artery disease” (CAD) is defined as a condition wherein at least one coronary artery has $>50\%$ luminal diameter stenosis, as diagnosed by coronary

angiography and includes conditions in which there is atheromatous narrowing and subsequent occlusion of the vessel. CAD includes those conditions which manifest as angina, silent ischaemia, unstable angina, myocardial infarction, arrhythmias, heart failure, and sudden death. Patients identified as having CAD herein Coronary artery disease is defined

- 5 Blood samples were taken from patients who were diagnosed with Coronary artery disease as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of Coronary artery disease was corroborated by a skilled Board certified physician .

- Total mRNA from a drop of peripheral whole blood taken from each patient was
10 isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a Affymetrix U133A Chip as described herein. Identification of genes differentially expressed in blood samples from patients with Coronary artery disease as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz
15 SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

- Figure 19 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having coronary artery disease (CAD) as described herein as compared with gene expression profiles from non-coronary artery disease
20 individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Non coronary artery disease individuals presented without coronary artery disease, but may have presented with other medical conditions and may be under various treatment regimes. Hybridizations to create said gene expression profiles were done using the
25 Affimetrix™ U1338 chip. A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who have coronary artery disease or do not have coronary artery disease. The “*” indicates those patients who abnormally clustered despite actual presentation. The number of hybridizations profiles determined for patients with CAD or without CAD are shown. 967 genes were identified as being differentially expressed with a p

value of < 0.05 as between the coronary artery disease patients and those individuals without coronary artery disease is noted. The identity of the differentially expressed genes is shown in Table 3L.

EXAMPLE 22

- 5 Affymetrix U133A Chip Microarray Data Analysis of gene expression profiles of blood samples from individuals having Rheumatoid arthritis as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with Rheumatoid arthritis but without
10 osteoarthritis as compared to blood samples taken from healthy patients

Rheumatoid arthritis (RA) is defined as a chronic, multisystem disease of unknown etiology with the characteristic feature of persistent inflammatory synovitis. Said inflammatory synovitis usually involves peripheral joints in a systemic distribution. Patients having RA as defined herein were identified as having one or more of the following;
15 (i) cartilage destruction, (ii) bone erosions and/or (iii) joint deformities.

Blood samples were taken from patients who were diagnosed Rheumatoid arthritis as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of Rheumatoid arthritis was corroborated by a skilled Board certified physician .

20 Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a Affymetrix U133A Chip as described herein. Identification of genes differentially expressed in blood samples from patients with Rheumatoid arthritis as compared to healthy patients was
25 determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 20 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having rheumatoid arthritis as described herein as compared with gene expression profiles from non-rheumatoid arthritis individuals. Expression profiles were generated using GeneSpring software analysis as described herein.

5 Each column represents the hybridization pattern resulting from a single individual. Normal individuals have no known medical conditions and were not taking any known medication. Non rheumatoid arthritis individuals presented without rheumatoid arthritis, but may have presented with other medical conditions and may be under various treatment regimes. Hybridizations to create said gene expression profiles were done using ChondroChip
10 (version2). A dendogram analysis is shown above. Samples are clustered and marked as representing patients who have rheumatoid arthritis or do not have rheumatoid arthritis. The “*” indicates those patients who abnormally clustered despite actual presentation. The number of hybridizations profiles determined for patients with rheumatoid arthritis and without rheumatoid arthritis are shown: 2,068 genes were identified as being differentially expressed
15 with a p value of < 0.05 as between the rheumatoid arthritis patients and a combination of those individuals without rheumatoid arthritis and normal is noted. The identity of the differentially expressed genes is shown in Table 3M.

EXAMPLE 23

20 Affymetrix U133A Chip Microarray Data Analysis of gene expression profiles of blood samples from individuals having depression as compared with gene expression profiles from normal individuals

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients with depression but without osteoarthritis as
25 compared to blood samples taken from healthy patients

As used herein “mood disorders” are conditions characterized by a disturbance in the regulation of mood, behaviour, and affect. “Mood disorders” can include depression, anxiety, schizophrenia, bipolar disorder, manic depression and the like.

As used herein "depression" includes depressive disorders or depression in association with medical illness or substance abuse in addition to depression as a result of sociological situations. Patients defined as having depression were diagnosed mainly on the basis of clinical symptoms including a depressed mood episode wherein a person displays a depressed mood on a daily basis for a period of greater than 2 weeks. A depressed mood episode may be characterized by sadness, indifference, apathy, or irritability and is usually associated with changes in a number of neurovegetative functions, including sleep patterns, appetite and weight, fatigue, impairment in concentration and decision making.

Blood samples were taken from patients who were diagnosed with depression as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of depression was corroborated by a skilled Board certified physician.

Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a Affymetrix U133A Chip as described herein. Identification of genes differentially expressed in blood samples from patients with depression as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002).

Figure 21 shows a diagrammatic representation of gene expression profiles of blood samples from individuals who were identified as having depression as described herein as compared with gene expression profiles from non-depression individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from a single individual. Normal individuals have no known medical conditions and were not taking any known medication. Non depression individuals presented without depression, but may have presented with other medical conditions and may be under various treatment regimes. Hybridizations to create said gene expression profiles were done using ChondroChip (version2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who have

depression, having non-depression or normal. The "*" indicates those patients who abnormally clustered despite actual presentation. The number of hybridizations profiles determined for patients with depression, non-depression and normal are shown. 941 genes were identified as being differentially expressed with a p value of < 0.05 as between the patients with depression and a combination of those individuals without depression and normal is noted. The identity of the differentially expressed genes is shown in Table 3N.

EXAMPLE 24

ChondroChip Microarray Data Analysis of gene expression profiles of blood samples from individuals having osteoarthritis as compared with gene expression profiles from normal individuals.

This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from patients who were identified as having various stages of osteoarthritis as compared to blood samples taken from healthy patients.

Osteoarthritis (OA), as used herein also known as "degenerative joint disease", represents failure of a diarthrodial (movable, synovial-lined) joint. It is a condition, which affects joint cartilage, and or subsequently underlying bone and supporting tissues leading to pain, stiffness, movement problems and activity limitations. It most often affects the hip, knee, foot, and hand, but can affect other joints as well.

OA severity can be graded according to the system described by Marshall (Marshall KW. J Rheumatol, 1996;23(4):582-85). Briefly, each of the six knee articular surfaces was assigned a cartilage grade with points based on the worst lesion seen on each particular surface. Grade 0 is normal (0 points), Grade I cartilage is soft or swollen but the articular surface is intact (1 point). In Grade II lesions, the cartilage surface is not intact but the lesion does not extend down to subchondral bone (2 points). Grade III damage extends to subchondral bone but the bone is neither eroded nor eburnated (3 points). In Grade IV lesions, there is eburnation of or erosion into bone (4 points). A global OA score is calculated by summing the points from all six cartilage surfaces. If there is any associated pathology, such as meniscus tear, an extra point will be added to the global score. Based on the total

score, each patient is then categorized into one of four OA groups: mild (1-6), moderate (7-12), marked (13-18), and severe (>18). As used herein, patients identified with OA may be categorized in any of the four OA groupings as described above.

5 Blood samples were taken from patients who were diagnosed with osteoarthritis as defined herein. Gene expression profiles were then analyzed and compared to profiles from patients unaffected by any disease. In each case, the diagnosis of osteoarthritis was corroborated by a skilled Board certified physician .

10 Total mRNA from a drop of peripheral whole blood taken from each patient was isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample were generated as described above. Each probe was denatured and hybridized to a 15K ChondroGene Microarray Chip (Chondrochip) as described herein. Identification of genes differentially expressed in blood samples from patients with disease as compared to healthy patients was determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical
15 Publishing Division, 2002).

Figure 22 shows a diagrammatic representation of gene expression profiles of blood samples from individuals having osteoarthritis as compared with gene expression profiles from normal individuals. Expression profiles were generated using GeneSpring software analysis as described herein. Each column represents the hybridization pattern resulting from
20 a single individual. Normal individuals have no known medical conditions and were not taking any known medication. Hybridizations to create said gene expression profiles were done using the ChondroChip (version 2). A dendrogram analysis is shown above. Samples are clustered and marked as representing patients who presented with different stages of osteoarthritis or normal. The “*” indicates those patients who abnormally clustered despite
25 actual presentation. The number of hybridizations profiles determined for either osteoarthritis patients or normal individuals are shown. 300 differentially expressed genes were identified as being differentially expressed with a p value of < 0.05 as between the osteoarthritis patients and normal individuals. The identity of the differentially expressed genes is shown in Table 30.

EXAMPLE 25

Microarray Data Analysis of gene expression profiles of blood samples from individuals undergoing therapeutic treatment as compared with gene expression profiles from individuals not undergoing treatment

5 This example demonstrates the use of the claimed invention to detect differential gene expression in blood samples taken from individuals undergoing therapeutic treatment as compared with gene expression profiles from individuals not undergoing treatment.

 Blood samples are taken from patients who are undergoing therapeutic treatment. Gene expression profiles are then analyzed and compared to profiles from patients not
10 undergoing treatment.

 Total mRNA from a drop of peripheral whole blood taken from each patient is isolated using TRIzol® reagent (GIBCO) and fluorescently labeled probes for each blood sample are generated as described above. Each probe is denatured and hybridized to a microarray for example the 15K Chondrogene Microarray Chip (Chondrochip), Affymetrix Genechip or
15 Blood chip as described herein. Identification of genes differentially expressed in blood samples from patients undergoing therapeutic treatment as compared to patients not undergoing treatment is determined by statistical analysis using the Wilcox Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002). Expression profiles are generated using GeneSpring
20 software analysis as described herein. The number of differentially expressed genes are then identified as being differentially expressed with a p value of < 0.05 .

 All patents, patent applications, and published references cited herein are hereby incorporated by reference in their entirety. While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by
25 those skilled in the art that various changes in form and details may be made therein without departing from the scope of the invention encompassed by the appended claims.

 One skilled in the art will appreciate readily that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those

objects, ends and advantages inherent herein. The present examples, along with the methods, procedures, treatments, molecules, and specific compounds described herein are presently representative of preferred embodiments, are exemplary, and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention as defined by the scope of the claims.

TABLE 2

Comparison of 1,800 Unique Genes Identified in the Blood Cell cDNA Library to Genes Previously Identified in Specific Tissues

Gene Identification	No. of ESTs	Accession No.	Tissue Distribution						
			Bl	Br	H	K	Li	Lu	
100 kDa coactivator	2	U22055		+				+	
10kD protein (BC10)	2	AF053470		+	+		+	+	
14-3-3 epsilon	2	U54778		+	+			+	
14-3-3 protein	11	U28964		+	+		+		
15 kDa selenoprotein (SEP15)	1	AF051894		+	+			+	
1-phosphatidylinositol-4-phosphate 5-kinase isoform C	1	S78798							
23 kD highly basic protein	21	X56932	+	+	+	+	+	+	
2-5A-dependent RNase	1	L10381							
2'-5'oligoadenylate synthetase 2 (OAS2)	4	M87284	B						
26S proteasome subunit 11	1	AF086708							
36 kDa phosphotyrosine protein	2	AJ223280	T		+				
3-7 gene product (non-exact 86%aa)	1	D64159							
3-phosphoglycerate dehydrogenase (PGAD)	1	AF006043	T	+	+			+	
3-prime-phosphoadenosine 5-prime-phosphosulfate synthase 1 (PAPSS1)	2	U53447	+	+	+	+		+	
46kd mannose 6-phosphate receptor (MPR46) (low match)	1	X56257							
5-aminoimidazole-4-carboxamide ribonucleotide	1	D89976							

transformylase									
5'-nucleotidase	3	D38524	T	+				+	
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (PFKFB4)	1	D49818		+					
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K)	1	AF041829							
71 kd heat shock cognate protein hsc70	23	Y00371							
76 kDa membrane protein (P76)	2	U81006		+	+	+	+	+	
8-oxoguanine DNA glycosylase (OGG1)	1	U96710	B					+	+
a disintegrin and metalloprotease domain 10 (ADAM10)	1	AF009615	T					+	
a disintegrin and metalloprotease domain 8 (ADAM8)	1	D26579	B	+					
A kinase anchor protein 95 (AKAP95)	2	Y11997	B, T activated		+				+
A kinase anchor protein, 149kD (AKAP149)	2	X97335		+	+	+			+
A4 differentiation-dependent protein (A4), triple LIM domain protein (LMO6), and synaptophysin (SYP); calcium channel alpha-1 subunit (CACNA1F)	1	U93305							
ABL and putative M8604 Met protein	1	U07561							
Absent in melanoma 1 (AIM1)	1	U83115	+	+					+
accessory proteins BAP31/BAP29 (DXS1357E)	2	Z31696		+	+				
acetyl-Coenzyme A acyltransferase (peroxisomal 3-oxoacyl-Coenzyme A thiolase)	2	X12966	+	+	+	+	+	+	

(ACAA)										
acetyl-Coenzyme A transporter (ACATN)	1	D88152	T lymphoma	+	+					
acidic 82 kDa protein	4	U15552								
acidic protein rich in leucines (SSP29)	1	Y07969	B	+	+		+	+		
Aconitase 2, mitochondrial (ACO2)	1	U80040	+	+	+	+		+		
actin binding protein MAYVEN	1	AF059569								
actin, beta (ACTB)	158	X04098	T, B	+	+		+			
actin, beta (ACTB) (non-exact, low match 73%)	1	M10277								
actin, gamma (low score)	1	K00791								
actin, gamma 1 (ACTG1)	4	X04098	+	+	+	+	+	+		high in many libraries
actin-binding LIM protein (ABLIM)	4	D31883		+	+	+		+		
Actinin, alpha 1 (ACTN1)	8	M95178		+	+	+		+		
actinin, alpha 4 (ACTN4)	1	D89980		+	+		+			
activated p21cdc42Hs kinase (ACK)	1	L13738	B	+					+	
activated RNA polymerase II transcription cofactor 4 (PC4)	1	X79805	+	+	+	+		+		
activating transcription factor 1 (ATF1)	1	X55544			+					
activating transcription factor 2 (ATF2)	1	X15875		+	+		+			
activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4)	2	M86842						+	+	
active BCR-related gene (ABR)	1	U01147	+	+	+	+		+		
acyl-CoA oxidase (AOX)	1	U03254								

acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM)	2	M16827							
acyl-Coenzyme A dehydrogenase, very long chain (ACADVL)	3	D43682	+	+	+	+	+	+	
acyloxyacyl hydrolase (neutrophil) (AOAH)	3	M62840	T		+		+	+	
adaptin, delta (ADTD)	2	U91930		+	+		+		
adaptin, delta (ADTD) (non-exact 59%)	1	AC005328							
adaptin, gamma (ADTG)	1	Y12226		+	+	+		+	
adaptor complex sigma3B (AP3S3)	2	X99459		+		+		+	
adaptor protein p150	1	Y08991							
adducin 1 (alpha) (ADD1)	2	L07261		+	+		+		
adducin 1 (alpha) (add1)	3	L29296	+	+	+	+		+	
adducin 3 (gamma) (ADD3)	3	U37122	B, W	+	+		+	+	
adenine nucleotide translocator 2 (fibroblast) (ANT2)	2	M57424		+	+		+		
adenine nucleotide translocator 2 (fibroblast) (ANT2) (non-exact 81%)	1	J02683							
adenine nucleotide translocator 2 (fibroblast) (ANT2) (non-exact, 79%)	1	J02683							
adenine nucleotide translocator 2 (fibroblast) (ANT2) (non-exact, 86%)	1	J02683							
adenine nucleotide translocator 3 (liver) (ANT3)	3	J03592		+	+		+	+	
adenosine deaminase, RNA-specific (ADAR)	6	U18121		+	+		+		
adenylate cyclase 3 (ADCY3)	2	AF033861		+	+	+	+	+	

adenylate cyclase 7 (ADCY7)	1	D25538							
adenylate kinase 2 (AK2)	2	U39945		+	+		+	+	
adenylate kinase 3 (AK3) (non-exact, 67%)	1	X60673							
adenylyl cyclase-associated protein (CAP)	28	M98474	T		+		+		
adipose differentiation-related protein; adipophilin (ADFP)	1	X97324			+		+	+	
ADP-ribosylation factor 1 (ARF1)	13	M84326		+	+		+	+	
ADP-ribosylation factor 3 (ARF3)	2	M33384		+	+		+		
ADP-ribosylation factor 4 (ARF4)	1	M36341	T lymphoma	+	+			+	
ADP-ribosylation factor 5 (ARF5)	1	M57567			+	+	+	+	
ADP-ribosylation factor domain protein 1, 64kD (ARFD1)	1	L04510		+					
ADP-ribosyltransferase (NAD ⁺ ; poly (ADP-ribose) polymerase) (ADPRT)	4	M32721	+	+	+	+	+	+	
adrenergic, beta, receptor kinase 1 (ADRBK1)	2	X61157	B	+			+		
adrenoleukodystrophy-like 1 (ALDL1)	1	AJ000327							
AE-binding protein 1 (AEBP1) (non-exact, 62%)	1	D86479							
AF-17	1	U07932							
A-gamma-globin	1	V00514							
A-gamma-globin (chromosome 11 allele)	1	J00176							
agammaglobulinaemia tyrosine kinase (ATK)	1	U78027							
AHNAK nucleoprotein	4	M80899	+	+	+	+		+	

(desmoyokin) (AHNAK)									
alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150) (ANPEP)	1	X13276			+		+		
alcohol dehydrogenase 5 (class III), chi polypeptide (ADH5)	1	M29872							
aldehyde dehydrogenase 1, soluble (ALDH1)	1	AF003341		+			+	+	
aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase) (ALDH10)	2	U75286							
aldehyde reductase 1 (low Km aldose reductase) (ALDR1)	3	J04795	B	+	+	+	+		
aldo-keto reductase family 1, member A1 (aldehyde reductase) (AKR1A1)	2	J04794	B	+	+		+		
aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) (AKR1C3)	1	D17793		+	+	+		+	
aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase) (AKR7A2)	1	Y16675		+	+		+	+	
aldolase A, fructose-bisphosphate (ALDOA)	7	X12447		+	+		+		
aldolase C, fructose-bisphosphate (ALDOC)	2	X05196		+	+		+		
alkaline phosphatase, liver/bone/kidney (ALPL)	1	4502062							
ALL-1 (=L04731;L04284 HRX)	4	Z69780							
alpha mannosidase II isozyme	1	D55649		+			+		
alpha thalassemia/mental retardation syndrome X-	3	U75653	+	+	+	+		+	

linked (ATRX)									
alpha-2 macroglobulin	1	Z11711							
alpha-2-globin	2	V00516							
alpha-2-macroglobulin receptor/lipoprotein receptor protein (A2MR/LRP)	1	U06985							
alpha-polypeptide of N- acetyl-alpha- glucosaminidase (HEXA)	1	M13520							
alpha-spectrin	1	X86901							
alpha-subunit of Gi2 a (GTP-binding signal transduction protein)	1	X07854							
aminin receptor 1 (67kD); Ribosomal protein SA (LAMR1)	2	J03799	T	+	+		+	+	
aminolevulinatase, delta-, dehydratase (ALAD)	1	X64467		+					
amino-terminal enhancer of split (AES)	2	X73358	+	+	+	+		+	
amino-terminal enhancer of split (AES)	3	U04241	B	+	+		+	+	
AMP deaminase isoform L (AMPD2)	8	M91029		+				+	
amphiphysin (Stiff-Mann syndrome with breast cancer 128kD autoantigen) (AMPH)	1	U07616	B	+				+	
amphiphysin (Stiff-Mann syndrome with breast cancer 128kD autoantigen) (AMPH)(non-exact, 68%)	1	U07616							
amphiphysin (Stiff-Mann syndrome with breast cancer 128kD autoantigen) (AMPH)(non-exact, 68%)	1	U07616							
amphiphysin II	4	U87558		+	+		+		
amphiphysin II (67%aa amphiphysin?)	1	AF068915							

amphiphysin II (non-exact 69% aa)	1	AF001383							
amphiphysin-like (AMPHL)	1	U68485		+	+				
amphiphysin-like (AMPHL) (low match)	1	AF068918							
AMY-1	1	D50692	B, T				+		
amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65) (APBB1)	1	L77864		+	+	+		+	
amyloid beta (A4) precursor-like protein 2 (APLP2)	6	L27631	T lymphoma	+	+		+	+	
ankyrin 3, node of Ranvier (ankyrin G) (ANK) (non-exact, 50%)	1	U43965							
annexin I (lipocortin I) (ANX1)	1	X05908		+	+	+		+	
annexin II	1	D28364							
annexin II (lipocortin II; calpactin I, heavy polypeptide) (ANX2)	7	D00017	+	+	+	+	+	+	high in many libraries.
annexin IV (placental anticoagulant protein II) (ANX4)	1	M19383		+	+	+	+	+	
annexin V (endonexin II) (ANX5)	2	M21731		+	+	+		+	
annexin V (endonexin II) (ANXV)	1	M19384		+	+	+		+	
annexin VI (p68) (ANX6)	6	Y00097		+	+	+		+	
annexin VII (synexin) (ANX7)	1	J04543		+	+	+		+	
antigen identified by monoclonal antibodies 12E7, F21 and O13 (MIC2)	2	M16279		+	+	+		+	
antigen identified by monoclonal antibodies 4F2, TRA1.10, TROP4, and T43 (MDU1)	3	J02939		+	+	+	+	+	

antigen TQ1	1								
anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2) (KIAA0106)	1	D14662		+	+	+	+	+	
APEX nuclease (multifunctional DNA repair enzyme) (APEX)	5	X66133		+	+		+	+	
Apolipoprotein L (APOL) (59%aa)	1	Z82215							
apoptosis inhibitor 1 (API1)	1	L49431		+	+	+	+	+	
apoptosis inhibitor 4 (survivin) (API4)	1	U75285	B, W	+	+		+		
apoptosis inhibitor 5 (API5)	1	U83857	T lymphoma	+			+		
apoptosis specific protein (ASP)	1	Y11588	B	+			+	+	
apoptotic protease activating factor (APAF1)	1	AF013263	B	+	+		+		
aquaporin 3 (AQP3)	1	AB001325	T				+		
aquaporin 9 (AQP9)	7	AB008775	T activated				+		
arachidonate 12-lipoxygenase (ALOX12)	1	M58704	T				+	+	
arachidonate 5-lipoxygenase-activating protein (ALOX5AP)	3	X52195	+	+		+		+	
ariadne homolog (ARI)	1	AJ009771	+	+	+	+		+	
ariadne-2 (D. melanogaster) homolog (all-trans retinoic acid inducible RING finger) (ARI2)	1	AF099149	+	+	+	+		+	
ARP1 (actin-related protein 1, yeast) homolog A (centractin alpha) (ACTR1A)	1	X82206		+			+		
ARP2 (actin-related protein 2, yeast) homolog (ACTR2)	9	AF006082		+	+		+	+	

ARP2/3 protein complex subunit 34 (ARC34)	5	AF006085	T activated, W	+	+		+		
Arp2/3 protein complex subunit p41 (ARC41)	6	AF006084	monocyte stimulated	+	+		+		
Arp2/3 protein complex subunit p41 (ARC41)) (low match)	1	AF006084							
Arp2/3 protein complex subunit p16 (ARC16)	20	AF017807		+	+		+	+	
Arp2/3 protein complex subunit p20 (ARC20)	2	AF006087		+	+		+	+	
Arp2/3 protein complex subunit p21(ARC21)	3	AF006086	W				+	+	
ARP3 (actin-related protein 3, yeast) homolog (ACTR3)	11	AF006083	W		+		+	+	
arrestin, beta 2 (ARRB2)	1	AF106941	B, T, W	+	+		+		
arsA (bacterial) arsenite transporter, ATP-binding, homolog 1 (ASNA1)	1	AF047469	B, T	+			+		
aryl hydrocarbon receptor nuclear translocator-like (ARNTL)	2	AF044288	B	+	+		+		
aryl hydrocarbon receptor-interacting protein (AIP)	1	U31913	+	+	+	+		+	
arylsulfatase A (ARSA)	1	X52151	T activated	+			+		
asialoglycoprotein receptor 2 (ASGR2)	1	M11025					+	+	
asparaginyl-tRNA synthetase (NARS)	3	D84273		+	+		+		
aspartyl-tRNA synthetase (DARS)	1	J05032	B	+	+		+		
ataxia telangiectasia mutated (includes complementation groups A, C and D) (ATM)	1	U82828	B, T		+		+		
ataxin-2-like protein A2LP (A2LG)	1	AF034373	B, T activated	+	+			+	
ATF6	1	AF005887		+			+		

ATP binding cassette transporter (ABCR) (non-exact 80%)	1	U88667							
ATP synthase (F1-ATPase) alpha subunit, mitochondrial	1	X59066							
ATP synthase beta subunit gene	1	M19482							
ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1)	1	X60221	+	+	+	+		+	
ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1 (ATP5G1)	1	X69907	T activated	+	+		+	+	
ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle (ATP5A1)	3	D14710							
ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle (ATP5A1) (low match)	1	D14710							
ATP synthase, H ⁺ transporting, mitochondrial F1 complex, beta polypeptide (ATP5B)	2	M27132							
ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1 (ATP5C1)	1	D16563	W	+	+	+	+		
ATP synthase, H ⁺ transporting, mitochondrial F1F0, subunit g (ATP5JG)	1	AF092124	+	+	+	+	+	+	
ATP/GTP-binding protein (HEAB)	2	U73524	+	+	+	+		+	
ATPase, Ca ⁺⁺ transporting, ubiquitous (ATP2A3)	5	Z69881		+					
ATPase, H ⁺ transporting, lysosomal (vacuolar proton	2	D89052	+	+	+	+		+	

pump) 21kD (ATP6F)									
ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD (ATP6E)	1	X76228		+	+	+		+	
ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD: Vacuolar proton-ATPase, subunit C; V-ATPase, subunit C (ATP6D)	5	X69151		+	+	+		+	
ATPase, H+ transporting, lysosomal (vacuolar proton pump), alpha polypeptide, 70kD, isoform 1 (ATP6A1)	3	L09235		+		+			
ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2 (ATP6B2)	6	X62949	+	+	+	+		+	
ATPase, H+ transporting, lysosomal (vacuolar proton pump), member J (ATP6J)	2	AF038954	+	+	+	+		+	high in testis
ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1 (ATP6S1)	1	D16469		+	+	+		+	
ATP-binding cassette 50 (TNF-alpha stimulated) (ABC50)	1	AF027302	+	+	+	+		+	
ATP-binding cassette protein M-ABC1 (mitochondrial)	1	AF047690							
ATP-dependent RNA helicase	1	AJ010840	T lymphoma		+		+		
autoantigen (Hs.75528)	2	L05425	T activated		+				
autoantigen (Hs.75528) (non-exact 84%)	1	L05425							
autoantigen (Hs.75682)	1	U17474	B	+				+	
autoantigen La/SS-B	1	Z35127							
axin (AXIN1)	1	AF009674	T	+					
axonemal dynein heavy	1	AJ000522						+	

chain (DNAH17)									
BAI1-associated protein 3 (BAIAP3) (non-exact 54%)	1	AB017111							
basement membrane-induced gene (ICB1)	1	AF044896							
basic leucine zipper nuclear factor 1 (JEM-1) (BLZF1)	2	JU79751							
basic transcription factor 3 (BTF3)	5	X74070	+	+	+	+	+	+	
basigin (BSG)	1	L10240		+			+		
BC-2	1	AF042384	B		+	+	+		
B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6)	1	U00115		+	+				
B-cell translocation gene 1, anti-proliferative (BTG)	1	X61123			+			+	
BCL2/adenovirus E1B 19kD-interacting protein 2 (BNIP2)	1	U15173	B	+			+	+	
BCL2/adenovirus E1B 19kD-interacting protein 3-like (BNIP3L)	2	AF067396		+	+	+		+	
beclin 1 (coiled-coil, myosin-like BCL2-interacting protein) (BECN1)	1	AF077301	B	+	+		+		
beta-1,2-N-acetylglucosaminyltransferase II (MGAT2)	2	U15128							
beta-2-microglobulin (B2M)	63	S82297	+	+	+	+	+	+	high in invasive prostate tumor
beta-hexosaminidase alpha chain (HEXA)	1	M16411							
beta-tubulin	7	V00599	+	+	+	+	+	+	high in many libraries
beta-tubulin (non-exact, 76%)	1	AF070561							
beta-tubulin, pseudogene	1	J00315							

BING4	1	Z97184							
biotinidase (BTD) (non-exact 62%)	1	U03274							
biotinidase (BTD) (non-exact 70%)	1	U03274							
biotinidase (BTD) (non-exact, 56%)	1	U03274							
BIOTINIDASE PRECURSOR	1	P43251							
biphenyl hydrolase-like (serine hydrolase) (BPHL)	1	X81372		+			+		
bone marrow stromal cell antigen 1 (BST1)	1	D21878					+		
box-dependent myc-interacting protein isoform BIN1-10 (BIN1)	1	AF043900							
box-dependent myc-interacting protein isoform BIN1-10 (BIN1) (non-exact, 64%)	1	AF043900							
brain my047 protein	1	AF063605	T	+	+		+		
branched chain keto acid dehydrogenase E1, alpha polypeptide (maple syrup urine disease) (BCKDHA)	3	Z14093	T	+	+		+		
BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase) (BAP1)	1	D87462	+	+	+	+			
BRCA1, Rho7 and vatl genes, and ipf35	1	L78833							
breakpoint cluster region protein, uterine leiomyoma, 1; barrier to autointegration factor (BCRP1)	2	AF044773		+	+				
breakpoint cluster region protein, uterine leiomyoma, 2 (BCRP2)	2	AF044774		+	+		+	+	
breast cancer anti-estrogen resistance 3 (BCAR3) (non-exact 73%)	1	U92715							

bromodomain-containing protein, 140kD (peregrin) (BR140)	2	M91585		+						
Bruton's agammaglobulinemia tyrosine kinase (<i>Btk</i>)	1	U13424								
Bruton's tyrosine kinase (BTK)	1	U78027								
Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3)	1	U78027								
BS4	1	AF108083								
BTG2 (BTG2)	6	Y09943	+	+	+	+			+	
BTK region clone ftp	1	U78027	+	+	+	+			+	
BTK region clone ftp-3	1	U01923		+	+			+		
BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog (BUB3)	4	AF053304	+	+	+	+			+	
butyrate response factor 1 (EGF-response factor 1) (BRF1)	4	X79067	+	+	+	+			+	
butyrophilin (BTF1)	7	U90543		+	+			+		
butyrophilin like receptor	1	AB020625.1								
CAG repeat containing (CTG4A)	2	U80744		+	+					
CAGH32	2	U80743		+	+			+		
calcium channel, voltage-dependent, L type, alpha 1D subunit (CACNA1D) (low match)	1	M83566								
calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma (CAMK2G)	1	AF069765		+	+	+			+	
calcium/calmodulin-dependent protein kinase kinase (KIAA0787)	1	AF101264	B	+	+			+		

calmodulin (=M19311)	7	D45887							
calmodulin 1 (phosphorylase kinase, delta) (CALM1)	6	M27319	B	+	+		+	+	
calnexin (CANX)	3	M94859	T	+			+	+	
calpain, large polypeptide L1 (CAPN1)	5	X04366		+	+		+	+	
calpain, large polypeptide L2 (CANP2)	5	M23254		+	+				
calpain, small polypeptide (CAPN4)	1	X04106		+	+		+	+	
calpastatin (CAST)	3	D16217					+		
Calponin 2	2	D83735		+		+		+	
calponin 2 (CNN2)	1	D83735	B, T	+			+		
calponin 2 (CNN2) (low score)	1	D83735							
calumenin (CALU)	3	AF013759	B		+		+	+	
cAMP response element- binding protein CRE-Bpa (H_GS165L15.1)	4	L05912							
cAMP-dependent protein kinase type II (Ht31)	1	M90360							
canicular multispecific organic anion transporter (CMOAT2)	1	AF009670				+	+	+	
capping protein (actin filament) muscle Z-line, alpha 1 (CAPZA1)	6	U56637	B, T		+			+	
capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2)	2	U03269	B	+	+				
capping protein (actin filament) muscle Z-line, beta (CAPZB)	1	U03271	+	+	+	+		+	
capping protein (actin filament), gelsolin-like (CAPG)	8	M94345	+	+		+		+	

carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase (CAD)	1	D78586	+	+	+	+		+	
carbonic anhydrase V, mitochondrial (CA5)	1	L19297		+			+		
carboxypeptidase D (CPD)	3	U65090	B	+	+				
carnitine/acylcarnitine translocase (CACT)	1	Y10319		+	+		+		
Cas-Br-M (murine) ecotropic retroviral transforming sequence (cbl)	2	X57110					+		
casein kinase 1, alpha 1 (CSNK1A1)	1	L37042	+	+	+	+		+	
casein kinase 2, alpha 1 polypeptide (CSNK2A1)	2	M55265	B	+			+	+	
casein kinase I gamma 3L (CSNK1G3L)	1	AF049090.1							
casein kinase II alpha subunit(=S72393)	1	X69951							
CASP8 and FADD-like apoptosis regulator (CFLAR)	4	AF015450		+	+	+	+	+	
caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase) (CASP1)	7	U13697	+			+			
caspase 10, apoptosis-related cysteine protease (CASP10)	1	U60519	B, T activated, T lymphoma				+		
caspase 3, apoptosis-related cysteine protease (CASP3)	3	U13737	B, T	+	+	+	+		
caspase 4, apoptosis-related cysteine protease (CASP4)	6	U25804	+	+	+	+		+	
caspase 5, apoptosis-related cysteine protease (CASP5)	1	U28015			+				
caspase 8, apoptosis-related cysteine protease	2	X98173		+		+		+	

(CASP8)										
caspase 9, apoptosis-related cysteine protease (CASP9)	1	U56390	B			+	+			
catalase (CAT)	5	X04076	B	+	+		+			
catechol-O-methyltransferase (COMT)	1	M65213		+	+		+			
catenin (cadherin-associated protein), alpha 1 (102kD) (CTNNA1)	6	D14705		+	+					
cathelicidin antimicrobial peptide (CAMP)	1	X89658	B							
cathepsin B (CTSB)	4	L16510			+		+	+		
cathepsin C (CTSC)	3	U79415		+	+	+		+		
cathepsin D (lysosomal aspartyl protease) (CTSD)	4	M11233		+	+		+			
cathepsin E (CTSE)	1	J05036					+			
cathepsin G (CTSG)	1	M16117	T, W		+					
cathepsin S (CTSS)	34	M86553	B, Monocyte stimulated, T lymphoma				+	+		
cathepsin W (lymphopain) (CTSW)	4	AF013611						+		
CBF1 interacting corepressor CIR (=U03644 recepin)	1	AF098297								
CCAAT/enhancer binding protein (C/EBP), alpha (CEBPA)	3	X87248		+	+	+		+		
CCAAT/enhancer binding protein (C/EBP), delta (CEBPB)	1	S63168			+		+	+		
CCAAT-box-binding transcription factor (CBF2)	2	M37197	T lymphoma			+	+			
CCR5 receptor (CCR5) (non-exact?)	1	AF011504								
CD14 antigen (CD14)	11	M86511	+	+	+	+		+		

CD18 (=M95293)	4	X64071							
CD1C antigen, c polypeptide (CD1C)	2	M28827						+	
CD2 antigen (cytoplasmic tail)-binding protein 2 (CD2BP2)	1	AF104222							
CD2 antigen (p50), sheep red blood cell receptor (CD2)	4	M14362	+		+	+		+	
CD2 cytoplasmic tail-binding protein 1 (CD2BP1)	2	AF038602					+		
CD20 antigen (CD20)	1	X12530							
CD20 receptor (S7)	1	X07203							
CD22 antigen (CD22)	1	U62631	B						
CD24 signal transducer	1	M58664							
CD33 antigen (gp67) (CD33)	1	M23197					+		
CD33 antigen-like 2; OB binding protein-2 (CD33L2) (non-exact, 68%)	1	U71383							
CD33L2 (61% aa)	1	D86359							
CD36 antigen (collagen type I receptor, thrombospondin receptor) (CD36)	7	M98398	T lymphoma		+		+	+	
CD37 antigen (CD37)	5	X14046	+	+		+		+	
CD38 alt	1	D84277							
CD39 antigen (CD39)	1	U87967	B	+			+	+	
CD3D antigen, delta polypeptide (TIT3 complex) (CD3D)	1	X03934			+	+		+	
CD3E antigen, epsilon polypeptide (TIT3 complex) (CD3E)	1	X03884	+			+			
CD3G antigen, gamma polypeptide (TIT3 complex) (CD3G)	2	X06026	W				+		

CD3Z antigen, zeta polypeptide (TiT3 complex) (CD3Z)	2	J04132	+			+			
CD3-zeta (clone pBS NK1)	1	X55510							
CD4 (low match)	1	S68043							
CD4 antigen (p55) (CD4)	4	M12807		+	+		+		
CD44 antigen (homing function and Indian blood group system) (CD44)	6	X56794	W				+	+	
CD48 antigen (B-cell membrane protein) (CD48)	3	X06341	+	+	+	+		+	
CD53 antigen (CD53)	10	L11670	+	+		+		+	
CD53 antigen (CD53) (low match)	1	M60871							
CD63 antigen (melanoma 1 antigen) (CD63)	3	M59907							
CD68 antigen (CD68)	2	S57235		+	+		+	+	
CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) (CD74)	72	K01144	+	+	+	+	+	+	high in many libraries
CD79A antigen (immunoglobulin-associated alpha) (CD79A)	2	M80462			+				
CD79B antigen (immunoglobulin-associated beta) (CD79B)	2	M89957	+						
CD8 antigen, alpha polypeptide (p32) (CD8A)	2	M27161	+			+		+	
CD8 antigen, beta polypeptide 1 (p37) (CD8B1)	1	X13445	W						
CD81 antigen (target of antiproliferative antibody 1) (CD81)	1	M33680		+	+			+	
CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83)	1	Q01151	B	+	+			+	

CD84 antigen (leukocyte antigen) (CD84)	1	U82988		+	+			+	
CD86 antigen	1	L25259		+					
CD9 antigen (p24) (CD9)	2	M38690			+		+	+	
CD97 antigen (CD97)	12	X84700	+	+		+			
CD97 antigen (CD97) (non-exact 59%)	1	P48960							
CD97 antigen (CD97) (non-exact 62%)	1	X94630	+	+		+			
CDC23 (cell division cycle 23, yeast, homolog) (CDC23)	1	AF053977		+			+	+	
CDC37 homolog	1	U63131	B	+	+		+	+	
Cdc42 effector protein 3 (CEP3)	2	AF104857	B	+	+		+		
CDC-like kinase (CLK)	1	L29219		+	+	+		+	
CDC-like kinase 2 (CLK2)	1	AF023268	B	+	+				
CDW52 antigen (CAMPATH-1 antigen) (CDW52)	13	X15183	T activated	+	+		+		
cell cycle progression restoration 8 protein(CPR8)	1	AF011794							
cell division cycle 10 (homologous to CDC10 of <i>S. cerevisiae</i>) (CDC10)	4	S72008	+	+	+	+		+	
cell division cycle 20, <i>S.cerevisiae</i> homolog (CDC20)	1	U05340		+	+	+			
cell division cycle 25B (CDC25B)	6	Z68092	+	+	+	+		+	
cell division cycle 2-like 1 (PITSLRE proteins) (CDC2L1) (non-exact 42%)	1	AF067514							
cell division cycle 42 (GTP-binding protein, 25kD) (CDC42)	5	M35543	+	+	+	+		+	
cell division protein (non-)	1	AF063015							

exact 68%)									
CELL-CYCLE NUCLEAR AUTOANTIGEN SG2NA (S/G2 NUCLEAR ANTIGEN)	1	Q13033							
centromere protein B (80kD) (CENPB)	1	X55039		+			+		
cep250 centrosome associated protein	3	AF022655	B	+			+		
ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease) (CLN2)	7	AF017456	+	+	+	+	+	+	high in bone
c-fgr (=M63877 nonreceptor protein- tyrosine kinase (fgr))	6	X52206							
CGI-19 protein	3	AF132953.1							
chaperonin containing TCP1, subunit 3 (gamma) (CCT3)	1	X74801		+	+			+	
chaperonin containing TCP1, subunit 4 (delta) (CCT4)	1	AF026291		+	+		+	+	
chaperonin containing TCP1, subunit 6A (zeta 1) (CCT6A)	4	L27706	B	+	+				
chaperonin containing TCP1, subunit 7 (eta) (CCT7)	4	AF026292	B	+				+	
Chediak-Higashi syndrome 1 (CHS1)	1	U67615	B, T lymphoma	+	+		+		
Chediak-Higashi syndrome 1 (CHS1) (low score)	1	U67615							
chemokine (C-C motif) receptor 2 (CCR2)	4	U03905							
chemokine (C-C motif) receptor 4 (CCR4) (low match) (may contain repeat)	1	X85740							
chemokine (C-C motif) receptor 7 (CCR7)	6	L31581							

chemokine (C-X3-C) receptor 1 (CX3CR1)	5	U20350		+					
chemokine (C-X-C motif), receptor 4 (fusin) (CXCR4)	5	M99293	+	+	+	+		+	
chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1)	2	M80927		+		+		+	
chitinase 3-like 2 (CHI3L2)	2	U49835		+		+		+	
chloride channel 1, skeletal muscle (CLCN1)	1	G18280							
chloride channel 6 (CLCN6)	1	D28475		+	+				
Chloride intracellular channel 1 (CLIC1)	1	U93205	+	+	+	+		+	
chondroitin sulfate proteoglycan 2 (versican) (CSPG2)	5	X15998			+				
chondroitin sulfate proteoglycan core protein	2	J02814			+			+	
chromatin assembly factor 1 p48 subunit (CAF-1 P48 subunit) (retinoblastoma binding protein p48) (retinoblastoma-binding protein 4) (MSI1 protein homolog)	1	Q09028							
chromodomain helicase DNA binding protein 1 (CHD1)	2	AF006513							
chromodomain helicase DNA binding protein 1-like (CHD1L)	1	AF054177							
chromodomain helicase DNA binding protein 2 (CHD2)	1	AF006514	B	+	+		+		
chromodomain helicase DNA binding protein 3 (CHD3)	1	AF006515							
chromodomain helicase DNA binding protein 4 (CHD4)	5	X86691	+	+	+	+		+	
chromosome 1 open	1	AF054176							

reading frame 7 (C1ORF7)									
chromosome 1 specific transcript KIAA0493	1	AB007962							
chromosome 17 open reading frame 1B (C17ORF1B)	1	AJ008112	T	+					
chromosome 4 open reading frame 1 (C4ORF1)	1	AF006621		+	+	+		+	
chromosome condensation 1-like (CHC1L)	2	AF060219		+	+	+		+	
chromosome X open reading frame 5 (CXORF5)	1	Y15164	B	+	+		+		
chromosome-associated polypeptide C(CAP-C)	2	AF092564	B	+	+		+	+	
cig42	1	AF026944							
cig5	3	AF026941							
citrate synthase (CS)	2	AF047042	B	+	+		+	+	
class I major histocompatibility antigen (HLA-Cw3)	2	U31372							
class I major histocompatibility antigen (HLA-Cw3) (low match)	1	U31372							
clathrin assembly protein lymphoid myeloid leukemia (CALM)	3	U45976	B	+	+			+	
clathrin heavy chain	1	X55878							
clathrin, heavy polypeptide-like 2 (CLTCL2)	1	D21260							
clathrin, light polypeptide (Lca) (CLTA) (low match)	1	M20472							
clathrin-associated/assembly/adapt or protein, medium 1 (CLAPM1)	3	D63475		+	+	+	+	+	
cleavage stimulation factor, 3' pre-RNA, subunit 2 64kD (CSTF2) (non-exact 82%)	1	M85085							

cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD (CSTF3)	1	U15782	B	+	+		+		
clk3	1	L29220	B	+	+				
clone 23815 (Hs.82845)	1	U90916		+	+			+	
clone 24592 mRNA sequence	1	D88378	+	+	+	+		+	
Clq/MBL/SPA receptor C1qR(p) ()	1	U94333							
clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) (CLU)	1	M64722	+	+	+	+	+	+	
CMP-sialic acid transporter (CMPST)	1	D87969	B	+	+				
CMRF35	3	X66171							
c-myc oncogene containing coxIII	1	X54629							
coagulation factor II (thrombin) receptor (F2R)	1	M62424		+	+			+	
coagulation factor V (proaccelerin, labile factor) (F5)	1	M14335		+		+	+		
coagulation factor XIII a subunit	3	M21998							
coagulation factor XIII, A1 polypeptide (F13A1)	6	M14354		+	+	+		+	
coated vesicle membrane protein (RNP24)	1	X92098	+	+	+	+	+	+	
coatamer protein complex, subunit alpha (COPA)	5	U24105	T	+			+		
Cofilin 1 (non-muscle) (CFL1)	13	X95404	+	+	+	+	+	+	high in fetal brain
cold inducible RNA-binding protein (CIRBP)	7	D78134		+	+			+	

cold shock domain protein A (CSDA)	3	X95325		+	+				
collagen, type IX, alpha 2 (COL9A2)	3	AF019406	B						
colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog (CSF1R)	3	X03663		+			+	+	
colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB)	5	M59941							
colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB) (low match)	1	M59941							
colony stimulating factor 3 receptor (granulocyte) (CSF3R)	16	X55720		+					
complement component 5 receptor 1 (C5a ligand) (C5R1)	1	M62505	L						
conserved gene amplified in osteosarcoma (OS4)	2	AF000152		+	+	+		+	
COP9 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 3 (COPS3)	2	AF031647		+	+			+	
COP9 homolog (HCOP9)	2	U51205	B	+	+	+	+	+	
COP11 protein, homolog of s. cerevisiae SEC23p (SEC23A)	4	X97064		+	+				
copine I (CPNE1)	2	U83246	B	+	+		+		
copine I (CPNE1) (low score)	1	U83246							
coproporphyrinogen oxidase (coproporphyrin, harderoporphyrin) (CPO)	1	D16611			+		+	+	
core-binding factor, beta subunit (CBFB)	1	L20298		+					

coronin	22	X89109	T, W	+	+		+		
coronin (low match)	1	U34690							
coronin (non-exact, 71%)	1	X89109							
cot (cancer Osaka thyroid) oncogene (COT)	1	D14497	+	+	+	+		+	
cryptochrome 1 (photolyase-like) (CRY1)	1	D84657		+	+			+	
CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1 (CTDP1)	1	AF081287		+	+	+		+	
C-terminal binding protein 1 (CTBP1)	1	U37408	B	+	+		+		
C-terminal binding protein 2 (CTBP2)	2	AF016507		+	+		+		
CUG triplet repeat, RNA- binding protein 1 (CUGBP1)	3	U63289		+	+	+		+	
cullin 1 (CUL1)	3	U58087		+	+	+		+	
cullin 3 (CUL3)	2	U58089		+	+	+		+	
cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1)	1	M74099	B	+					
cyclin D2 (CCND2)	2	D13639		+	+	+		+	
cyclin D3 (CCND3)	5	M92287	B, T lymphoma		+		+		
cyclin G1 (CNNG1)	1	D78341	B	+	+			+	
cyclin I	3	D50310	B	+			+		
cyclin T2 (CNNT2)	1	AF048732	B, T lymphoma	B					
cyclin-dependent kinase 2 (CDK2)	1	X62071							
cyclin-dependent kinase inhibitor (p27Kip1)	1	S76986							
cyclin-dependent kinase inhibitor 1A (p21, Cip1)	2	S67388	+	+	+	+	+	+	

(CDKN1A)									
CYP2D7-CYP2D6 intergenic region (partial)	1	X90926							
cystatin B (stefin B) (CSTB)	1	L03558			+		+	+	
cysteine and glycine-rich protein 3 (cardiac LIM protein) (CSRP3)	5	L54057			+				
cytidine deaminase (CDA)	2	L27943					+		
cytochrome b	1	AF042500							
cytochrome b (CYTB) (isolate Aus5)	1	AF042518							
cytochrome b(-245) beta chain N-terminal region (X- linked granulomatous disease gene)	2	X05895							
cytochrome b-245, beta polypeptide (chronic granulomatous disease) (CYBB)	2	X04011	+			+		+	
cytochrome C	1	P00001							
cytochrome c oxidase subunit IV (COX4)	1	U90915	T	+	+		+	+	
cytochrome c oxidase subunit Vb (COX5B)	2	M59250					+		
cytochrome c oxidase subunit VII-related protein (COX7RP)	6	AB007618	+	+	+	+		+	
cytokine suppressive anti- inflammatory drug binding protein 1 (p38 MAP kinase) (CSBP1)	1	L35263	lymphocyte	+	+		+		
Cytoplasmic antiproteinase=38 kda intracellular serine proteinase inhibitor	1	S69272			+				
cytotoxic granule- associated RNA-binding protein p40-TIA-1	1	S70114							
D123 (D123)	1	D14878	+	+		+		+	

D2-2	1	AF019226							
D38	1	X74802							
damage-specific DNA binding protein 1 (127kD) (DDB1)	2	AJ002955	+	+	+	+	+	+	
DCHT (low match)	1	AF017635							
DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1 (DDXBP1)	1	U78524		+	+	+	+	+	
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide (72KD) (P72)	2	U59321	T	+	+		+	+	
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1)	1	X70649		+	+			+	
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15 (DDX15)	2	AB001636							
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16 (DDX16)	2	AB011149	+	+	+	+		+	
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 (DDX3)	3	U50553	+	+	+	+		+	
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD) (DDX5)	37	X15729	+	+	+	+		+	
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD) (DDX5) (low match)	1	AF015812							
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6)	2	D17532	+	+					
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase, 54kD) (DDX8)	1	D50487		+	+	+		+	
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II;	3	L13848	+	+	+	+		+	

leukophysin) (DDX9)									
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y chromosome (DBY)	1	AF000985		+	+		+		
Death associated protein 3 (DAP3)	2	X83544	+	+	+	+	+	+	
death effector domain-containing protein (DEDD)	1	AF083236		+	+	+		+	
death-associated protein 6 (DAXX)	2	AF039136		+	+	+		+	
dedicator of cyto-kinesis 2 (DOCK2)	4	D86964	+	+		+		+	
defender against cell death 1 (DAD1)	1	D15057			+		+	+	
Defensin, alpha 1, myeloid-related sequence (DEFA1)	4	L12690				+	+	+	
DEK gene (D6S231E)	1	X64229	B		+		+		
delta sleep inducing peptide, immunoreactor (DSIPI)	4	Z50781	+	+	+	+		+	
dendritic cell protein (GA17)	3	AF064603	+	+	+	+		+	
deoxycytidine kinase (DCK)	1	M60527							
deoxyribonuclease II, lysosomal (DNASE2)	3	AB004574							
DGS-I	2	L77566		+					
diacylglycerol kinase	3	D16440							
diacylglycerol kinase alpha (DAGK1) (clone 24)	3	AF064771		+					
diacylglycerol kinase alpha (DAGK1) (clone 24) (low match)	1	AF064771							
diaphanous (Drosophila, homolog) 1 (DIAPH1)	1	AF051782	B, monocyte stimulated	+	+		+	+	
diaphorase (NADH) (cytochrome b-5 reductase) (DIA1)	1	Y09501	+	+	+	+	+	+	

differentiated Embryo Chondrocyte expressed gene 1 (DEC1)	1	AB004066		+			+	+	
differentiated Embryo Chondrocyte expressed gene 1 (DEC1) (low match)	1	AB004066							
differentiation antigen CD20	1	L23415							
DiGeorge syndrome critical region gene 2 (DGCR2)	1	X84076		+	+			+	
dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD)	2	J03620		+			+	+	
dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) (DLAT)	1	Y00978	B	+			+		
dihydropyrimidinase-like 2 (DPYSL2)	1	D78013		+	+		+	+	
dinG gene	1	Y10571							
diphtheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 2 (DPH2L2)	3	AF053003	B	+	+		+	+	
disintegrin-protease (non-exact 72%)	1	Y13323							
DJ-1 protein	2	AF021819	+	+	+	+		+	
Dmx-like 1 (DMXL1)	1	AJ005821	+		+	+			
DNA (cytosine-5)-methyltransferase 1 (DNMT1)	3	X63692	T activated, lymphoma	+			+	+	
DNA fragmentation factor, 40 kD, beta subunit (DFFB)	1	AF064019							
DNA fragmentation factor, 45 kD, alpha subunit	2	U91985	T	+	+			+	

(DFFA)									
DNA mismatch repair protein (hMLH1)	1	U17840							
DNA segment on chromosome X (unique) 648 expressed sequence	3	M64241	+	+	+	+	+	+	high in many libraries
DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis (D5S346))	3	M73547		+	+	+		+	
DNA-damage-inducible transcript 1 (DDIT1) (low match)	1	L24498							
DnaJ protein	1	AJ001309							
DnaJ protein	1	AJ001309							
docking protein 2, 56kD (DOK2)	1	AF034970							
dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST)	1	D89060	+	+	+	+	+	+	activated T cell
dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit (DPM1)	1	D86198	T activated	+	+		+		
down-regulated by activation (immunoglobulin superfamily) (DORA)	1	AJ223183					+		
down-regulated in adenoma DRA (low match)	1	P40879							
D-type cyclin-interacting protein 1 (DIP1)	1	AF082569	B				+	+	
dual specificity phosphatase 1 (DUSP1)	4	X68277	+	+	+	+	+	+	
dual specificity phosphatase 11 (RNA/RNP complex 1-interacting) (dusp11)	1	AF023917	+	+	+	+		+	
dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-	1	L05147		+	+		+	+	

related) (DUSP3)									
dual specificity phosphatase 6 (DUSP6)	6	X93920	+	+	+	+	+	+	
dynactin 1 (p150, Glued (Drosophila) homolog) (DYTN1)	3	X98801							
dynactin 1 (p150, Glued (Drosophila) homolog) (DYTN1) (low match)	1	X98801	B	+	+				
dynamain 2 (DNM2)	1	L36983							
dynamitin (dynactin complex 50 kD subunit) (DCTN-50) (non-exact 88%)	1	U50733							
dynein, axonemal, heavy polypeptide 17-like (non-exact, 57%aa)	1	X99947							
dynein, cytoplasmic, light intermediate polypeptide 2 (DNCL12)	1	AF035812	B	+	+			+	
dynein, cytoplasmic, light intermediate polypeptide 2 (DNCL12) (non-exact, 69%)	1	AF035812							
dyskeratosis congenita 1, dyskerin (DKC1)	1	U59151	B	+			+	+	
dystonia 1, torsion (autosomal dominant) (DYT1)	1	AF007871		+	+	+		+	
dystrobrevin, beta (DTNB)	1	AF022728		+					
dystrophia myotonica-containing WD repeat motif (DMWD)	1	L19267		+	+		+	+	
dystrophia myotonica-protein kinase (DMPK)	1	L08835	+	+	+			+	
dystrophin (muscular dystrophy, Duchenne and Becker types) (DMD) (low match, 59%aa)	1	X14298							
E1B-55kDa-associated protein	1	AJ007509	W	+	+		+	+	

E2F transcription factor 3 (E2F3)	2	D38550		+	+	+	+	+	
E2F transcription factor 4, p107/p130-binding (E2F4)	1	X86096	B	+			+		
E2F transcription factor 5, p130-binding (E2F5)	2	U15642	+	+		+		+	
E74-like factor 1 (ets domain transcription factor) (ELF1)	1	M82882	B		+		+	+	
E74-like factor 4 (ets domain transcription factor) (ELF4)	3	U32645		+	+			+	
E74-like factor 4 (ets domain transcription factor) (ELF4) (non-exact, 71%)	1	U32645							
early development regulator 2 (homolog of polyhomeotic 2) (EDR2)	4	U89278	+	+	+	+		+	
EBV induced G-protein coupled receptor (EBI2)	1	L08177	W						
ecotropic viral integration site 2B (EVI2B)	3	M60830		+		+			
ectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1)	1	J04456						+	
EGF-like-domain, multiple 4 (EGFL4)	1	AB011541							
eIF-2-associated p67 homolog	3	U13261	B	+				+	
elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN) (low match)	1	M24782		+	+				
elav-type RNA-binding protein (ETR-3)	3	U69546							
electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II) (ETFA)	2	J04058		+					
ELK3, ETS-domain protein (SRF accessory protein 2)	2	Z36715			+			+	

(ELK3)									
elongation factor 1-beta	1	L26404							
elongation factor Ts (mitochondrial protein)	1	AF110399							
elongation factor Tu- nuclear encoded mitochondrial	1	X84694							
eMDC II protein	1	AJ242015.1							
ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p80/85 src substrate) (EMS1)	1	M98343		+	+		+	+	
endogenous retroviral element HC2	1	Z70664							
endosulfine alpha (ENSA)	1	X99906	T	+					
endothelial differentiation, sphingolipid G-protein- coupled receptor, 1 (EDG1)	2	M31210		+	+	+		+	
endothelial differentiation, sphingolipid G-protein- coupled receptor, 1 (EDG1) (low match 66%)	1	M31210							
endothelial monocyte- activating polypeptide (EMAPII)	1	U10117	+	+	+	+		+	
enolase 1, (alpha) (ENO1)	12	M14328	+	+	+	+	+	+	
enolase 2, (gamma, neuronal) (ENO2)	1	X51956		+					
enolase-alpha	1	D28437							
enoyl Coenzyme A hydratase 1, peroxisomal (ECH1)	2	U16660							
enoyl Coenzyme A hydratase, short chain, 1, mitochondrial (ECHS1)	1	D13900	+	+	+	+	+	+	
ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (SHORT CHAIN ENOYL-COA	1	P30084							

HYDRATASE) (SCEH) (ENOYL-COA HYDRATASE 1) (low match, non-exact 56%)									
epidermal growth factor receptor pathway substrate 15 (EPS15)	2	U07707		+		+		+	
EPIDIDYMAL SECRETORY PROTEIN E1 PRECURSOR (EPI-1) (HE1) (EPIDIDYMAL SECRETORY PROTEIN 14.6) (ESP14.6)	2	Q15668							
epithelial membrane protein 3 (EMP3)	1	U87947	+	+	+	+		+	
Epoxide hydrolase 1, microsomal (xenobiotic) (EPHX1)	1	L29766						+	only
ERCC2 (=L47234)	1	X52221							
ERF-2	3	U07802	+	+	+	+		+	high in gall bladder
ERp28 protein	1	X94910	+	+	+	+		+	
erythrocyte membrane protein	2	M81635							
erythroleukemic cells K562	2	L25343							
EST (Hs.189509)	2	U24166							
estrogen receptor-related protein (hERRa1)	1	L38487							
ESTs, Highly similar to ADENYLOSUCCINATE SYNTHETASE	1	X66503	B, T	+	+				
ESTs, Moderately similar to cysteine-rich fibroblast growth factor receptor	1	U28811	+	+	+	+		+	
ET binding factor 1 (SBF1)	1	U93181	+	+				+	
ets domain protein ERF	1	U15655	+	+	+	+		+	
eukaryotic translation elongation factor 1 alpha 1 (EEF1A1)	326	X03558	T	+	+			+	

eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) (low match)	1	X03558							
eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) (low match)	1	X03558							
eukaryotic translation elongation factor 1 beta 2 (EEF1B2)	5	X60489	+	+	+	+		+	
eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D)	1	Z21507	+	+	+	+	+	+	
eukaryotic translation elongation factor 1 gamma (EEF1G)	31	Z11531							
eukaryotic translation elongation factor 2 (EEF2)	2	X51466		+				+	
eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD) (EIF2S1)	1	J02645							
eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD) (EIF2S2)	1	M29536							
eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD) (EIF2S3)	3	L19161		+	+				
eukaryotic translation initiation factor 3, subunit 10 (theta, 150/170kD) (EIF3S10)	2	U78311							
eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD) (EIF3S2)	3	U36764	+	+	+	+	+	+	high in white blood cells
eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) (EIF3S3)	6	U54559	+	+	+	+		+	high in spleen
eukaryotic translation initiation factor 3, subunit 4 (delta, 44kD) (EIF3S4)	9	AF020833		+	+	+		+	
eukaryotic translation initiation factor 3, subunit 6 (48kD) (EIF3S6)	4	U94175	+	+	+	+		+	high in bladder

eukaryotic translation initiation factor 3, subunit 6 (EIF3S6)	1	U62962		+	+	+		+	Highly represented (1.4833 pct) in library 36 human gall bladder
eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67kD) (EIF3S7)	3	U54558	+	+	+	+		+	
eukaryotic translation initiation factor 3, subunit 8, 110KD (EIF3S8)	5	U46025	+	+	+	+	+	+	high in testis
eukaryotic translation initiation factor 4 gamma, 1 (EIF4G)	1	AF012088							
eukaryotic translation initiation factor 4 gamma, 1 (EIF4G) (low match)	1	AF012088							
eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1)	2	D12686							
eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2)	6	U73824	+	+	+	+	+	+	
eukaryotic translation initiation factor 4 gamma, 2 (EIFG2)	2	U76111	+	+	+	+	+	+	
eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1)	29	D13748							
eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2)	11	D30655	+	+	+	+	+	+	
eukaryotic translation initiation factor 4B (EIF4B)	18	X55733	+	+	+	+		+	
eukaryotic translation initiation factor 4E (EIF4E)	1	P06730							
Eukaryotic translation initiation factor 4E binding protein 2 (EIF4EBP2)	3	L36056	T, B	+				+	+
eukaryotic translation initiation factor 4H (EIF4H)	2	Q15056							
eukaryotic translation initiation factor 5 (EIF5)	2	U49436	+	+	+	+	+	+	

eukaryotic translation termination factor 1 (ETF1)	2	U90176	+	+	+	+		+	
EV12 protein	1	M55266		+					
Ewing sarcoma breakpoint region 1 (EWSR1)	1	X66899	+	+	+	+		+	
EWS/FLI1 activated transcript 2 homolog (EAT-2)	2	AF020264							
EWS-E1A-F chimeric protein	1	U35622							
excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence) (ERCC1)	1	M28650	+	+	+	+		+	
excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome)) (ERCC5)	1	X69978		+	+	+		+	
exostoses (multiple)-like 3 (EXTL3)	1	AF001690		+	+	+		+	
F11	1	X77744				+			
F1-ATPase beta subunit (F-1 beta)	2	X03559							
Fanconi anaemia group A	2	Z83095							
Fanconi anemia, complementation group A (FANCA)	1	X99226	+	+	+	+			
far upstream element (FUSE) binding protein 1 (FUBP1)	2	U05040	+		+			+	
farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPS)	1	J05262	+	+	+	+		+	

farnesyl-diphosphate farnesyltransferase 1 (FDFT1)	2	X69141	+	+	+	+	+	+	
farnesyltransferase, CAAX box, beta (FNTB)	2	L00635		+	+				
Fas ligand (gene and promoter region)	1	AF044583							
Fas-ligand associated factor 1	1	U70667							
fatty-acid-Coenzyme A ligase, long-chain 1 (FACL1)	4	D10040	+	+	+	+	+	+	
Fc fragment of IgA, receptor for (FCAR)	1	X54150							
Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide (FCER1G)	1	M33195	+	+	+	+		+	
Fc fragment of IgE, low affinity II, receptor for (CD23A) (FCER2)	2	X04772	+	+					
Fc fragment of IgG, low affinity IIa, receptor for (CD32)	6	M31932	+	+	+	+	+	+	
Fc fragment of IgG, low affinity IIa, receptor for (CD32) (FCGR2A)	1	X62572	+	+	+	+	+	+	
Fc fragment of IgG, low affinity IIIa, receptor for (CD16) (FCGR3A)	34	X07934	+	+	+	+		+	
Fc fragment of IgG, receptor, transporter, alpha (FCGRT)	3	U12255		+	+	+	+	+	high in many libraries
fc-fgr	1	Z13983							
Fc-gamma-receptorIIIB (FCGR3B)	2	M90746							
feline sarcoma (Snyder- Theilen) viral (v- fes)/Fujinami avian sarcoma (PRCII) viral (v- fps) oncogene homolog(FES) c-fes/fps)	3	X06292							

female sterile homeotic-related gene 1 (mouse homolog) (FSRG1)	2	X96670	+	+	+	+		+	
ferritin L-chain	9	Y09188							
ferritin, heavy polypeptide 1 (FTH1)	4	M11146	+	+	+	+	+	+	
fertilin alpha pseudogene	1	Y09232							
fetal Alzheimer antigen (FALZ)	2	U05237		+					
fetal Ig heavy chain variable region	1	M34024							
fibrillarin (FBL)	1	X56597	+	+	+	+	+	+	
fibrinogen-like protein 2 (T49)	3	Z36531				+			
fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome) syndrome, Pfeiffer syndrome, Jackson-Weiss) (FGFR2)	1	M35718	+	+	+	+	+	+	
ficolin (collagen/fibrinogen domain-containing) 1 (FCN1)	19	D83920				+		+	
filamin A, alpha (actin-binding protein-280) (FLNA)	2	X53416							
filamin B, beta (actin-binding protein-278) (FLNB)	1	AF043045		+	+		+		
Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30 (FAU)	2	X65923	+	+	+	+	+	+	Highly represented in intraepithelial neoplasia and invasive prostate tumor
FK-506 binding protein	1	M80199	+	+	+	+		+	
FK506-binding protein 1A (12kD) (FKBP1A)	2	M34539							
FK506-binding protein 1B	1	M92423		+		+		+	

(12.6 kD) (FKBP1B)									
FK506-binding protein 5 (FKBP5)	4	U71321		+	+	+		+	
Flightless I (Drosophila) homolog (FLII)	3	U80184		+					
Flightless I (Drosophila) homolog (FLII) (low match)	1	U80184							
FLN29 (FLN29)	2	AB007447		+		+		+	
flotillin 2 (FLOT2)	5	M60922	+	+	+	+	+	+	
folate receptor 2 (fetal) (FOLR2)	1	AF000380		+	+	+		+	
forkhead, (Drosophila) homolog (rhabdomyosarcoma) like 1 (FKHRL1)	1	AF032886	+	+		+		+	
Formyl peptide receptor 1 (FPR1)	9	M60627	+	+	+	+		+	
formyl peptide receptor-like 1 (FPRL1)	1	M84562							Found only in libraries from placenta
formyl peptide receptor-like 1 (FPRL1) (low score)	1	M84562							
fragile X mental retardation 1 (FMR1)	1	L29074	+	+		+		+	
fragile X mental retardation, autosomal homolog 1 (FXR1)	1	U25165	+	+	+	+			
Friend leukemia virus integration 1 (FLI1)	3	M93255	+	+					
fructose-bisphosphatase 1 (FBP1)	1	D26054				+		+	
FSHD-associated repeat DNA, proximal region	1	U85056							
fucose-1-phosphate guanylyltransferase (FPGT)	1	AF017445		+	+	+			
full length insert cDNA clone ZA78A09	1	AF086122							

full length insert cDNA YP07G10	1	AF075061							
fumarate hydratase (FH)	1	U59309		+	+	+		+	
FUS (low match)	1	X99006							
FYN-binding protein (FYB- 120/130) (FYB)	16	U93049		+		+			
G alpha interacting protein. (GAIP) (low score)	1	X91809							
G protein beta subunit-like protein 12.3	2	D28398							
G protein-coupled receptor 64 (HE6) (non-exact 59%)	1	X81892				+			
G protein-coupled receptor kinase 6 (GPRK6)	2	L16862	+	+	+			+	
G1 to S phase transition 1 (GSPT1)	2	X17644		+	+	+	+	+	
GA-binding protein transcription factor, beta subunit 2 (47kD) (GABPB2)	1	D13316		+	+	+	+	+	
galactose-1-phosphate uridylyltransferase (GALT)	2	M60091							
galactosidase, beta 1 (GLB1)	3	M27508		+			+	+	
galactosyltransferase (=X13223 N- acetylglucosamide-(beta 1- 4)-galactosyltransferase)	1	M13701							
galectin-9 isoform	1	AB006782	+			+		+	
gamma2-adaptin (G2AD)	1	AF068706	+	+		+		+	
gamma-actin	2	M37130							
gamma-aminobutyric acid (GABA) B receptor 1 (GABBR1)	2	AJ012187		+	+			+	
GATA-binding protein 2 (GATA2)	1	M68891				+		+	
GATA-binding protein 3 (GATA3)	1	M69106			+	+		+	

GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 1 (GCN5L1)	3	D64007	+	+	+	+		+	
GDP dissociation inhibitor 1 (GDI1)	1	D45021	+	+	+	+		+	high in adult brain
GDP dissociation inhibitor 2 (GDI2)	4	Y13286							
GDS-related protein (HKE1.5)	4	U68142	+	+	+	+		+	
gelsolin (amyloidosis, Finnish type) (GSN)	3	X04412		+	+	+	+	+	
general transcription factor II, I (GTF2I)	4	Y14946	+	+	+	+	+	+	
general transcription factor II, i, pseudogene 1 (GTF2IP1)	1	AF038968	+	+	+	+	+	+	high in fetal brain
general transcription factor IIF, polypeptide 1 (74kD subunit) (GTF2F1)	4	X64037	+	+	+	+		+	
general transcription factor IIH, polypeptide 3 (34kD subunit) (GTF2H3)	2	Z30093	B, T						
general transcription factor IIH, polypeptide 4 (52kD subunit) (GTF2H4)	3	Y07595		+		+		+	
general transcription factor IIIA (GTF3A)	1	U14134	+	+		+		+	
general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD) (GTF3C1)	1	U02619		+		+			
general transcription factor IIIC, polypeptide 2 (beta subunit, 110kD) (GTF3C2)	3	D13636	+	+	+	+	+	+	
germline immunoglobulin heavy chain (IGHV@)	1	L06612							
germline immunoglobulin heavy chain, variable region	1	X92236							
germline immunoglobulin heavy chain, variable region, (21-2)	1	X92343							

GLE1 (yeast homolog)-like, RNA export mediator (GLE1L)	1	AF058922		+	+				
glia maturation factor, beta (GMFB)	1	AB001106	+	+		+		+	
glioma-associated oncogene homolog (zinc finger protein) (GLI)	1	X07384							
glioma-associated oncogene homolog (zinc finger protein) (GLI) (low score)	1	X07384							
globin, alpha 2	1	V00516							
glucocorticoid receptor (=M69104)	1	M32284							
glucocorticoid receptor (GRL)	2	U80947	+	+	+	+		+	
glucos phosphate isomerase (CONTAINS LARGE REPEAT)	1	L09105							
glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) (GNS)	1	Z12173	+						
glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) (GNS) (non-exact 56%)	1	Z12173							
glucose transporter-like protein-III (GLUT3)	1	M20681		+	+	+	+	+	
glucose transporter-like protein-III (GLUT3) (low match)	1	M20681							
glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II) (GAA)	1	Y00839	+	+		+		+	
glucosidase, beta; acid (includes glucosylceramidase) (GBA)	1	K02920	+	+	+	+		+	
glutamate dehydrogenase 1 (GLUD1)	1	M20867		+	+	+	+	+	

glutamate-ammonia ligase (glutamine synthase) (GLUL)	12	X59834	+	+	+	+		+	
glutamate-ammonia ligase (glutamine synthase) (GLUL) (low score)	1	Y00387							
glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC)	1	M90656				+			
glutamine cyclotransferase	1	X71125		+	+				
glutamine-fructose-6-phosphate transaminase 1 (GFPT1)	1	M90516		+		+			
glutaminyI-tRNA synthetase	1	X72396							
glutaminyI-tRNA synthetase (QARS)	6	X76013	+	+	+	+		+	
glutamyl-prolyl-tRNA synthetase (EPRS)	1	X54326							
glutathione peroxidase 1 (GPX1)	2	M21304	+	+	+	+	+	+	
glutathione peroxidase 4 (phospholipid hydroperoxidase) (GPX4)	1	X71973	+	+	+	+		+	
glutathione S-transferase pi (GSTP1)	1	U30897		+	+	+	+	+	
glutathione S-transferase subunit 13 homolog	1	AF070657							
glyceraldehyde-3-phosphate dehydrogenase (GAPD)	12	J02642					+		
glycogenin (GYG)	1	U31525		+	+	+		+	
glycophorin C (Gerbich blood group) (GYPC)	1	X12496		+	+	+		+	
glycoprotein M6B (GPM6B)	1	U45955		+	+				
glycyl-tRNA synthetase (GARS)	1	U09587		+	+	+		+	

glyoxalase I (lactoyl glutathione lyase) (GLYI)	1	L07837	+	+	+	+		+	
golgi autoantigen, golgin subfamily a, 1 (GOLGA1)	1	U51587		+		+			
golgi autoantigen, golgin subfamily a, 2 (GOLGA2) (non-exact, 70%)	1	L06147							
golgi autoantigen, golgin subfamily a, 4 (GOLGA4)	1	U31906							
golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1 (GOLGB1)	1	X75304		+	+	+		+	
gp25L2 protein	4	X90872							
grancalcin	8	M81637		+	+	+			
granulin (GRN)	16	X62320	+	+	+	+		+	
granulin (GRN) (low match)	1	X62320							
Granulysin (NKG5)	5	M85276	+					+	
granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA)	1	M18737	+	+	+	+		+	
GRB2-related adaptor protein (GRAP)	1	U52518	T only						
Grb2-related adaptor protein 2 (GRAP2)	1	AF090456	T				+		
GRO1 oncogene (melanoma growth stimulating activity, alpha) (GRO1)	1	X54489				+		+	
growth arrest and DNA-damage-inducible gene (GADD153)	1	S40706							
growth arrest-specific 7 (GAS7)	4	AB007854		+	+				
growth factor receptor-bound protein 2 (GRB2)	1	X62852	B	+			+	+	
GS1 (protein of unknown	1	M86934		+	+	+			

function)									
GS3955	4	D87119		+	+	+		+	
GTP binding protein 1 (GTPBP1)	1	U87964		+	+	+			
GTP binding protein similar to <i>S. cerevisiae</i> HBS1 (HBS1)	1	U87791		+	+	+		+	
GTPase activating protein-like (GAPL)	1	AB011110		+	+	+		+	high fetal brain
GTP-binding protein (low match)	1	Z49068							
GTP-binding protein G(K), alpha subunit (=G(I) ALPHA-3)(=GTP-binding regulatory protein Gi alpha-3 chain)	1	P08754							
Gu protein (GURDB)	2	U41387	+		+	+		+	
guanine nucleotide binding protein	1								
guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 (GNAI2)	4	J03004	+	+	+	+		+	
guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3 (GNAI3)	7	M20597	+	+	+	+		+	
guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1 (GNAS1)	2	X04409	B, T	+			+	+	
guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 2 (GNAT2)	1	Z18859							
guanine nucleotide binding protein (G protein), beta 5 (GNB5)	2	AF017656		+	+	+		+	
guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1)	5	M36430	+	+	+	+	+	+	

guanine nucleotide binding protein (G protein), q polypeptide (GNAQ)	2	AF011496		+	+	+			
guanine nucleotide binding protein-like 1 (GNL1)	1	L25665	+	+	+	+		+	
guanine nucleotide exchange factor	1	L13857	+	+	+	+			
guanine nucleotide regulatory factor (LFP40)	1	X15610	+	+	+	+		+	
guanine nucleotide regulatory factor (LFP40)	1	U72206	+	+	+	+		+	
GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3 (P205) (RECEPTOR OF ACTIVATED PROTEIN KINASE C 1) (RACK1)	1	P25388							
GUANINE-MONOPHOSPHATE SYNTHETASE (GMPS)	1	U10860			+				
guanosine monophosphate reductase (GMPR) (non-exact, 72%)	1	M24470							
guanosine-diphosphatase like protein	1	AF016032							
guanylate binding protein 1, interferon-inducible, 67kD (GBP1)	2	M55542		+	+	+	+	+	
guanylate binding protein 2, interferon-inducible (GBP2)	6	M55543	+	+	+	+		+	
H2A histone family, member C (H2AFC)	1	Z83742							
H2A histone family, member Y (H2AY)	2	AF041483	+	+	+	+		+	
H2B histone family, member L (H2BFL)	2	Z80783	+	+	+	+	+	+	high in adrenal gland tumor
h2-calponin	1	D86059							
H-2K binding factor-2	1	L08904		+	+	+		+	
H3 histone family, member K (H3FK)	1	Z83735							

H3 histone, family 3A (H3F3A)	7	M11353	+	+	+	+		+	high in ovary
H3 histone, family 3B (H3.3B) (H3F3B)	15	Z48950	+	+	+	+		+	high in endothelial cells
hbc647	1	U68494		+	+	+	+		
heat shock 27kD protein 1 (HSPB1)	1	U12404		+	+		+	+	
heat shock 40kD protein 1 (HSPF1)	4	D85429	+	+	+	+	+	+	high in testis
heat shock 60kD protein 1 (chaperonin) (HSPD1)	3	M22382	+	+	+	+	+	+	
heat shock 70kD protein 1 (HSPA1A)	7	M59828	+	+	+	+	+	+	high in activated T cells
heat shock 70kD protein 5 (glucose-regulated protein, 78kD) (HSPA5)	13	X87949		+	+		+		
heat shock 70kD protein 6 (HSP70B') (HSPA6)	4	X51757	+	+	+				
heat shock 70kD protein 9B (mortalin-2) (HSPA9B)	2	L15189		+	+	+	+	+	
HEAT SHOCK COGNATE 71 KD PROTEIN	1	P11142							
heat shock factor binding protein 1 (HSBP1)	2	AF068754							
heat shock protein 90	13	M27024	+	+	+	+	+	+	high in many libraries
heat shock protein, DNAJ-like 2 (HSJ2)	1	D13388		+	+		+	+	
Hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (HERC1)	1	U50078		+	+	+			
hect domain and RLD 2 (HERC2)	1	AB002391	+	+	+	+		+	
helicase-like protein (HLP)	1	X98378	+	+		+		+	
helix-loop-helix protein HE47 (E2A)	1	M65214						+	

hematopoietic cell-specific Lyn substrate 1 (HCLS1)	18	X16663	+		+	+		+	
heme oxygenase (decycling) 1 (HMOX1)	1	X06985		+		+	+	+	
HEMOGLOBIN ALPHA CHAIN	1	P19015							
hemoglobin beta (beta globin)	5	AF117710							
hemoglobin, alpha 1 (HBA1)	301	V00491			+		+	+	
hemoglobin, alpha 1 (HBA1) (low match)	1	V00491							
hemoglobin, alpha 1 (low match)	1	V00493							
hemoglobin, alpha 1 (non- exact, 76%)	1	J00153							
hemoglobin, alpha 1 (non- exact, 82%)	1	V00493							
hemoglobin, beta (HBB)	129	V00497	+	+	+	+	+	+	high in many libraries
hemoglobin, beta (HBB) (low match)	1	V00497							
hemoglobin, beta (HBB) (low match)	1	L48220							
hemokine (C-X-C motif), receptor 4 (fusin) (CXCR4)	1	D10924	+	+	+	+		+	
hemopoietic cell kinase (HCK)	5	M16591				+		+	
hepatitis C-associated microtubular aggregate protein p44	2	D28908							
hepatoma-derived growth factor	1	D16431	+	+	+	+		+	
Hermansky-Pudlak syndrome (HPS)	2	U65676							
HERV-E integrase (non- exact 76%aa)	1	AF026246							
heterogeneous nuclear protein similar to rat helix	2	S63912		+	+	+		+	

destabilizing protein (FBRNP)									
heterogeneous nuclear ribonucleoprotein (C1/C2) (HNRPC)	4	M16342							
heterogeneous nuclear ribonucleoprotein A/B (HNRPAB)	1	M65028	+	+	+	+	+	+	
heterogeneous nuclear ribonucleoprotein A1 (HNRPA1)	20	X12671	+	+	+	+	+	+	High in alveolar rhabdomyosarcoma
heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1)	3	M29064	+	+	+	+	+	+	High in activated T cell, fetal brain
heterogeneous nuclear ribonucleoprotein D (hnRNP D)	2	D55673	+	+	+	+	+	+	
heterogeneous nuclear ribonucleoprotein D-like (HNRPDL)	5	D89092	+	+	+	+	+	+	
heterogeneous nuclear ribonucleoprotein F (HNRPF)	1	L28010	+	+	+	+		+	
heterogeneous nuclear ribonucleoprotein F (HNRPF) (83%)	1	L28010							
heterogeneous nuclear ribonucleoprotein G (HNRPG)	2	Z23064		+	+	+		+	
heterogeneous nuclear ribonucleoprotein H (HNRPH) (FTP-3)	3	P55795							
heterogeneous nuclear ribonucleoprotein H (HNRPH) (low match)	1	P31943							
heterogeneous nuclear ribonucleoprotein H1 (H) (HNRPH1)	2	L22009	+	+	+	+		+	
heterogeneous nuclear ribonucleoprotein K (HNRPK)	21	S74678	+	+	+	+	+	+	
heterogeneous nuclear ribonucleoprotein R	1	AF000364		+	+	+	+	+	

(HNRPR)									
heterogeneous nuclear ribonucleoprotein U (scaffold, attachment factor A) (HNRPU)	3	X65488	+	+	+	+	+	+	
hexokinase 1 (HK1)	2	X66957		+	+	+		+	
hexokinase 2 (HK2)	3	Z46376	+	+	+	+		+	
hexokinase 3 (HK3)	2	U51333							
hexosaminidase A (alpha polypeptide) (HEXA)	1	S62047							
HGMP07I gene for olfactory receptor	2	U76377							
High density lipoprotein binding protein (HDLBP)	2	M64098	+	+	+	+	+	+	
high-mobility group (nonhistone chromosomal) protein 1 (HMG1)	5	X12597	+	+	+	+	+	+	
high-mobility group (nonhistone chromosomal) protein 1 (HMG1) (non-exact 60%)	1	D63874							
High-mobility group (nonhistone chromosomal) protein 17 (HMG17)	2	M12623	+	+	+	+		+	
high-mobility group (nonhistone chromosomal) protein 2 (HMG2)	2	M83665	+	+	+	+	+	+	
high-mobility group (nonhistone chromosomal) protein isoforms I and Y	2	L17131	+	+	+		+	+	
high-risk humanpapilloma viruses E6 oncoproteins targeted protein E6TP1 beta (=AB007900 KIAA0440)	1	AF090990.1							
histidine ammonia-lyase (HAL)	1	D16626			+, only				
histidyl-tRNA synthetase (HARS)	2	Z11518	+	+	+	+	+	+	
histocompatibility antigen	1	U31372							

(HLA-Cw3), class I									
histone deacetylase 1 (HDAC)	4	U50079	+	+	+	+		+	
histone deacetylase 1 (HDAC1)	2	D50405	+	+	+	+		+	
histone deacetylase 5 (NY-CO-9)	1	AF039691		+	+				
HK2 gene for hexokinase II	1	Z46362							
HL9 monocyte inhibitory receptor precursor	2	U91928				+			
HLA class I heavy chain (HLA-Cw*1701)	1								
HLA class I locus C heavy chain	1	X58536							
HLA class II SB 4-beta chain	1	X03022							
HLA class III region containing NOTCH4 gene	1	U89335	+	+	+	+		+	
HLA-A	1	Z72423							
HLA-A	2	AJ006020							
HLA-A*7402	1	AJ223060							
HLA-A11	1	U02934							
HLA-B	2	X75953							
HLA-B	1	X83401							
HLA-B	1	X78426							
HLA-B associated transcript-1 (D6S81E)	1	Z37166	+	+	+	+	+	+	
HLA-B associated transcript-2 (D6S51E)	2	M33509	+	+	+	+			
HLA-B*1529	4	D44501							
HLA-Bw72 antigen	119	L09736	+	+	+	+	+	+	high in many libraries
HLA-C gene (HLA-Cw*0701 allele)	1	D83957							

HLA-Cw*0701	9	Z46810							
HLA-Cw*0801	1	D64151							
HLA-Cw*1203	1	D64146							
HLA-DC classII histocompatibility antigens alpha-chain (=K01160)	2	X00370							
HLA-DR alpha-chain	17	M60333	+	+	+	+	+	+	high in spleen
HLA-F (leukocyte antigen F)	3	X17093			+	+		+	
HMG box containing protein 1	3	AF019214							
hMLH1 (=U83845)	1	AB017806.1							
Hmob33	3	Y14155							
HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 1 (HRMT1L1)	2	U80213	+	+	+	+		+	
hnRNP C1/C2	2	D28382							
homeobox (=X58250 Mouse homeo box protein, put. transcription factor involved in embryogenesis and hematopoiesis)	1	M60721							
homeobox protein (HLX1) (=M60721)	1	U14326							
homeodomain-interacting protein kinase 3 (HIPK3)	1	AF004849	+		+	+		+	
homolog of Drosophila past (PAST)	2	AF001434	+	+	+	+		+	
homolog of yeast (S. cerevisiae) ufd2 (UFD2)	3	D50916		+	+	+		+	
HPV16 E1 protein binding protein	1	U96131		+	+			+	
HRIHFB2157	1	AB015344		+	+			+	
HRX-like protein (=AF010403 ALR)	1	Y08836							

hsc70 gene for 71 kd heat shock cognate protein	3	Y00371							
HSPC012	1	AF077036.1							
HSPC021	1	AF077207.1							
HsPex13p	1	U71374							
htra2-beta-2	1	U87836	+	+	+	+		+	
HU-K4	1	U60644							
hunc18b2	1	U63533		+	+	+		+	
HUNKI	1	Y12059	+	+		+	+	+	
huntingtin-interacting protein HYPA/FBP11 (HYPA)	1	AF049528							
hVps41p (HVPS41)	1	U87309							
hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit (HADHA)	1	U04627		+	+		+		
hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB)	1	D16481	+	+	+	+		+	
hydroxysteroid (17-beta) dehydrogenase 1 (HSD17B1)	1	U34879		+			+		
hypothetical protein	1								
hypothetical protein (AL008729) (dJ257A7.2)	1								
hypothetical protein (CIT987SK_2A8_1 chromosome 8)	1	U96629							
hypothetical protein (clone 24640)	1	AF055004							

hypothetical protein (clone ICRFp507G2490).	1	Z70222							
hypothetical protein (dJ1042K10.4) (non-exact 76%)	1	AL022238							
hypothetical protein (dJ465N24.1 similar to predicted yeast and worm proteins)	2	AL031432							
hypothetical protein (dJ487J7.1.1)	2	AL008730							
hypothetical protein (dJ753P9.2)	2	AL023653							
hypothetical protein (DKFZp586l111)	1	AL050131.1							
hypothetical protein (J257A7.2)	1	AL008729							
hypothetical protein (KIAA0440) (=AF026504 R.norvegicus SPA-1 like protein)	1	AB007900							
hypothetical protein (L1H 3' region)	1								
hypothetical protein (S164)	1	P49756							
hypothetical protein (similar to thrombospondin) (non-exact 56%)	1	AF109907							
hypothetical protein 3	1								
hypothetical protein B (HSU47926) (non-exact, 56%)	1	U47926							
hypothetical protein from BCRA2 region (CG005)	3	U50532	+	+	+	+		+	
hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) (HIF1A)	1	AF050115							
Ia-associated invariant gamma-chain (clones lambda-y (1,2,3))	1	M13555							

iduronate 2-sulfatase (Hunter syndrome) (IDS)	2	M58342	+	+	+	+		+	
Ig heavy chain V region (=D11016)	1	L20779							
Ig heavy chain variable region	2	M34024							
Ig heavy chain variable region (VH4DJ) (clone T14.4)	1	Z75378							
Ig heavy chain variable region (VH4DJ) (clone T22.18)	1	Z75392							
Ig J chain	1	M12378							
Ig kappa	1	S49007							
IG kappa light chain variable region A20	1	X63398							
Ig kappa light chain, V- and J-region (=X59315)	1	D90158							
Ig lambda light chain variable region (26-34)ITIIIF120)	1	Z85052							
Ig mu-chain VDJ4-region	1	M16949							
Ig rearranged anti-myelin kappa-chain (V-J4-region, hybridoma AE6-5)	1	M29469							
Ig rearranged H-chain mRNA V-region	2	M97920							
Ig rearranged light-chain V region (=D90158)	1	M74020							
IGF-II mRNA-binding protein 3 (KOC1) (non-exact, 75%)	1	U97188	+	+	+				
IgG Fc binding protein (FC(GAMMA)BP)	1	D84239	+	+		+		+	
IgG heavy chain variable region (vH26)	1	M83136							
IgM heavy chain (C mu, membrane exons)	1	X14939							

IkB kinase-beta (IKK-beta)	1	AF029684							
IL-1 receptor type II	1	U14177							
IL2-inducible T-cell kinase (ITK)	2	S65186							
immediate early protein (ETR101)	1	M62831	+		+	+		+	
immunoglobulin light chain (lambda)	1	D87018							
Immunoglobulin (CD79A) binding protein 1 (IGBP1)	1	Y08915	B, T	+	+		+		
immunoglobulin C (mu) and C (delta) heavy chain (=K02878)	2	X57331							
immunoglobulin G Fc receptor IIIB	1	Z46223							
immunoglobulin gamma 3 (Gm marker) (IGHG3)	3	Y14737	+			+		+	high in many libraries
immunoglobulin gamma heavy chain variable region (=X61011)	1	Z66542							
immunoglobulin heavy chain (VI-3B)	1	X62109							
immunoglobulin heavy chain J region	1	X86356							
immunoglobulin heavy chain J region, B1 haplotype	2	X86355							
immunoglobulin heavy chain variable region (IGH) (clone 21u-48)	1	AF062126							
immunoglobulin heavy chain variable region (IGH) (clone 23u-1)	1	AF062212							
immunoglobulin heavy chain variable region V1-18 (IGHV@) (=X60503)	2	M99641							
immunoglobulin heavy chain variable region V3-43 (IGHV@)	2	M99672							

immunoglobulin heavy chain variable region V3-7 (IGHV@)	3	M99649							
immunoglobulin IgH heavy chain Fd fragment	1	U07986							
immunoglobulin kappa light chain	1	X58081							
immunoglobulin kappa light chain V-segment A27	1	X12686							
immunoglobulin light chain	1	D86990							
immunoglobulin light chain (low match)	1	D86996							
immunoglobulin light chain variable region (lambda IIIb subgroup) from IgM rheumatoid factor	1	L29157							
immunoglobulin M heavy chain V region=anti-lipid A antibody	1	S50735							
immunoglobulin mu (IGHM)	9	X57086	+	+		+		+	
immunoglobulin mu binding protein 2 (IGHMBP2)	1	L24544	T	+			+		
immunoglobulin superfamily, member 2 (IGSF2)	1	Z33642							
Immunoglobulin VH mRNA (487 bp) (=M99652 immunoglobulin heavy chain variable region V3-11 (IGHV@))	1	X61013							
imogen 38 (IMOGEN38)	1	Z68747		+	+	+		+	
IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1)	1	J05272	+	+	+	+			
IMP (inosine monophosphate) dehydrogenase 2 (IMPDH2)	2	L39210	+	+	+	+		+	
inc finger protein 151 (pHZ-67) (ZNF151)	1	Y09723	+	+	+	+		+	

inc finger protein, C2H2, rapidly turned over (ZNF20)	1	AF011573		+	+				
inducible poly(A)-binding protein (IPABP)	1	U33818	+	+	+	+		+	
inducible poly(A)-binding protein (IPABP) (low match)	1	U33818							
inducible protein (Hs.80313)	2	L47738	+	+	+	+		+	
inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (ID2)	4	M97796	+	+	+	+	+	+	
inhibitor of kappa light, polypeptide gene enhancer in B-cells, kinase complex-associated protein (IKBKAP)	2	AF044195							
inositol 1,3,4-trisphosphate 5/6-kinase	1	U51336	+	+	+	+	+	+	
inositol 1,4,5 trisphosphate receptor type 1 (ITPR1)	1	U23850		+	+	+			
inositol 1,4,5-trisphosphate 3-kinase B (ITPKB)	2	X57206	B	+	+		+		
inositol monophosphatase	1	S38980							
inositol polyphosphate-5-phosphatase, 145kD (INPP5D)	2	U84400	+	+	+	+		+	
Ins(1,3,4,5)P4-binding protein	1	X89399		+				+	
insulin-like growth factor 2 receptor (IGF2R)	5	Y00285	+	+	+	+		+	
integral membrane protein 1 (ITM1)	1	L38961			+	+		+	
integral membrane protein 2C (ITM2C)	1	AF038953	T		+		+	+	
integral membrane protein Tmp21-I (p23)	3	U61734	+	+	+	+	+	+	
integrin beta 4 binding protein (ITGB4BP)	2	AF047433			+			+	

integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41B) (ITGA2B)	3	M34480		+			+		
integrin, alpha 5 (fibronectin receptor, alpha polypeptide) (ITGA5)	4	X06256	+	+	+		+	+	
integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL)	6	Y00796							
integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide) (ITGAM)	1	M18044							
integrin, alpha X (antigen CD11C (p150), alpha polypeptide) (ITGAX)	1	M81695	+	+				+	
integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2 MSK12) (ITGB1)	2	X07979							
integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	32	M15395	+	+		+		+	
integrin, beta 7 (ITGB7)	1	M68892	+						
Integrin-linked kinase (ILK)	1	U40282	+	+	+	+		+	
intercellular adhesion molecule 1 (CD54), human rhinovirus receptor (ICAM1)	1	J03132	+			+	+	+	
intercellular adhesion molecule 2 (ICAM2)	1	X15606	+	+	+	+		+	
intercellular adhesion molecule 3 (ICAM3)	6	X69819	+					+	
intercellular adhesion molecule 4, Landsteiner-Wiener blood group (ICAM4)	1	L27670						+	

Interferon consensus sequence binding protein 1 (ICSBP1)	1	M91196	W, T lymphoma						
Interferon consensus sequence binding protein 1 (ICSBP1) (low match)	1	M91196							
interferon regulatory factor 2 (IRF2)	4	X15949	+	+	+	+			
interferon regulatory factor1 (IRF1)	4	L05072	+	+	+	+		+	
interferon regulatory factor5 (IRF5)	1	U51127	+	+		+			
interferon, gamma-inducible protein 16 (IFI16)	2	M63838	+	+	+	+		+	
interferon, gamma-inducible protein 30 (IFI30)	9	J03909	+	+		+		+	
INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1) (non-exact 62%)	1	P32455							
interferon-induced protein 17 (IFI17)	3	X84958		+	+	+		+	
interferon-induced protein 54 (IFI54)	5	M14660							
interferon-inducible (1-8D)	5	X57351	T		+		+	+	
interferon-inducible (1-8U)	1	X57352			+		+	+	
interferon-related developmental regulator 1 (IFRD1)	5	Y10313		+	+			+	
interferon-stimulated transcription factor 3, gamma (48kD) (ISGF3G)	2	M87503		+		+		+	
interleukin 1 receptor, type II (IL1R2)	1	U64094				+			
Interleukin 10 receptor, beta (I.10RB)	1	U08988	T activated		+			+	
interleukin 12 receptor, beta 1 (IL12RB1)	2	U03187	+						only found in T cell

interleukin 13 receptor, alpha 1 (IL13RA1)	2	Y09328		+	+	+	+	+	
interleukin 16 (lymphocyte chemoattractant factor) (IL16)	6	U82972		+					
interleukin 18 receptor 1 (IL18R1)	1	U43672							
interleukin 2 receptor, beta (IL2RB)	9	M26062							
interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG)	6	D11086	+		+			+	
interleukin 4 receptor (IL4R)	3	X52425	+	+		+		+	
interleukin 6 receptor (IL6R)	5	X12830		+				+	
interleukin 6 signal transducer (gp130, oncostatin M receptor) (IL6ST)	1	M57230							
interleukin 7 receptor (IL7R)	14	M29696	+					+	
interleukin 7 receptor (IL7R) (low match)	1	AF043123							
interleukin 8 (IL8)	8	Y00787	+		+		+		High in activated T cells, bone and pancreatic islets
interleukin 8 receptor alpha (IL8RA)	11	L19591							
interleukin 8 receptor, beta (IL8RB)	14	M94582							
interleukin enhancer binding factor 2, 45kD (ILF2)	3	U10323	+	+	+	+	+	+	high in uterus
interleukin enhancer binding factor 3, 90kD (ILF3)	2	U10324							
interleukin-1 receptor-associated kinase 1 (IRAK1)	2	L76191		+	+	+		+	

interleukin-1 receptor-associated kinase 1 (low match)	1	U52112							
interleukin-10 receptor, alpha (IL10RA)	5	U00672	+	+	+	+			
interleukin-11 receptor, alpha (IL11RA)	7	Z38102		+	+				
INTERLEUKIN-14 PRECURSOR (IL-14) (HIGH MOLECULAR WEIGHT B-CELL GROWTH FACTOR) (HMW-BCGF) (non-exact 46%)	1	P40222							
intestinal carboxylesterase; liver carboxylesterase-2 (ICE)	1	U60553		+			+		
inversin protein (non-exact 52%)	1	AF084367							
IQ motif containing GTPase activating protein 1 (IQGAP1)	6	L33075							
IQ motif containing GTPase activating protein 2 (IQGAP2)	1	U51903		+		+			
isocitrate dehydrogenase 1 (NADP+), soluble (IDH1)	1	AF020038	+	+	+	+	+	+	
isocitrate dehydrogenase 2 (NADP+), mitochondrial (IDH2)	2	X69433	+	+	+	+	+	+	
isocitrate dehydrogenase 3 (NAD+) alpha (IDH3A)	2	U07681			+				
isocitrate dehydrogenase 3 (NAD+) gamma (IDH3G)	1	Z68907	+	+	+	+		+	
isolate Aus3 cytochrome b (CYTB)	1	AF042516							
isolate TzCCR5-179 CCR5 receptor (CCR5)	1	AF011524							
isopentenyl-diphosphate delta isomerase (IDI1)	5	X17025	+	+	+	+		+	
Janus kinase 1 (a protein)	4	M64174	+	+	+	+		+	

tyrosine kinase) (JAK1)									
Janus kinase 2 (a protein tyrosine kinase) (JAK2)	1	AF005216							
Jk-recombination signal binding protein (RBPJK)	2	L07876							
JM1 protein	1	AJ005890		+		+			
jumonji (mouse) homolog (JMJ)	1	U57592		+	+	+		+	
jun D proto-oncogene (JUND)	1	X51346	+	+	+	+		+	
jun dimerization protein	1	AF111167							only found in germ
junction plakoglobin (JUP)	1	M23410		+	+	+		+	
kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4)) (KAI1)	1	U20770	+	+	+	+	+	+	
karyopherin (importin) beta 1 (KPNB1)	2	L39793	+	+	+	+	+	+	
karyopherin (importin) beta 2 (KPNB2)	1	U72395	+	+	+	+			
karyopherin alpha 1 (importin alpha 5) (KPNA1)	1	S75295	+	+	+		+		
karyopherin alpha 2 (RAG cohort 1, importin alpha 1) (DPNA2)	1	U09559							
karyopherin alpha 3 (importin alpha 4) (KPNA3)	1	D89618		+			+		
karyopherin alpha 4 (KPNA4)	1	M17887		+	+				
Katanin (80 kDa) (KAT)	1	AF052432		+	+	+		+	
KE03 protein	2	AF064604							
Kelch-like ECH-associated protein 1 (KIAA0132) (66%aa)	1	D50922							

Keratin 8 (KRT8)	1	X74929		+	+	+	+	+	
ketoheokinase (fructokinase) (KHK)	1	X78678		+		+	+		
KIAA0001 (KIAA0001) (72% aa)	1	Q15391							
KIAA0001 (KIAA0001) (76% aa)	1	Q15391							
KIAA0001 (KIAA0001) (non-exact 72%)	1	Q15391							
KIAA0002 (KIAA0002)	5	D13627		+	+	+		+	
KIAA0005 (KIAA0005)	4	D13630		+	+	+		+	
KIAA0010 (KIAA0010)	1	D13635		+				+	
KIAA0016 (KIAA0016)	1	D13641	+	+	+	+		+	
KIAA0017 (KIAA0017)	2	D87686							
KIAA0022 (KIAA0022)	2	D14664		+	+	+			
KIAA0023 (KIAA0023)	1	D14689		+					
KIAA0024 (KIAA0024)	1	D14694	+	+	+	+		+	
KIAA0025 (KIAA0025)	1	D14695		+	+	+	+	+	
KIAA0026 (KIAA0026)	2	D14812		+	+	+		+	
KIAA0027	1	D25217		+					
KIAA0032 (KIAA0032)	2	D25215		+	+	+			
KIAA0040 (KIAA0040)	1	D25539	+	+	+	+		+	
KIAA0050 (KIAA0050)	4	D26069							
KIAA0053 (KIAA0053)	17	D29642	+		+	+			
KIAA0057 (KIAA0057)	1	D31762	+	+	+	+	+	+	high in fetal lung
KIAA0058 (KIAA0058)	11	D31767	+	+	+	+		+	
KIAA0063 (KIAA0063)	3	D31884	+	+	+	+		+	
KIAA0064 (KIAA0064)	1	D31764	+	+	+	+		+	
KIAA0066	1	D31886	+	+	+	+		+	

KIAA0068	1	D38549		+	+	+	+	+	
KIAA0073	3	D38552		+	+	+		+	
KIAA0081	2	D42039		+		+		+	
KIAA0084	2	D42043	+	+	+	+		+	
KIAA0085	26	U30498	+	+	+	+	+	+	
KIAA0088	3	D42041	+	+	+	+	+	+	
KIAA0090	2	D42044	+	+	+	+	+	+	
KIAA0092 (KIAA0092)	1	D42054		+	+	+		+	
KIAA0094	3	D42084			+	+			
KIAA0095 (KIAA0095)	1	D42085							
KIAA0096	1	D43636	+	+	+	+		+	
KIAA0097 (KIAA0097)	1	X92474	T	+	+		+		
KIAA0099 (KIAA0099)	3	D43951	+	+	+	+	+	+	
KIAA0102 (KIAA0102)	2	D14658		+		+	+	+	
KIAA0105	1	D14661	B	+			+	+	
KIAA0120	2	P37802							
KIAA0120 (non-exact, 65%)	1	M83106							
KIAA0121 (KIAA0121)	1	D50911	+	+	+	+		+	
KIAA0123	1	D21064		+	+	+		+	
KIAA0128	1	D50918	+	+	+	+		+	
KIAA0129 (KIAA0129)	1	D50919	+	+	+	+			
KIAA0130 (KIAA0130)	1	AF055995		+	+	+			
KIAA0136	2	D50926							
KIAA0137 (KIAA0137)	1	AB004885		+	+	+		+	
KIAA0140 (KIAA0140)	1	D50930	+	+		+		+	
KIAA0141 (KIAA0141)	3	D50931							

KIAA0144 (KIAA0144)	3	D63478	+	+	+	+		+	
KIAA0144 (KIAA0144) (low match)	1	D63478							
KIAA0144 (non-exact 61%)	1	Q14157							
KIAA0144 (non-exact 65%)	1	Q14157							
KIAA0146	2	D63480		+	+	+		+	
KIAA0148 (KIAA0148)	1	D63482		+				+	
KIAA0154	2	D63876	+	+	+	+		+	
KIAA0156	1	D63879		+	+	+		+	
KIAA0160	2	D63881							
KIAA0161 (KIAA0161)	1	D79983	+	+		+			
KIAA0164 (KIAA0164)	3	D79986							
KIAA0167 (KIAA0167)	1	D79989		+					
KIAA0168 (KIAA0168)	3	D79990		+	+	+		+	
KIAA0169	3	D79991							
KIAA0171 (KIAA0171)	3	D79993		+	+	+		+	
KIAA0174 (KIAA0174)	7	D79996	+	+	+	+		+	
KIAA0179	2	D80001		+	+	+		+	
KIAA0181	1	D80003		+	+	+		+	
KIAA0183	4	D80005	+	+	+	+	+	+	
KIAA0184	1	D80006	+	+	+	+		+	
KIAA0191 (72% aa)	1	D83776							
KIAA0191 (non-exact 77%)	1								
KIAA0193 (KIAA0193)	1	D83777	+	+	+	+		+	
KIAA0200 (KIAA0200)	1	D83785		+	+	+		+	
KIAA0210 (KIAA0210)	3	D86965							
KIAA0217	2	D86971	+	+	+	+		+	

KIAA0219	2	U77700		+	+	+		+	
KIAA0222 (KIAA0222)	1	D86975							
KIAA0223	2	D86976							
KIAA0229	1	D86982	+	+					
KIAA0232 (KIAA0232)	1	D86985		+	+	+		+	
KIAA0233 (KIAA0233)	1	D87071							
KIAA0235	2	D87078	+	+	+	+			
KIAA0239	1	D87076	+	+					
KIAA0239 (non-exact 80%)	1	D87076							
KIAA0240	1	D87077							
KIAA0242	4	D87684	+	+	+	+	+	+	
KIAA0248	2	D87435		+	+	+		+	
KIAA0249 (KIAA0249)	3	D87436	+	+	+	+		+	
KIAA0253	5	D87442	+	+	+	+	+	+	
KIAA0254 (KIAA0254)	1	D87443		+	+	+			
KIAA0255(KIAA0255)	4	D87444		+	+	+		+	
KIAA0262 (KIAA0262)	3	D87451	+	+	+	+		+	
KIAA0263 (KIAA0263)	1	D87452	+	+	+	+		+	
KIAA0264	3	D87453		+	+	+		+	
KIAA0268	1	D87742	+	+		+		+	
KIAA0269	1	Q92558							
KIAA0275 (KIAA0275)	13	D87465	+	+		+		+	
KIAA0304 (KIAA0304)	2	AB002302	+	+	+	+	+	+	
KIAA0308	2	AB002306		+	+			+	
KIAA0310 (KIAA0310)	1	AB002308		+	+	+		+	
KIAA0314 (=U96635 M.musculus ubiquitin protein ligase Nedd-4)	3	AB002312							

KIAA0315 (KIAA0315)	4	AB002313		+	+	+	+	+	
KIAA0325 (=L08505 R.norvegicus cytoplasmic dynein heavy chain (MAP 1C))	2	AB002323							
KIAA0329 (KIAA0329)	1	AB002327		+	+	+		+	
KIAA0330	1	AB002328	+	+	+			+	
KIAA0332	1	AB002330		+	+	+		+	
KIAA0333	2	AB002331		+	+	+	+	+	
KIAA0336 (KIAA0336)	3	AB002334	+	+	+	+		+	
KIAA0336 (KIAA0336) (low match)	1	AB002334							
KIAA0342 (KIAA0342)	1	AB002340		+	+			+	
KIAA0344 (KIAA0344)	2	AB002342				+		+	
KIAA0354 (KIAA0354)	1	AB002352	+	+	+	+		+	
KIAA0365 (KIAA0365)	3	AB002363	+	+	+	+	+	+	
KIAA0370	6	AB002368		+	+	+	+	+	
KIAA0372 (KIAA0372)	1	AB002370							
KIAA0373 (KIAA0373)	1	AB002371		+		+			
KIAA0375 (KIAA0375)	1	AB002373		+		+			
KIAA0377 (KIAA0377)	1	AB002375		+		+	+		
KIAA0379	1	AB002377				+			
KIAA0379 (non-exact, 65%)	1	AB002377							
KIAA0380 (KIAA0380)	1	AB002378	+	+		+		+	
KIAA0380 (KIAA0380) (60%aa)	1	AB002378							
KIAA0382 (KIAA0382)	2	AB002380		+	+	+		+	
KIAA0383	1	AB002381							
KIAA0386 (KIAA0386)	5	AB002384							

KIAA0392	1	AB002390							
KIAA0397 (KIAA0397)	4	AB007857		+	+	+	+	+	
KIAA0403	3	AB007863							
KIAA0404	1	AB007864		+		+			
KIAA0409	1	AB007869		+		+			
KIAA0421	1	AB007881	+	+	+			+	
KIAA0424 (non-exact 82%)	1	AB007884							
KIAA0428 (KIAA0428)	9	Y13829							
KIAA0429 (KIAA0429)	2	AB007889	+	+	+	+		+	
KIAA0430 (KIAA0430)	2	AB007890							only in ovary
KIAA0432 (KIAA0432)	2	U86753	T	+	+				
KIAA0435 (KIAA0435)	1	AB007895							
KIAA0438 (KIAA0438)	1	AB007898		+	+	+		+	
KIAA0447 (KIAA0447)	3	AB007916	+	+	+	+		+	
KIAA0449	1	AB007918		+				+	
KIAA0456	1	AB007925		+	+	+		+	
KIAA0458 (KIAA0458)	1	AB007927							
KIAA0462	1	AB007931	+	+	+	+		+	
KIAA0465	1	AB007934		+	+	+	+	+	
KIAA0476 (KIAA0476)	1	AB007945		+	+	+			
KIAA0489	1	AB007958							
KIAA0494 (KIAA0494)	1	AB007963	+	+	+	+		+	
KIAA0515	1	AB011087	+	+	+	+		+	
KIAA0521	3	AB011093	+	+				+	
KIAA0525	1	AB011097		+		+			
KIAA0530	1	AB011102		+	+	+			
KIAA0532	1	AB011104	+	+	+	+		+	

KIAA0537 (KIAA0537)	1	AB011109							
KIAA0540	1	AB011112	+	+	+	+		+	
KIAA0543	1	AB011115			+	+		+	
KIAA0544	1	AB011116		+	+	+		+	
KIAA0549	2	AB011121		+	+	+		+	
KIAA0551	2	AB011123		+				+	
KIAA0554	8	AB011126		+	+	+		+	
KIAA0561	1	AB011133		+		+			
KIAA0562 (KIAA0562)	1	AB011134							
KIAA0563 (KIAA0563)	1	AB011135							
KIAA0569 (KIAA0569)	2	AB011141		+	+	+		+	
KIAA0571 (KIAA0571)	2	AB011143		+	+	+			
KIAA0573	1	AB011145		+		+		+	
KIAA0576	1	AB011148							
KIAA0580	1	AB011152							
KIAA0584	1	AB011156		+					
KIAA0592	3	AB011164	+	+	+	+		+	
KIAA0596	1	AB011168		+	+				
KIAA0598 (KIAA0598)	1	AB011170		+	+	+			
KIAA0608	1	AB011180			+	+			
KIAA0614	2	AB014514	+	+	+	+		+	
KIAA0615 (KIAA0615)	1	AB014515							
KIAA0621	1	AB014521		+	+			+	
KIAA0648	1	AB014548		+	+	+		+	
KIAA0652 (KIAA0652)	1	AB014552	+	+	+	+		+	
KIAA0668	1	AB014568							
KIAA0669	1	AB014569							

KIAA0671 (KIAA0671)	1	AB014571			+	+		+	
KIAA0675 (KIAA0675)	1	AB014575		+		+	+		
KIAA0676	1	AB014576		+	+	+		+	
KIAA0677 (KIAA0677)	2	AB014577		+	+	+	+	+	
KIAA0678	1	AB014578	+	+	+	+		+	
KIAA0679	6	AB014579		+	+	+		+	
KIAA0680 (KIAA0680)	1	AB014580							
KIAA0692	1	AB014592	+	+	+	+		+	
KIAA0697	1	AB014597							
KIAA0699	1	AB014599	+	+	+	+		+	
KIAA0700	1	AB014600		+	+	+		+	
KIAA0737 (KIAA0737)	3	AF014837	+	+	+	+		+	
KIAA0748 (KIAA0748)	2	AB018291		+					
KIAA0763 (KIAA0763)	2	AB018306	+	+	+	+		+	
KIAA0769 (KIAA0769)	2	AB018312		+	+	+		+	
KIAA0782	1	AB018325	+	+		+			high in BPH stroma
KIAA0796	1	AB018339		+	+	+		+	
KIAA0798 (KIAA0798)	1	AB018341							
KIAA0823	1	AB020630							
KIAA0854	1	AB020661	+	+	+	+		+	
KIAA0856	1	AB020663		+	+	+		+	
KIAA0860	1	AB020667		+		+			
KIAA0862	1	AF054828		+	+	+			
KIAA0871 (non-exact 88%)	1	AB020678							
KIAA0873	1	AB020680		+	+	+		+	
KIAA0892	1	AB020699	+	+	+	+		+	
KIAA0906	1	AB020713	+	+	+	+		+	

KIAA0991	1	AB023208.1								
killer cell lectin-like receptor subfamily B, member 1 (KLRB1)	1	U11276			+	+			+	
killer cell lectin-like receptor subfamily C, member 4 (KLRC4)	1	U96846								
kinectin 1 (kinesin receptor) (KTN1)	1	D13629								
kinesin family member 5B (KIF5B)	2	X65873		+	+	+				
kinesin-like DNA binding protein	1	AB017430	+	+	+	+			+	
Krueppel-related DNA-binding protein (TF6) (low match)	1	M61869								
Kruppel related gene (clone pHKR1RS)	1	M20675								
Kruppel-like zinc finger protein Zf9	3	U51869	+	+	+	+	+	+		
Kruppel-like zinc finger protein Zf9 (non-exact 76%)	1	U44975		+	+			+	+	
kruppel-type zinc finger protein, ZK1	1	AB011414.1								
L apoferritin	3	X03742								
lactate dehydrogenase A (LDHA)	3	X02152		+	+	+	+	+		
lactate dehydrogenase A (LDHA) (non-exact, 81%)	1	X02152								
lactate dehydrogenase B (LDHB)	6	X13794	+	+	+	+	+	+		high in fetal lung fibroblast
lactotransferrin (LTF)	1	U07643	+			+			+	high in bone marrow
laminin binding protein (low score)	1	D28372								
laminin receptor 1 (67kD); Ribosomal protein SA (LAMR1)	20	X15005	+	+	+	+	+	+		high in many libraries

laminin receptor homolog {3' region}	1	S35960							
laminin, gamma 1 (formerly LAMB2) (LAMC1)	2	J03202	+	+	+			+	
latent transforming growth factor beta binding protein 1 (LTBP1)	2	M34057		+	+	+		+	
LAZ3/BCL6 (=Z79582;D28522/4)	1	Z79581							
LDLC	2	Z34975	+	+	+	+		+	
lecithin-cholesterol acyltransferase (LCAT) (non-exact, 66%)	1	M17959							
lectin, galactoside-binding, soluble, 2 (galectin 2) (LGALS2)	1	M87842				+			
lectin, galactoside-binding, soluble, 3 binding protein (galectin 6 binding protein) (LGALS3BP)	1	L13210	+	+	+	+		+	
leucine rich repeat (in FLII) interacting protein 1 (LRRFIP1)	5	AJ223075	+	+	+	+	+	+	
leucocyte immunoglobulin- like receptor-5 (LIR-5)	2	AF072099				+			
leucocyte immunoglobulin- like receptor-6a (LIR-6)	7	AF025530							
leucocyte immunoglobulin- like receptor-7 (LIR-7)	2	U82275		+					only found in CNS
leukemia virus receptor 1 (GLVR1)	1	L20859	+	+	+	+		+	
leukocyte adhesion protein p150,95 alpha subunit	1	M29484							
leukocyte antigen, HLA-A2	3	Y13267							
leukocyte immunoglobulin- like receptor (MIR-10)	3	AF025528		+					
leukocyte tyrosine kinase (LTK)	1	X60702	+						found only in blood

leukocyte-associated Ig-like receptor 1 (LIAR1)	3	AF013249				+			
leukotriene A4 hydrolase (LTA4H)	6	J03459	+	+	+	+	+	+	
leupaxin (LDPL)	2	AF062075	+			+		+	
ligase I, DNA, ATP-dependent (LIG1)	1	M36067	B, T	+	+		+	+	
LIM and SH3 protein 1 (LASP1)	2	X82456	+	+	+	+	+	+	
LIM domain kinase 2 (LIMK2)	2	AC002073	+	+	+	+		+	
line-1 protein	1								
Line-1 repeat mRNA with 2 open reading frames	1	U93566	+	+	+	+	+	+	
Line-1 repeat with 2 open reading frames	1	M22332	+	+	+	+	+	+	high in gastric tumor
LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	1	P08547							
lipase A, lysosomal acid, cholesterol esterase (Wolman disease) (LIPA)	4	X76488	+	+	+	+		+	
lipase, hormone-sensitive (LIPE)	1	L11706	+	+				+	
LMP7	1	L11045							
Lon protease-like protein (LONP)	2	X74215	+	+	+	+		+	
low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor) (LRP1)	2	AF058414					+		only in liver
low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1) (LRPAP1)	1	M63959		+	+		+	+	
low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-	1	M63959							

associated protein 1) (LRPAP1) (non-exact, 75%)									
low-affinity Fc-gamma receptor IIA	1	L08107							
LPS-induced TNF-alpha factor (PIG7)	9	AF010312	+	+	+	+	+	+	
Lst-1	1	U00921	+	+	+	+		+	
L-type amino acid transporter subunit LAT1	1	AF104032							
lung resistance-related protein (LRP)	1	X79882	+	+	+	+		+	
Lymphocyte antigen 75 (LY75)	1	AF011333	B						
lymphocyte antigen 9 (LY9)	2	L42621							
lymphocyte antigen HLA- B*4402 and HLA-B*5101	2	L42345							
lymphocyte cytosolic protein 1 (L-plastin) (LCP1)	42	J02923							
lymphocyte cytosolic protein 2 (SH2 domain- containing leukocyte protein of 76kD) (LCP2)	4	U20158	T lymphoma, T activated						
lymphocyte glycoprotein T1/Leu-1	2	X04391	+		+				
lymphocyte-specific protein 1 (LSP1)	16	M33552	+	+	+	+		+	
lymphocyte-specific protein tyrosine kinase (LCK)	7	M36881		+				+	
lymphoid phosphatase LyP1	1	AF001847							
lymphoid-restricted membrane protein (LRMP)	4	U10485	+		+	+			
lymphoid-specific SP100 homolog (LYSP100-A)	1	U36500						+	
lymphoma proprotein convertase (LPC)	2	U33849	+	+	+	+		+	

LYSOSOMAL PROTECTIVE PROTEIN PRECURSOR (CATHEPSIN A) (CARBOXYPEPTIDASE C)	1	P10619							
lysosomal-associated membrane protein 1 (LAMP1)	1	J04182	+	+	+	+	+	+	
Lysosomal-associated membrane protein 2 (LAMP2)	1	J04183		+	+	+	+	+	
lysozyme (renal amyloidosis) (LYZ)	39	M19045	+	+	+	+		+	
lysyl-tRNA synthetase (KARS)	2	D32053	+	+	+	+		+	
M phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) (MPP- 10)	1	X98494							
M1-type and M2-type pyruvate kinase	2	X56494							
m6A methyltransferase (MT-A70)	7	AF014837	+	+		+			
mab-21 (C. elegans)-like 1 (MAB21L1)	1	U38810		+	+	+		+	
MacMarcks	1	X70326	+	+	+	+	+	+	
macrophage-associated antigen (MM130)	1	Z22968		+	+	+		+	
MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A) (MEF2A)	1	U49020		+	+	+		+	
MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C)	1	L08895		+	+	+		+	
major cytoplasmic tRNA- Val(IAC) (=M33940)	1	X17516							
major histocompatibility complex class I beta chain	1	M95531							

(HLA-B)									
major histocompatibility complex, class I, A (HLA-A)	41	Z93949	+	+	+	+		+	high in villous adenoma
major histocompatibility complex, class I, A (HLA-A) (low match)	1	Z72422							
major histocompatibility complex, class I, C (HAL-C)	82	M24097	+	+	+	+	+	+	
major histocompatibility complex, class I, E (HLA-E)	77	M20022	+	+	+	+		+	
major histocompatibility complex, class II, DM BETA (HLA-DMB)	2	U15085	+	+	+	+		+	
major histocompatibility complex, class II, DP beta 1 (HLA-DPB1)	10	M57466	+	+	+	+		+	
major histocompatibility complex, class II, DR beta 1 (HLA-DRB1)	9	V00522	+	+	+	+		+	
Major histocompatibility complex, class II, Y box-binding protein I; DNA-binding protein B (YB1)	2	M24070		+	+		+	+	
malate dehydrogenase 1, NAD (soluble) (mdh1)	1	D55654	+	+	+	+	+	+	
malate dehydrogenase 1, NAD (soluble) (MDH1)	3	D55654		+	+		+	+	
malonyl-CoA decarboxylase precursor	2	AF097832							
maltase-glucoamylase (mg)	1	AF016833				+			
manic fringe (Drosophila) homolog (MFNG)	1	U94352	+	+	+	+		+	
mannose phosphate isomerase (MPI)	1	X76057		+	+	+		+	
mannose phosphate isomerase (mpi)	2	X76057		+	+	+		+	
mannose-6-phosphate receptor (cation dependent) (M6PR)	3	X56253		+	+		+	+	

mannose-P-dolichol utilization defect 1 (MPDU1)	1	AF038961		+	+	+		+	
mannosidase, alpha B, lysosomal (MANB)	1	U60885		+		+	+	+	
mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT1)	1	M55621	+	+	+	+	+	+	
map 4q35 repeat region	1	AF064849							
MAP kinase-interacting serine/threonine kinase 1 (MKNK1)	2	AB000409		+	+	+	+	+	
MAP/ERK kinase kinase 3 (MEKK3)	5	U78876		+					
MAP/ERK kinase kinase 5 (MEKK5)	1	D84476		+	+		+		
MAP/microtubule affinity-regulating kinase 3 (MARK3)	4	M80359		+	+			+	
Marenostrin protein	1	Y14441							
MASL1	1	AB016816							
MAX dimerization protein (MAD)	3	L06895						+	
MaxiK potassium channel beta subunit	1	AF035046							
MBP-2 for MHC binding protein 2	1	X65644		+	+	+		+	
Meis (mouse) homolog 3 (MEIS3)	1	U68385		+	+	+		+	
melanoma-associated antigen p97 (melanotransferrin)	1	M12154							
membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) (MCP)	4	X59405		+	+	+		+	
membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen CA125)	4	D14696		+	+	+	+	+	

(M17S2)									
membrane metallo- endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME)	2	J03779	B		+	+	+	+	
membrane protein, palmitoylated 1 (55kD) (MPP1)	2	M64925		+	+	+	+	+	
meningioma expressed antigen (MGEA)	1	U94780				+			
meningioma-expressed antigen 11 (MEA11)	1	U73682	+	+		+	+		
Menkes Disease (ATP7A) putative Cu ⁺⁺ -transporting P-type ATPase	1	L06133		+					
metallothionein 2A (MT2A)	1	V00594		+	+	+	+	+	
metaxin 1 (MTX1)	1	U46920		+		+		+	
methionine adenosyltransferase II, alpha (MAT2A)	2	X68836	+	+	+	+		+	
methyl-CpG binding domain protein 1 (MBD1) (non-exact 59%aa)	1	Y10746							
methylene tetrahydrofolate dehydrogenase (NAD ⁺ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2)	2	X16396	+	+	+	+		+	
methylenetetrahydrofolate dehydrogenase (NADP ⁺ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase (MTHFD1)	1	J04031		+	+	+	+	+	
methyltransferase, putative	2	AJ224442							
MHC antigen (HLA-B) (=L42024)	1	U14943							
MHC class 1 region	2	AF055066							
MHC class I antigen (HLA-	1	U70863							

MHC class I histocompatibility antigen (HLA-B) (clone C21/14)	1	U06697							
MHC class I HLA B71	2	L07950							
MHC class I HLA-A (Aw33.1)	1	Flp							
MHC class I HLA-B	1	U18660							
MHC class I HLA-B (HLA-B-07ZEL allele) (=X86704)	1	U18661							
MHC class I HLA-B (HLA-B-08NR allele)	1	U28759							
MHC class I HLA-B*3512	1	L76094							
MHC class I HLA-B41 variant (=U17572)	3	U17572							
MHC class I HLA-B44.2 chain	1	M24038							
MHC class I HLA-B51-cd3.3	1	L41086							
MHC class I HLA-C allele	2	Z33459							
MHC class I HLA-Cw*0304 (=M84172; M99389)	1	D64150							
MHC class I HLA-Cw*0803	3	Z15144							
MHC class I HLA-Cw6	1	M28206							
MHC class I HLA-J antigen	1	L56139							
MHC class I lymphocyte antigen A2 (A2.1) variant DK1	1	M19670							
MHC class I mic-B antigen	1	X91625							
MHC class I polypeptide-related sequence A (MICA)	1	L14848				+			
MHC class I protein HLA-C heavy chain (C*0701new allele) (=AF017331)	1	U61274							
MHC class II DNA Sequence (clone A37G7-1C11)	1	L18885							

MHC class II DQ-alpha associated with DRw6, DQw1 protein	1	M16995	+		+	+		+	
MHC class II DQ-beta associated with DR2, DQw1 protein	2	M17564		+		+		+	
MHC class II HAL-DQ-LTR5 (DQ,w8) DNA fragment, long terminal repeat region	1	M33842							
MHC class II hla-dr alpha-chain (=J00197;M60334;K011171;J00194;M60333;X00274)	1	J00195							
MHC class II HLA-DRB1	1	AF007883							
MHC class II HLA-DRw11-beta-I chain (DRw11.3)	1	M21966							
MHC class II lymphocyte antigen (DPw4-beta-1)	1	M23907							
MHC CLASS II TRANSACTIVATOR CIITA (non-exact 57%)	1	P33076							
MHC HLA-E2.1 (=X87679)	1	M32507							
MHC HLA-E2.1 (alpha-2 domain) (low match)	1	M32507							
Mi-2 autoantigen 240 kDa protein (non-exact 84%)	1	U08379							
microsomal stress 70 protein ATPase core (stch)	1	U04735							
microtubule-associated protein 4 (MAP4)	1	U19727	+	+	+	+		+	
microtubule-associated protein 7 (MAP7)	1	X73882							
mineralocorticoid receptor (aldosterone receptor) (MLR)	2	M16801		+		+		+	
minichromosome maintenance deficient (S. cerevisiae) 3 (MCM31)	1	X62153		+	+	+		+	
minichromosome maintenance deficient (S.	1	AB011144		+	+	+		+	

cerevisiae) 3-associated protein (MCM3AP)									
minichromosome maintenance deficient (S. cerevisiae) 5 (cell division cycle 46) (MCM5)	2	X74795	+	+	+	+	+	+	
mitochondrial cytochrome b (CYTB)	1	AF042517							
mitochondrial 16S rRNA	11	Z70759							
mitochondrial ATP synthase (F1-ATPase) alpha subunit	2	X59066							
mitochondrial ATP synthase c subunit (P1 form)	1	X69907							
mitochondrial cytochrome b (CYTB)	6	AF042508							
mitochondrial cytochrome b small subunit of complex II	1	AB006202							
mitochondrial CYTOCHROME C OXIDASE POLYPEPTIDE I	1	P00395							
mitochondrial CYTOCHROME C OXIDASE POLYPEPTIDE II	1	P00403							
mitochondrial cytochrome C oxidase subunit II	2	P00403							
mitochondrial cytochrome oxidase subunit II (COII) (=U12692 Hsa4 mitochondrion cytochrome oxidase subunit II)	5	U12691							
mitochondrial DNA loop attachment sequences (clone LAS34)	1	X89763							
mitochondrial DNA polymerase accessory subunit precursor (MtPolB) nuclear gene encoding mitochondrial protein,	1	U94703		+					
mitochondrial DNA,	1	X93334							

complete genome									
mitochondrial genes for several tRNAs (Phe, Val, Leu) and 12S and 16S ribosomal RNAs.	8	V00710							
mitochondrial genes for tRNA (Phe) and 12S rRNA (fragment)	3	V00660							
mitochondrial inner membrane preprotein translocase Tim17a	1	AF106622							
mitochondrial isolate Afr7 cytochrome b(CYTB)	1	AF042503							
mitochondrial loop attachment sequence (clone LAS88)	1	X89843							
mitochondrial NADH dehydrogenase subunit 2 (ND2)	14	AF014893							
mitochondrial translational initiation factor 2 (MTIF2)	1	L34600		+	+	+		+	
mitochondrion cytochrome b	1	U09500							
mitogen inducible gene mig-2	1	Z24725		+	+	+		+	
mitogen inducible gene mig-2 (non-exact, 71%)	1	Z24725							
mitogen-activated protein kinase-activated protein kinase 3 (MAPKAPK3)	2	U43784		+	+	+		+	
MLN51	2	X80199		+	+	+	+	+	
MLN64 (=D38255 CAB1)	1	X80198	+	+	+	+			
moesin (MSN)	14	M69066	+	+	+	+		+	
monocytic leukaemia zinc finger protein (MOZ)	2	U47742		+	+	+		+	
MOP1 ()	2	U29165							
motor protein (Hs.78504)	2	D21094	+	+	+	+		+	

mouse double minute 2, human homolog of; p53-binding protein (MDM2)	1	U39736			+	+			
M-phase phosphoprotein 6 (MPP-6)	1	X98263		+	+	+		+	
M-phase phosphoprotein, mpp11	1	X98260							
MPS1	1	L20314							
Mr 110,000 antigen	2	D64154		+		+	+	+	
MRC OX-2, V-like region (=M17227)	1	X05324							
mu-adaptin-related protein-2; mu subunit of AP-4 (MU-ARP2)	1	Y08387							
multifunctional polypeptide similar to SAICAR synthetase and AIR carboxylase (ADE2H1)	1	X53793	+	+	+	+		+	
murine leukemia viral (bmi-1) oncogene homolog (BMI1)	1	L13689		+		+		+	
mutant (Daudi) beta2 - microglobulin	44	X07621							
mutated in colorectal cancers (MCC)	1	M62397		+	+			+	
myeloid cell leukemia sequence 1 (BCL2-related) (MCL1)	9	L08246	+	+	+	+	+	+	
myeloid cell nuclear differentiation antigen (MND4)	11	M81750	+					+	
myeloid differentiation primary response gene (88) (MYD88)	4	U70451		+	+	+		+	
myeloid leukemia factor 2 (MLF2)	3	U57342		+		+		+	
myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 7 (MLLT7)	8	U89867		+	+	+		+	

MYH9 (cellular myosin heavy chain)	1	M81105							
myomesin (M-protein) 2 (165kD) (MYOM2)	1	X69089							
myosin IE (MYO1E)	11	X98411		+		+			
myosin light chain kinase (MLCK)	1	U48959	+		+	+		+	
myosin phosphatase, target subunit 1 (MYPT1)	2	D87930		+	+	+		+	
myosin regulatory light chain (=U26162)	2	D50372							
myosin VIIa (low match 71)	1	U55208							
myosin, heavy polypeptide 9, non-muscle (MYH9)	3	M81105	+	+	+	+		+	
myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB)	6	X54304	+	+	+	+	+	+	
myosin-I beta	1	X98507	+	+	+	+		+	
myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L) (MACS)	1	D10522		+	+				
myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible protein p78) (MX1)	1	M30817	+	+	+	+		+	
myxovirus (influenza) resistance 2, homolog of murine (MX2)	3	M30818			+				
N-acetylgalactosaminidase, alpha- (NAGA)	2	M62783		+	+		+	+	
N-acetylglucosamine receptor 1 (thyroid) (NAGR1)	1	L03532		+	+	+		+	
NACP/alpha-synuclein	2	U46896							
N-acylaminoacyl-peptide hydrolase (APEH)	1	D38441		+	+		+	+	
N-acylsphingosine amidohydrolase (acid	11	U47674	+	+	+	+		+	

ceramidase) (ASAH)									
NAD ⁺ -specific isocitrate dehydrogenase beta subunit precursor (encoding mitochondrial protein)	1	U49283	+	+	+	+	+	+	
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13) (NDUFA5)	1	U53468.1	+	+	+	+	+	+	
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGDH) (NDUFB5)	1	AF047181		+	+	+	+	+	
NADH dehydrogenase (ubiquinone) Fe-S protein 2 (49kD) (NADH-coenzyme Q eductase) (NDUFS2)	1	AF050640		+	+	+	+	+	
NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD) (NDUFV2)	1	M22538			+	+	+	+	
NADH:ubiquinone dehydrogenase 51 kDa subunit (NDUFV1)	2	AF053070	+	+	+	+	+	+	
NADH-CYTOCHROME B5 REDUCTASE (B5R) (50%aa)	1	P00387							
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1	1	P03886							
Nardilysin (N-arginine dibasic convertase) (NRD1)	2	U64898	+	+	+	+		+	
nascent-polypeptide-associated complex alpha polypeptide (NACA)	5	X80909		+	+		+	+	
natural killer cell group 7 sequence (NKG7)	8	S69115				+		+	
natural killer cell transcript 4 (NK4)	19	M32011	+						
natural killer-associated transcript 3 (NKAT3)	1	U30274	+						blood only
natural killer-associated	1	AF022045	+						blood only

transcript 5 (NKAT5)									
natural killer-tumor recognition sequence (NKTR)	1	L04288	B		+			+	+
N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2 (NDST2)	2	AF042084	+	+		+			+
Ndr protein kinase	3	Z35102		+					
Nedd-4-like ubiquitin-protein ligase WWP1	1	U96113							
nel (chicken)-like 2 (NELL2)	3	D83018		+	+				
N-ethylmaleimide-sensitive factor attachment protein, alpha (NAPA)	1	U39412		+				+	
N-ethylmaleimide-sensitive factor attachment protein, gamma (NAPG)	1	U78107		+	+	+			
neural precursor cell expressed, developmentally down-regulated 5 (NEDD5)	3	X92544	+	+	+	+			+
neural precursor cell expressed, developmentally down-regulated 8 (NEDD8)	1	D23662	+	+	+	+	+	+	
neuregulin 1 (NRG1)	1	U02330		+			+	+	
neuroblastoma RAS viral (v-ras) oncogene homolog (NRAS)	4	AB020692	+	+	+	+			+
Neuroblastoma RAS viral (v-ras) oncogene homolog (NRAS) (low match)	1	X68286							
Neurofibromin 2 (bilateral acoustic neuroma) (NF2)	1	S73853		+					+
neuronal apoptosis inhibitory protein (NAIP)	2	U19251	+	+	+				+
neuronal cell adhesion molecule (NRCAM)	1	AB002341		+	+	+			+
neuropathy target esterase	1	AJ004832		+	+	+			+

(NTE)										
neuropeptide Y3 receptor, 5'UTR (low score)	1	D28433								
neurotrophic tyrosine kinase, receptor, type 1 (NTRK1)	14	X03541	+	+	+	+	+	+		
neutrophil cytosolic factor 4 (40kD)	2	U50720								
NG31	1	AF129756								
NGAL (=X83006)	1	X99133								
nibrin (NBS)	1	AF051334								
NIK	1	AB014587		+	+	+		+		
Ninjurin 1; nerve injury-induced protein-1	1	U72661		+	+	+		+		
nitrilase 1 (NIT1) (=AF069984)	1	AF069987								
NKG2-D (low match) (non-exact, 58%)	1	X54870								
Nmi	1	U32849								
N-myristoyltransferase 1 (NMT1)	1	AF043324		+	+	+	+	+		
No arches-like (zebrafish) zinc finger protein (NAR)	1	U79569		+	+	+		+		
non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1)	1	D50420	+	+	+	+	+	+		
non-muscle (fibroblast) tropomyosin	1									
non-muscle alpha-actinin	1	U48734								
non-muscle myosin alkali light chain (Hs.77385)	3	M22918	+	+	+	+	+	+		High in fetal adrenal gland and BPH stroma
non-neuronal enolase (EC 4.2.1.11)	1	X16289								
non-receptor tyrosine phosphatase 1	1	M33689								

normal keratinocyte subtraction library mRNA, clone H22a	3	X53778	+	+	+	+	+	+	high in many libraries
notch group protein (N)	3	M99437							
novel protein	1	X99961							
novel T-cell activation protein	1	X94232		+	+	+		+	
N-ras protein NRU	1	A60196							
N-sulfoglucosamine sulfohydrolase (sulfamidase) (SGSH)	1	U60111		+				+	
nsulin induced gene 1 (INSIG1)	1	U96876	+	+	+	+	+	+	
ntegrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) (ITGA14)	3	L12002	+			+			
nterferon, gamma-inducible protein 16 (IFI16)	1	M63838	+	+	+	+		+	
nterleukin 1, beta (IL1RB)	1	M15330							
nuclear antigen H731-like protein	2	U83908		+	+	+		+	
nuclear antigen Sp100 (SP100)	4	U36501	+			+	+	+	
Nuclear antigen Sp100 (SP100) (85%aa)	1	P23497							
Nuclear antigen Sp100 (SP100) (89%aa)	1	P23497							
nuclear autoantigenic sperm protein (histone-binding) (NASP)	1	M97856	+		+				
nuclear corepressor KAP-1 (KAP-1) (=U95040; X97548 TIF1beta zinc finger protein)	1	U78773							
Nuclear domain 10 protein (NDP52)	4	U22897	+	+	+	+	+	+	
Nuclear factor (erythroid-derived 2)-like 2 (NFE2L2)	1	S74017		+	+	+	+	+	

Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) (NFKB1)	2	M58603		+	+		+	+	
nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA)	3	M69043		+	+	+		+	
nuclear factor related to kappa B binding protein (NFRKB)	1	U08191		+	+	+		+	
nuclear mitotic apparatus protein 1 (NUMA1)	3	Z11583	+	+	+	+	+	+	
nuclear receptor coactivator 2 (GRIP1)	1	X97674							
nuclear receptor coactivator 3 (AIB3)	2	AF010227	+	+	+			+	
nuclear receptor coactivator 4 (ELE1)	22	X77548		+	+	+	+	+	
nuclear receptor interacting protein 1 (NRIP1)	1	X84373		+		+		+	
nuclear respiratory factor 1 (NRF1)	1	U02683	B	+	+				
nuclear RNA helicase, DECD variant of DEAD box family (DDXL)	4	U90426	+	+	+	+		+	
nuclear transcription factor, Y, alpha (NFYA)	1	X59711	B						
nuclear transcription factor, X-box binding 1 (NFX1)	3	U15306		+	+		+		
nuclear transport factor 2 (placental protein 15) (PP15)	1	X07315	+	+	+	+		+	
nucleobindin (=M96824)	1	U31336							
nucleobindin 1 (NUCB1)	2	M96824	+	+	+	+		+	
nucleolar phosphoprotein p130 (P130)	1	Z34289		+	+				
nucleolar protein (KKE/D repeat) (NOP56)	1	Y12065	+	+	+	+		+	

nucleolar protein (MSP58)	1	AF015308							
nucleolar protein 1 (120kD) (NOL1)	1	M32110	+	+					
nucleolar protein p40	1	U86602	+	+	+	+		+	
nucleolin (NCL)	2	M60858	+	+	+	+		+	
nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1)	14	M28699	+	+	+	+		+	
nucleophosmin-retinoic acid receptor alpha fusion protein NPM-RAR long form	1	U41742							
nucleoporin (NUP358) (=D42063 RanBP2 (Ran-binding protein 2)).	2	L41840							
nucleoporin 153kD (NUP153)	1	Z25535							
nucleoporin 98kD (NUP98)	1	U41815							
nucleosome assembly protein	1	D28430							
nucleosome assembly protein 1-like 1 (NAP1L1)	1	M86667		+	+	+		+	
nucleosome assembly protein 1-like 4 (NAP1L4)	2	U77456	+	+	+	+		+	
nucleosome assembly protein, 5'UTR	1	D28430							
olfactory receptor (OR7-141)	1	U86281							
OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (OR17-4) (non-exact 65%)	1	P34982							
oligodendrocyte myelin glycoprotein (OMG)	7	L05367		+					
O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) (OGT)	1	U77413	+	+		+	+	+	

oncofetal trophoblast glycoprotein 5T4 precursor (non-exact 55%)	1	A53531							
Oncogene TIM (TIM) (non-exact 84%)	1	U02082							
ORF (Hs.77868)	1	M68864	+	+	+	+	+	+	
ORF1; MER37; putative transposase similar to pogo element Length = 454	1	U49973							
origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L)	2	U27459				+			
origin recognition complex, subunit 4 (yeast homolog)-like (ORC4L) (low match)	1	AF022108							
ornithine aminotransferase (gyrate atrophy) (OAT)	2	M23204		+	+	+			
ornithine decarboxylase (ODC)	1	M20372							
ornithine decarboxylase antizyme, ORF 1 and ORF 2	11	D78361	+	+	+	+	+	+	High in pancreas, and activated T cells
orphan receptor (Hs.100221)	2	U07132	+	+	+	+		+	
OS-9 precursor	6	AB002806	+	+	+	+	+	+	
osteonectin (=X82259 BM-40)	1	D28381							
ovel centrosomal protein RanBPM (RANBPM)	1	AB008515		+	+	+		+	
over-expressed breast tumor protein	1	L34839							
oviductal glycoprotein 1, 120kD (OVGP1)	1	U09550			+	+	+		
oxidase (cytochrome c) assembly 1-like (OXAIL)	1	X80695		+	+	+	+	+	
oxoglutarate dehydrogenase (lipoamide) (OGDH)	4	D10523	T	+	+		+	+	

oxysterol binding protein (OSBP)	1	M86917	+	+			+		
OZF	1	X70394		+	+	+		+	
OZF (non-exact zinc finger)	1	X70394							
p21/Cdc42/Rac1-activated kinase 1 (yeast Ste20-related) (PAK1)	2	U51120	+	+		+			
P35-related protein (= S80990 ficolin)	1	D63392							
p40	1	U93569							
p40phox (=U50720)	1	X77094							
P47 LBC oncogene	4	U03634							
p53-induced protein (PIG11)	1	AF010315	+	+	+	+			
p54nrb (low match)	1	Y11287							
p62 nucleoporin	1	X58521							
p63 mRNA for transmembrane protein	1	X69910	+	+	+	+		+	
PAC clone DJ0701O16 from 7q33-q36 (non-exact 54%)	1	Q07108							
palmitoyl-protein thioesterase (ceroid-lipofuscinosis, neuronal 1, infantile; Hattia-Santavuori disease) (PPT)	10	U44772		+	+	+		+	
papillary renal cell carcinoma (translocation-associated) (PRCC)	1	X99720	+	+	+	+	+	+	
PAR protein	1	AF115850		+		+			
partial EST (clone c-1gh04)	1	Z43627							
PAX3/forkhead transcription factor gene fusion	1	U02368							
paxillin (PXN)	4	D86862		+	+	+		+	
PBK1 protein	2	AJ007398	+	+	+	+		+	

PBS-EST (nz92e01.s1 NCI_CGAP_GCB1 clone IMAGE:1302936) (low score)	1	AA732534							
PDZ domain protein (Drosophila inaD-like) (INALD)	1	AJ224747	+			+		+	
PEBP2aC Runt domain encoding gene (=Z35728)	1	Z38108							
peptidase D (PEPD)	1	J04605							
peptidylprolyl isomerase A (cyclophilin A) (PPIA)	3	Y00052		+	+	+	+	+	high in many libraries
peptidylprolyl isomerase D (cyclophilin D) (PPID)	2	L11667	T	+	+		+	+	
peptidylprolyl isomerase E (cyclophilin E) (PPIE)	1	AF042386		+	+		+	+	
PERB11.1 (=U56942 MHC class I chain-related protein A)	1	U69630							
perforin 1 (preforming protein) (PRF1)	14	M28393							
peroxisomal acyl-CoA thioesterase (PTE1)	2	X86032							
Peroxisomal acyl- coenzyme A oxidase	1	X71440		+	+	+	+	+	
peroxisomal farnesylated protein (PXF)	1	X75535		+	+	+	+	+	
phorbol-12-myristate-13- acetate-induced protein (PMAIP1)	1	D90070	B, W						
phosphate carrier (mitochondrial gene?)	1	X77337							
Phosphate carrier, mitochondrial (PHC)	3	X60036	+	+	+	+		+	
phosphate cytidyltransferase 1, choline, alpha isoform (PCYT1A)	1	L28957	T		+		+		
PHOSPHATIDATE CYTIDYLYLTRANSFERAS	1	Q92903							

E (CDP-DIGLYCERIDE)										
phosphatidylinositol 3-kinase delta catalytic subunit	2	U57843								
phosphatidylinositol 4-kinase, catalytic, beta polypeptide (PIK4CB)	3	AB005910	+	+	+	+		+		
phosphatidylinositol glycan, class H (PIGH)	1	L19783		+	+	+	+	+		
phosphatidylinositol transfer protein (PI-TPbeta)	2	D30037								
phosphatidylinositol transfer protein, membrane-associated (PITPNM)	2	X98654	B, T lymphoma	+						
phosphatidylinositol transfer protein, membrane-associated (PITPNM) (non-exact 64%)	1	X98654								
phosphatidylinositol-4-phosphate 5-kinase, type II, alpha (PIP5K2A)	1	U14957			+			+		
phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B)	1	U85245		+	+	+		+		
phosphodiesterase 7A (PDE7A)	1	L12052	B, W	+	+			+		
phosphodiesterase 1B (PDES1B)	1	U56976		ONLY						
phosphoglucomutase 1 (PGM1)	2	M83088		+	+	+		+		
phosphogluconate dehydrogenase (PGD)	1	U30255			+					
phosphoglycerate kinase 1 (PGK1)	12	V00572								
phosphoglycerate mutase 1 (brain) (PGAM1)	3	J04173	+	+	+	+	+	+		
phosphoglycerate mutase 2 (muscle) (PGAM2)	1	M55673		+	+			+		
phosphoinositide-3-kinase, catalytic, alpha polypeptide	1	Z29090		+	+	+				

(PIK3CA)									
phosphoinositide-3-kinase, catalytic, delta polypeptide (PIK3CD)	4	U86453		+	+	+		+	
phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG)	1	X83368							
phospholipase C	1	X14034							
phospholipase C, delta 1 (PLCD1)	2	U09117		+	+	+		+	
phospholipase C, gamma 1 (formerly subtype 148) (PLCG1)	1	M34667	+	+	+	+		+	
phospholipid scramblase	1	AF008445							
phosphoribosyl pyrophosphate synthetase-associated protein 1 (PRPSAP1)	1	D61391		+	+			+	
phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART)	3	X54199		+	+	+	+	+	
phosphorylase kinase, alpha 2 (liver), glycogen storage disease IX (PHKA2)	3	D38616		+	+	+	+	+	
phosphorylase, glycogen; brain (PYGB)	1	U47025	+	+	+			+	
phosphorylase, glycogen; brain (PYGB) (low match, non-exact, 75%)	1	U47025							
phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL)	1	Y15233		+	+	+		+	
phosphorylation regulatory protein HP-10	2								
phosphatidylinositol transfer protein (PITPN)	1	D30036	+	+	+	+		+	

pigment epithelium-derived factor (PEDF)	1	U29953	+	+	+	+	+	+	
pim-1 oncogene (PIM1)	1	M24779	+	+	+			+	
pinin, desmosome associated protein (PNN)	1	U77718	B, monocyte, T lymphoma						
placenta (Diff33)	5	U49188		+	+	+		+	
placenta (Diff33) (non-exact, 69%)	1	U49188							
placenta (Diff48)	18	U49187	+						
placenta (Diff48) (low match)	1	U49187							
placenta(Diff48) (low match)	1	U49187							
plasminogen activator, urokinase receptor (PLAUR)	1	X74039		+		+		+	
platelet factor 4 (PF4)	1	M25897			+			+	
platelet/endothelial cell adhesion molecule (CD31 ntigen) (PECAM1)	8	M37780		+	+	+	+	+	
platelet-activating factor acetylhydrolase 2 (40kD) (PAFAH2)	4	U89386		+	+	+			
platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (45kD) (PAFAH1B1)	1	U72342	+	+	+	+	+	+	
platelet-activating factor receptor (PTAFR)	1	D10202		+				+	
pleckstrin (PLEK)	10	X07743			+	+		+	
pleckstrin (PLEK) (low match)	1	X07743							
pleckstrin homology, Sec7 and coiled/coil domains 1(cytohesin 1) (PSCD1)	4	M85169	+	+		+		+	
pleckstrin homology, Sec7 and coiled/coil domains,	4	L06633	+			+			

binding protein (PSCDBP)									
pM5 protein	1	X57398	+	+	+	+		+	
PMP69	2	Y14322							
poly (ADP-ribose) polymerase (NAD (+) ADP- ribosyltransferase) (=X16674)	1	X56140							
poly(A) polymerase (PAP)	1	X76770	+	+	+	+		+	
poly(A)-binding protein-like 1 (PABPL1)	19	Y00345	+	+	+	+	+	+	
poly(rC)-binding protein 1 (PCBP1)	3	X78137	+	+	+	+	+	+	
polyadenylate binding protein	1	U75686							
polycystic kidney disease 1 (autosomal dominant) (PKD1)	5	U24498							
polymerase (DNA directed), beta (POLB)	1	D29013		+			+	+	
polymerase (DNA directed), gamma (POLG)	6	D84103							
polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A)	1	X63564	+	+	+	+	+	+	
polymyositis/scleroderma autoantigen 2 (100kD) (PMSCL2)	1	L01457	+	+	+	+	+	+	
polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I) (PTB)	1	X65372	+	+	+	+	+	+	
positive regulator of programmed cell death ICH-1L (Ich-1)	3	U13021			+				
postmeiotic segregation increased 2-like 12 (PMS2L12)	1	M16514	+	+	+	+		+	
postmeiotic segregation increased 2-like 8 (PMS2L8)	1	U38964	+	+	+	+		+	

potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15)	1	D87291				+		+	
potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1)	1	AF051426		+	+	+		+	
POU domain, class 2, associating factor 1 (POU2AF1)	1	Z49194				+			
POU domain, class 2, transcription factor 1 (POU2F1)	2	X13403		+		+			
PPAR binding protein (PPARBP)	1	Y13467	+	+	+	+		+	
PPAR gamma2	1	D83233							
pre-B-cell colony-enhancing factor (PBEF)	8	U02020							
prefoldin 1 (PFDN1)	1	Y17392	+	+	+	+	+	+	
prefoldin 5 (PRFLD5)	3	D89667	B	+	+		+		
prefoldin subunit 3 (=U96759 von Hippel-Lindau binding protein (VBP-1))	1	Y17394							
pregnancy-associated plasma protein A (PAPPA)	1	U28727		+		+			high in placenta
pre-mRNA splicing factor SF3a (60kD), similar to S. cerevisiae PRP9 (spliceosome-associated protein 61) (SF3A60)	1	U08815	+	+	+	+		+	
pre-mRNA splicing factor SF3a (60kD), similar to S. cerevisiae PRP9 (spliceosome-associated protein 61) (SF3A60) (low score)	1	U08815							
pre-mRNA splicing factor SRp20, 5'UTR	2	D28423							
preprotein translocase (TIM17)	3	X97544	+	+	+	+		+	

prion protein	1	X82545							
prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler- Scheinker syndrome, fatal familial insomnia) (PRNP)	1	M13899		+	+	+		+	
pristanoyl-CoA oxidase (low match)	1	Y11411							
pristanoyl-CoA oxidase (low score)	1	Y11411							
procollagen-lysine, 2- oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers- Danlos syndrome type VI) (PLOD)	1	M98252		+	+	+		+	
procollagen-proline, 2- oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide 1 (P4HA1)	1	M24486	+	+	+	+	+	+	
procollagen-proline, 2- oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) (P4HB)	4	X05130	+	+	+	+	+	+	
profilin 1 (PFN1)	1	J03191	+	+	+	+	+	+	
progesterone receptor- associated p48 protein (P48)	2	U28918		+					
prohibitin (PHB)	1	S85655		+	+	+	+	+	
proliferating cell nuclear antigen (PCNA)	3	J04718	+	+	+	+		+	
proliferation-associated gene A (natural killer- enhancing factor A) (PAGA)	4	L19184	+	+	+	+	+	+	
proline-rich protein BstNI subfamily 2 (PRB2) (non- exact, 43%aa)	1	S62936							
proline-serine-threonine phosphatase interacting protein 1 (PSTPIP1)	1	U94778							

prolyl endopeptidase (PREP)	2	X74496		+		+		+	
prolylcarboxypeptidase (angiotensinase C) (PRCP)	5	L13977		+	+	+	+	+	
promyelocytic leukemia (PML)	1	M80185	+	+	+	+		+	
properdin P factor, complement (PFC)	4	X57748	+						
pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP)	1	M54995			+	+		+	
pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP)	7	M54995	+		+		+		
proprotein convertase subtilisin/kexin type 7 (PCSK7)	4	U40623							
prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP)	89	D00422	+	+	+	+	+	+	
prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1)	1	U63846	B	+			+	+	
prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2)	2	L15326							
prostaglandin-endoperoxide synthase-1 (=L08404; U84208) (all promoters)	1	D64068							

prostate carcinoma tumor antigen (pcta-1)	2	L78132								
protease inhibitor 1 (anti-elastase), alpha-1-antitrypsin (PI)	17	K02212		+	+	+	+	+		high in many libraries
protease inhibitor 2 (anti-elastase), monocyte/neutrophil (ELANH2) (low match)	1	M93056				+		+		
proteasome (prosome, macropain) 26S subunit, ATPase, 1 (PSMC1)	3	L02426	B	+	+			+		
proteasome (prosome, macropain) 26S subunit, ATPase, 3 (PSMC3)	1	M34079	+	+	+	+		+		
proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4)	2	AF020736								
proteasome (prosome, macropain) 26S subunit, ATPase, 5 (PSMC5)	5	L38810	+	+	+	+	+	+		
proteasome (prosome, macropain) 26S subunit, ATPase, 6 (PMSC6)	2	D78275	+	+	+	+		+		
proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11)	1	AF001212	T	+			+			
proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 (PSMD2)	2	D78151		+	+			+		
proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 (PSMD5)	1	S79862	T	+	+		+			
proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PMSD7)	1	D50063		+	+	+		+		high in many libraries
proteasome (prosome, macropain) 26S subunit, on-ATPase, 12 (PMSD12)	1	AB003103		+	+	+		+		
proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) (PSME1)	3	L07633	+	+	+	+		+		

proteasome (prosome, macropain) subunit, alpha type, 3 (PSMA3)	2	D00762		+	+	+		+	
proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5)	3	X61970	+	+	+	+		+	
proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7)	3	AF054185		+	+	+	+	+	
proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) (low match)	1	AF022815							
proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1)	1	D00761	+	+	+	+	+	+	
proteasome (prosome, macropain) subunit, beta type, 10 (PSMB10)	1	X71874	+	+		+	+	+	
proteasome (prosome, macropain) subunit, beta type, 6 (PSMB6)	1	D29012		+	+	+		+	
proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7) (PSMB8)	1	U17497	+	+	+	+		+	
proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2) (PSMB9)	3	Z14977	+			+		+	
proteasome (prosome, macropain) subunit, beta type, 7 (PSMB7)	1	D38048	+	+	+	+	+	+	
protective protein for beta-galactosidase (galactosialidosis) (PPGB)	3	M22960	+	+	+	+	+	+	
protein A alternatively spliced form 2 (A-2)	1	U47925		+					
protein activator of the interferon-induced protein kinase (PACT)	1	AF072860		+	+	+		+	high in testis
protein disulfide isomerase-	2	D49489	+	+	+	+	+	+	

related protein (P5)									
protein geranylgeranyltransferase type I, beta subunit (PGGT1B)	1	L25441	+	+	+				
protein homologous to chicken B complex protein, guanine nucleotide binding (H12.3)	20	M24194	+	+	+	+	+	+	high in many libraries
protein kinase A anchoring protein	1	AF037439		+					
protein kinase C substrate 80K-H (PRKCSH)	2	U50317	+	+	+	+		+	
protein kinase C, beta 1 (PRKCB1)	6	X06318	+	+	+	+		+	
protein kinase C, delta (PRKCD)	1	D10495	+	+	+	+		+	
protein kinase C, eta (PRKCH)	1	M55284			+			+	
protein kinase C, mu (PRKCM) (non-exact 78%)	1	X75756							
Protein kinase C-like 1 (PRKCL1)	2	D26181	+	+	+	+		+	
protein kinase, AMP-activated, gamma 1 non-catalytic subunit (PRKAG1)	1	U42412	B, T lymphoma	+	+				
protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) (PRKAR1A)	4	M18468		+	+	+	+	+	
protein kinase, DNA-activated, catalytic polypeptide (PRKDC)	1	U47077		+	+		+	+	
protein kinase, mitogen-activated 1 (MAP kinase 1; p40, p41) (PRKM1)	1	Z11695	B	+			+		
protein kinase, mitogen-activated 6 (extracellular signal-regulated kinase, p97) (PRKM6)	1	L77964		+		+	+	+	
protein kinase, mitogen-activated, kinase 3 (MAP	1	U66839	+	+	+	+	+		

kinase kinase 3) (PRKMK3)									
protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA)	5	M63960	+	+	+	+	+	+	
protein phosphatase 1, regulatory subunit 10 (PPPR10)	3	Y13247		+	+	+		+	
protein phosphatase 1, regulatory subunit 7 (PPP1R7)	2	Z50749	+	+	+	+	+	+	
protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform (PPP2CB)	1	X12656	+	+	+	+	+	+	
protein phosphatase 2 (formerly 2A), regulatory subunit B" (PR 72), alpha isoform and (PR 130), beta isoform (PPP2R3)	1	L07590			+	+		+	
protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A)	2	L42373	+	+	+	+		+	
protein phosphatase 2, regulatory subunit B (B56), delta isoform (PPP2R5D)	3	D78360		+	+	+		+	
protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C)	1	D26445	+	+	+	+		+	
protein phosphatase 2A regulatory subunit alpha-isotype (alpha-PR65)	5	J02902	+	+	+	+		+	
protein phosphatase 4 (formerly X), catalytic subunit (PPP4C)	2	AF097996	+	+	+	+		+	
protein tyrosine kinase 2 beta (PTK2B)	4	L49207		+		+		+	
protein tyrosine phosphatase epsilon	1	X54134							
protein tyrosine phosphatase type IVA, member 2 (PTP4A2)	2	L48723	+	+	+	+		+	

protein tyrosine phosphatase, non-receptor type 1 (PTPN1)	1	M31724	+	+	+	+			
protein tyrosine phosphatase, non-receptor type 12 (PTPN12)	1	M93425		+	+	+		+	high in testis
protein tyrosine phosphatase, non-receptor type 12 (PTPN12) (non-exact, 70%)	1	M93425							
protein tyrosine phosphatase, non-receptor type 2 (PTPN2)	2	M25393		+	+	+		+	
protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte) (PTPN4)	1	M68941			+	+		+	
protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	7	M74903	+	+	+	+		+	
protein tyrosine phosphatase, non-receptor type 7 (PTPN7)	1	D11327	+			+		+	
protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA)	1	M34668	+	+	+	+		+	
protein tyrosine phosphatase, receptor type, c polypeptide (PTPRC)	44	Y00638	+	+		+		+	
protein tyrosine phosphatase, receptor type, M (PTPRM)	1	X58288		+	+	+		+	
protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2)	2	U81561		+		+		+	
protein with polyglutamine repeat (ERPROT213-21)	1	U94836	+	+	+	+		+	
protein-kinase, interferon-inducible double stranded RNA dependent inhibitor (PRKRI)	1	U28424		+	+	+	+	+	

protein-L-isoaspartate (D-aspartate) O-methyltransferase (PCMT1)	4	D13892		+	+				
proteoglycan 1, secretory granule (PRG1)	7	J03223		+		+		+	
prothymosin, alpha (gene sequence 28) (PTMA)	12	M14483	+	+	+	+	+	+	
prp28, U5 snRNP 100 kd protein (U5-100K)	7	AF026402	+	+	+	+		+	
PRP4/STKWD splicing factor (HPRP4P)	1	AF001687		+	+	+		+	
PTK7 protein tyrosine kinase 7 (PTK7)	1	U40271		+	+	+		+	
purinergic receptor P2X, ligand-gated ion channel, 4 (P2RX4)	3	AF000234		+	+	+		+	
purinergic receptor P2X, ligand-gated ion channel, 7 (P2RX7)	1	Y12851	+						macrophage only
puromycin-sensitive aminopeptidase (PSA)	1	Y07701		+	+			+	
putative ATP(GTP)-binding protein	2	AJ010842		+				+	
putative brain nuclearly-targeted protein (KIAA0765)	1	AB018308	+	+	+	+		+	
putative chemokine receptor; GTP-binding protein (HM74)	1	D10923	+						
putative dienoyl-CoA isomerase (ECH1)	1	AF030249							
putative G-binding protein	1	AF065393							
Putative human HLA class II associated protein I (PHAP1)	1	U73477	B	+			+		
Putative L-type neutral amino acid transporter (KIAA0436)	1	AB007896							
putative mitochondrial space protein 32.1	1	AF050198							

PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24)	1	Q04900							
putative nucleic acid binding protein	2	X76302	+	+	+	+		+	
putative outer mitochondrial membrane 34 kDa translocase Htom34	1	U58970		+	+	+		+	
putative p150 (non-exact 88%)	1	U93568							
putative translation initiation factor (SUI1)	1	L26247	+	+	+	+	+	+	High in moderately differentiated colon adenocarcinoma
putative tumor suppressor protein (123F2)	1	AF061836		+	+	+		+	
pyrroline 5-carboxylate reductase	1	M77836	+	+	+	+		+	
pyruvate dehydrogenase (lipoamide) alpha 1 (PDHA1)	1	D90084		+	+	+	+	+	
pyruvate dehydrogenase (lipoamide) beta (PDHB)	2	J03576	+	+	+	+		+	
Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein (PDX1)	3	Y13145		+	+				
pyruvate kinase, muscle (PKM2)	11	M23725					+		
RAB, member of RAS oncogene family-like (RABL)	1	U18420		+	+	+		+	
RAB1, member RAS oncogene family (RAB1)	3	M28209		+	+	+		+	
RAB11A, member RAS oncogene family (RAB11A)	2	X56740	+	+	+	+		+	high in spleen
RAB11B, member RAS oncogene family (Rab11B)	1	D45418		+				+	
RAB27A, member RAS	3	U38654				+			

oncogene family (RAB27A)									
RAB5B, member RAS oncogene family (RAB5B)	1	X54871		+	+	+		+	
RAB6, member RAS oncogene family (RAB6)	1	M28212		+				+	
RAB7, member RAS oncogene family (RAB7)	1	X93499	+	+	+	+		+	
RAB7, member RAS oncogene family-like 1 (RAB7L1)	2	D84488		+	+	+		+	
RAB9, member RAS oncogene family (RAB9)	1	U44103							
RAD50 (S. cerevisiae) homolog (RAD50)	2	U63139		+	+	+			
RAD51 (S. cerevisiae) homolog C (RAD51C)	1	AF029669		+	+	+		+	
Radin blood group (RD)	2	L03411		+	+	+		+	
RAE1 (RNA export 1, S.pombe) homolog (RAE1)	3	U84720	+	+	+	+		+	
ralA-binding protein (RLIP76)	2	L42542	+	+	+	+			
RAN binding protein 2-like 1 (RANBP2L1)	2	AF012086							
Ran GTPase activating protein 1 (RANGAP1)	3	X82260	+	+	+	+		+	
RAN, member RAS oncogene family (RAN) (low match)	1	M31469							
RanBP2 (Ran-binding protein 2) (=U19248; L41840 sapiens nucleoporin (NUP358))	1	D42063							
ransforming growth factor, beta receptor II (70-80kD) (TGFB2)	4	D50683	+	+	+	+		+	
RAP1A, member of RAS oncogene family (RAP1A)	10	M22995	+	+	+	+	+	+	
RAR-related orphan	1	U16997						+	

receptor C (RORC)										
RAS guanyl releasing protein 2 (calcium and DAG-regulated)	1	Y12336	+	+						
ras homolog gene family, member A (ARHA)	12	X05026	+	+	+	+	+	+		high in ovary
ras homolog gene family, member G (rho G) (ARHG)	1	X61587	+	+	+	+				
ras homolog gene family, member H (ARHH)	2	Z35227	+	+	+				+	
ras inhibitor (RIN1)	2	M37191		+						
Ras-GTPase activating protein SH3 domain-binding, protein 2 (KIAA0660)	2	AF053535	+	+	+	+			+	
Ras-GTPase-activating protein SH3-domain-binding protein (G3BP)	3	U32519	+	+	+	+			+	
ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) (RAC2)	11	M29871			+				+	
RAS-RELATED PROTEIN RAP-1B (GTP-BINDING PROTEIN SMG P21B)	1	P09526								
RBQ-1	1	X85133		+	+	+				
rearranged T cell receptor beta variable region (TCRB) (=X58810)	1	L06891								
regulator of Fas-induced apoptosis (TOSO)	1	AF057557	B					+		
regulator of G protein signalling 6 (RGS6)	1	AF073920		+						
regulator of G-protein signalling 14 (RGS14)	2	AF037195	+	+	+	+				
regulator of G-protein signalling 2, 24kD (RGS2)	6	L13391	+	+	+	+			+	
regulator of G-protein signalling 5 (RGS5) (49% aa)	1	O15539								

regulatory factor X, 4 (influences HLA class II expression) (RFX4)	1	M69297			+	+				
regulatory factor X, 5 (influences HLA class II expression) (RFX5)	2	X85786	T	+	+				+	
replication protein A1 (RPA1)	1	M63488	+	+	+	+			+	
replication protein A3 (14kD) (RPA3) (low match)	1	L07493								
reproduction 8 (D8S2298E)	1	D83767		+	+	+				
requiem, apoptosis response zinc finger gene (REQ)	2	U94585	+	+	+	+			+	
requiem, apoptosis response zinc finger gene (REQ) (=AF001433) (low match)	1	U94585								
restin (Reed-Steinberg cell- expressed intermediate filament-associated protein) (RSN)	1	M97501	B, T	+	+					
retinoblastoma 1 (including osteosarcoma) (RB1)	3	L11910	+	+	+	+				
retinoblastoma binding protein 2 homolog 1 (RBBP2H1)	1	AF087481								
retinoblastoma-binding protein 1 (RBBP1)	1	S66427	+	+						
retinoblastoma-binding protein 2 (RBBP2)	5	S66431	+	+	+	+			+	
retinoblastoma-binding protein 4 (RBBP4)	1	X71810		+	+	+			+	
retinoblastoma-binding protein 4 (RBBP4)	1	X74262		+	+	+			+	
retinoblastoma-binding protein 7 (RBBP7)	1	U35143								
retinoblastoma-like 2 (p130) (RBL2)	1	X76061		+	+	+			+	
retinoic acid receptor responder (tazarotene)	1	AF060228		+		+	+	+		

nduced) 3 (RARRES3)									
retinoic acid receptor, alpha (RARA)	1	X06538	+	+		+			
retinoic acid responsive (NN8-4AG)	1	U50383		+		+		+	
retinoid X receptor beta (RXR-beta)	2	X66424		+	+	+		+	
REV3 (yeast homolog)-like, catalytic subunit of DNA polymerase zeta (REV3L)	1	AF035537							
Rho GDP dissociation inhibitor (GDI) beta (ARHGDIB)	23	L07916	+	+	+	+	+	+	
Rho GTPase activating protein 4 (ARHGAP4)	2	X78817	+	+					
Rho GTPase activating protein 4 (ARHGAP4) (low match)	1	P98171							
Rho-associated, coiled-coil containing protein kinase 2 (ROCK2)	1	AB014519							
ribonuclease 6 precursor (RNASE6PL)	2	U85625	+	+	+	+	+	+	
ribonuclease 6 precursor (RNASE6PL) (low match)	1	U85625							
ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) (RNASE2)	1	X55988					+		
ribonuclease/angiogenin inhibitor (RNH)	3	M36717	+	+	+	+		+	
ribonucleoside diphosphate reductase M1 subunit	1	X65708							
ribonucleotide reductase M2 polypeptide (non-exact 91%)	1	P31350							
ribophorin I (RPN1)	1	Y00281	+	+	+	+		+	
ribophorin II (RPN2)	1	Y00282	+	+	+	+	+	+	

ribosomal 18S rRNA	3	M10098								
ribosomal 28S RNA	1	M11167								
ribosomal phosphoprotein P0, 5'UTR (low match)	1	D28418								
Ribosomal protein	1									
ribosomal protein L10 (RPL10)	30	L25899	+	+	+	+	+	+		high in many libraries
RIBOSOMAL PROTEIN L10A (CSA-19)	2	P53025								
ribosomal protein L11 (RPL11)	4	X79234	+	+	+	+	+	+		Alveolar rhabdomyosarcoma
ribosomal protein L12 (RPL19)	2	L06505	+	+	+	+	+	+		
ribosomal protein L13 (PRL13)	1	P26373	+	+	+	+	+	+		high in many libraries
ribosomal protein L14 (RPL14)	4	D87735	+	+	+	+	+	+		high in many libraries
ribosomal protein L17 (RPL17)	4	X53777	+							blood only
ribosomal protein L18 (RPL18)	10	L11566	+	+	+	+			+	
ribosomal protein L18a (RPL18A)	5	L05093		+	+	+	+	+		High in fetal adrenal gland and skin
ribosomal protein L18a homologue	2	X80821				+				
ribosomal protein L19 (RPL19)	15	X63527	+	+	+	+	+	+		
ribosomal protein L21 (RPL21)	6	U14967	+	+	+	+	+	+		
ribosomal protein L22 (RPL22)	3	D17652	+	+	+	+			+	
ribosomal protein L23 (RPL23)	2	X55954	+	+	+	+	+	+		high in many libraries
ribosomal protein L23a (RPL23A)	5	U37230	+	+	+	+	+	+		high in many libraries
ribosomal protein L26	8	X69392	+	+	+	+	+	+		

(RPL26)										
ribosomal protein L27 (RPL27)	6	L05094	+	+	+	+		+		
ribosomal protein L27a (RPL27A)	10	U14968	+	+	+	+	+	+		
ribosomal protein L28 (RPL28)	6	U14969	+	+	+	+		+		
ribosomal protein L29 (RPL29)	6	U10248	+	+	+	+	+	+		
ribosomal protein L3 (RPL3)	81		+	+	+	+	+	+		high in many libraries
ribosomal protein L3 homologue	81	X06323								
ribosomal protein L30 (RPL30)	6	X79238	+	+	+	+	+	+		high in lymphoma
ribosomal protein L30 (RPL30) (low score)	1	X79238								
ribosomal protein L31 (RPL31)	10	X15940	+	+	+	+	+	+		High in alveolar rhabdomyosarcoma
ribosomal protein L32 (RPL32)	3	X03342	+	+	+	+	+	+		
ribosomal protein L33-like (RPL33L)	1	AF047440		+	+	+		+		
ribosomal protein L34 (RPL34)	5	L38941		+	+	+	+	+		
ribosomal protein L34 (RPL34) (low match)	1	L38941								
ribosomal protein L37 (RPL37)	5	D23661	+	+	+	+	+	+		high in barstead prostate
ribosomal protein L37a	4	X66699	+	+	+	+	+	+		high in many libraries
ribosomal protein L38 (RPL38)	1	Z26876	+	+	+	+	+	+		high in many libraries
ribosomal protein L4 (RPL4)	27	D23660	+	+	+	+	+	+		high in many libraries
ribosomal protein L41 (RPL41)	4	AF026844	+	+	+	+	+	+		high in many libraries

ribosomal protein L5 (RPL5)	14	U14966	+	+	+	+	+	+	High in alveolar rhabdomyosarcoma
ribosomal protein L5 (RPL5) (low match)	1	U14966							
ribosomal protein L6 (RPL6)	7	X69391	+	+	+	+	+	+	high in many libraries
ribosomal protein L7 (RPL7)	14	X52967	+	+	+	+	+	+	high in conorm
ribosomal protein L7a (RPL7A)	15	M36072	+	+	+	+	+	+	High in uterus, and seminoma
ribosomal protein L8 (RPL8)	5	Z28407	+	+	+	+	+	+	high in ovary
ribosomal protein L9 (RPL9)	10	U09953		+	+	+	+	+	
ribosomal protein S10 (RPS10)	5	U14972	+	+	+	+	+	+	high in many libraries
ribosomal protein S11 (RPS11)	4	X06617	+	+	+	+	+	+	high in many libraries
ribosomal protein S11 (RPS11) (low match)	1	AB007152							
ribosomal protein S12 (RPS12)	3	X53505	+	+	+	+	+	+	high in many libraries
ribosomal protein S13 (RPS13)	2	L01124		+	+	+	+	+	
ribosomal protein S14 (RPS14)	12	M13934	+	+	+	+	+	+	
ribosomal protein S15 (RPS15)	2	M32405	+	+	+	+	+	+	
ribosomal protein S16 (RPS16)	3	M60854	+	+	+	+	+	+	High in prostate invasive tumor
ribosomal protein S17 (RPS17)	2	M13932	+	+	+	+	+	+	high in many libraries
ribosomal protein S18	8	X69150							
ribosomal protein S19 (RPS19)	7	M81757	+	+	+	+	+	+	high in many libraries
ribosomal protein S2 (RPS2)	4	X17206	+	+	+	+	+	+	high in many libraries

RIBOSOMAL PROTEIN S2 (RPS4)	2	P15880								
ribosomal protein S20 (RPS20)	7	L06498	+	+	+	+	+	+	+	high in many libraries
ribosomal protein S21 (RPS21)	3	L04483	+	+	+	+	+	+	+	high in CD34+/CD38- hematopoietic cells and skin tumor
ribosomal protein S23 (RPS23)	3	D14530		+	+	+		+		
ribosomal protein S24 (RPS24)	7	M31520	+	+	+	+	+	+	+	high in uterus
ribosomal protein S25 (RPS25)	3	M64716	+	+	+	+	+	+	+	high in barstead prostate
ribosomal protein S26 (RPS26)	2	X69654		+	+	+	+	+	+	
ribosomal protein S27 ((metalloproteinase 1) (RPS27)	5	U57847	+	+	+	+	+	+	+	
ribosomal protein S28 (RPS28)	3	U58682	+	+	+	+		+		
ribosomal protein S29 (RPS29)	2	U14973	+	+	+	+	+	+	+	
ribosomal protein S3 (RPS3)	9	X55715	+	+	+	+	+	+	+	high in many libraries
ribosomal protein S3 (RPS3) (low match)	1	U14990								
ribosomal protein S3A (RPS3A)	21	Z83334		+	+	+	+	+	+	high in many libraries
ribosomal protein S3A (RPS3A) (low score)	1	M77234								
ribosomal protein S4, X-linked (RPS4X)	9	M58458	+	+	+	+		+		high in ovary and Synovial sarcoma
ribosomal protein S4, Y-linked (RPS4Y)	2	M58459	+	+	+	+	+	+	+	
ribosomal protein S5 (RPS5)	4	U14970	+	+	+	+	+	+	+	high in lymphoma
RIBOSOMAL PROTEIN S6 (PHOSPHOPROTEIN)	1	P10660								

NP33)										
ribosomal protein S6 (RPS6)	22	M20020	+	+	+	+	+	+		
ribosomal protein S6 (RPS6) (non-exact 86%)	1	M77232								
ribosomal protein S6 kinase, 90kD, polypeptide 1 (RPS6KA1)	3	L07597	+	+	+	+		+		
ribosomal protein S6 kinase, 90kD, polypeptide 2 (RPS6KA2)	1	X85106								
ribosomal protein S7 (RPS7)	4	Z25749		+	+	+	+	+		
ribosomal protein S8 (RPS8)	6	X67247		+	+	+	+	+		
ribosomal protein S9 (RPS9)	8	U14971								colón tumor
ribosomal protein, large, P0 (RPLP0)	18	M17885	T		+			+		
ribosomal protein, large, P1 (RPLP1)	12	M17886	T	+	+		+			
ribosomal RNA 18S (=M10098; K03432) (=polyadenylating sequence)	11	X03205								
ribosomal RNA 28S	2	M11167								
ribosomal RNA, 16S	1	U25123								
ring finger protein (non-exact 58%)	1	AJ001019								
ring finger protein 3 (RNF3)	1	AJ001019								
ring finger protein 4 (RNF4)	3	AB000468		+	+	+		+		
ring zinc-finger protein (ZNF127-Xp)	3	U41315		+	+	+		+		
RNA (guanine-7-) methyltransferase (RNMT)	1	AB007858		+	+	+		+		
RNA binding motif protein 5 (RBM5)	4	U23946	+	+	+	+		+		

RNA binding motif, single stranded interacting protein 2 (RBMS2)	1	D28483		+		+		+	
RNA helicase (putative), (Myc-regulated DEAD box protein) (MRD8)	1	X98743	+	+	+	+		+	
RNA helicase-related protein	1	AF083255		+	+	+		+	
RNA pol II largest subunit	2	X74872							
RNA polymerase I subunit (RPA40)	1	AF008442		+	+			+	
RTVP-1 protein	2	X91911	+	+	+	+		+	
S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) (S100A10)	2	M81457			+		+	+	
S100 calcium-binding protein A11 (calgizzarin) (S100A11)	1	X80201		+	+	+		+	
S100 calcium-binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)(S100A4)	3	M80563	B		+		+		
S100 calcium-binding protein A8 (calgranulin A) (S100A8)	7	M21005			+	+		+	high in bone marrow
S100 calcium-binding protein A9 (calgranulin B) (S100A9)	14	X06233			+	+			high in invasive larynx squamous cell carcinoma
S164 gene	1	AF109907							
S-adenosylmethionine decarboxylase 1 (AMD1)	3	M88003	+	+	+	+		+	
SB classII histocompatibility antigen alpha-chain	5	M27487	+	+	+	+		+	
SC35-interacting protein 1 (SRRP129)	5	AF030234	+	+	+	+	+	+	
scaffold attachment factor B (SAFB)	1	U72355	+	+	+	+		+	

scaffold attachment factor B (SAFB) (non-exact 78%)	1	U72355							
scRNA molecule, transcribed from Alu repeat	1	L13713							
SEC14 (S. cerevisiae)-like (SEC14L)	4	D67029		+	+	+		+	
SEC23-like protein B (SEC23B)	2	X97065	+	+	+	+		+	
SEC63 (SEC63)	1	AF100141		+	+			+	
secreted protein, acidic, cysteine-rich (osteonectin) (SPARC)	7	M25746		+	+	+	+	+	high in bone marrow stroma
secretory carrier membrane protein 1 (SCAMP1)	1	AF038966		+		+			
secretory carrier membrane protein 2 (SCAMP2)	1	AF005038	+	+	+	+	+	+	
secretory carrier membrane protein 3 (SCAMP3)	1	AF005039							
secretory granule proteoglycan core (clones lambda-PG[6;7,8])	1	M33649							
selectin L (lymphocyte adhesion molecule 1) (SELL)	43	X17519	+			+		+	
selectin P ligand (SELPLG)	13	U02297	+	+					
sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (SEMA4D)	2	U60800		+		+		+	
Ser/Arg-related nuclear matrix protein (plenty of prolines 101-like) (SRM160)	4	AF048977		+	+	+	+	+	
serine palmitoyltransferase subunit I (SPTI)	1	Y08685		+	+	+		+	
serine palmitoyltransferase, subunit II (LCB2)	1	AB011098	+	+	+	+		+	

serine protease	1	J02907							
serine protease inhibitor, Kunitz type, 2 (SPINT2)	1	U78095	+	+	+	+		+	
serine/threonine kinase 10 (STK10)	1	AB015718	+	+	+	+		+	
serine/threonine kinase 19 (STK19)	1	L26260	+	+	+	+			
serine/threonine kinase 4 (STK4)	1	U18297		+				+	
serine/threonine protein kinase KKIALRE (KKIALRE)	1	X66358		+	+	+		+	
serine/threonine protein-kinase (NIK)	1	Y10256		+	+	+			
SERINE/THREONINE-PROTEIN KINASE RECEPTOR R3 PRECURSOR (SKR3)	1	P37023							
serologically defined colon cancer antigen 16 (NY-CO-16)	2	AF039694							
serologically defined colon cancer antigen 33 (SDCCAG33)	1	AF039698	B, T	+	+		+		
serologically defined colon cancer antigen 33 (SDCCAG33) (low score)	1	AF039698							
serologically defined colon cancer antigen 33 (SDCCAG33) (low score)	1	AF039698							
serum deprivation response (phosphatidylserine-binding protein) (SDPR) (=S67386)	1	AF085481.1							
serum/glucocorticoid regulated kinase (SGK)	2	Y10032	+	+	+	+		+	
SET domain, bifurcated 1 (SETDB1)	2	D31891	+	+	+			+	
SH2 domain protein 1A, Duncan's disease lymphoproliferative	1	AF073019	T					+	

syndrome) (SH2D1A)									
SH3 binding protein (SAB)	2	AB005047	+	+	+	+		+	
SH3 domain protein 1B (SH3D1B)	4	U61167	+			+		+	
SH3BGR PROTEIN (=21-GLUTAMIC ACID-RICH PROTEIN;21-GARP) (non-exact 82%aa)	1	P55822							
SH3-binding domain glutamic acid-rich protein like (SH3BGRL)	1	AF042081	+	+	+	+		+	
SH3-domain GRB2-like 1 (SH3GL1)	1	U65999	+	+	+	+		+	
SHC (Src homology 2 domain-containing) transforming protein 1 (SHC1)	2	X68148		+	+	+		+	
siha binding protein 1 (SiahBP1)	2	U51586		+	+	+		+	
siha binding protein 1 (SiahBP1) (non-exact, 69%)	1	U51586							
Sialomucin CD164 (CD164)	9	D14043							
sialophorin (gpL115, leukosialin, CD43) (SNP)	2	J04536							
sialyltransferase (STHM)	1	U14550			+	+		+	
sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) (SIAT1)	2	X17247	+	+	+	+	+	+	
sialyltransferase 4A (beta-galactosidase alpha-2,3-sialyltransferase) (SIAT4A)	1	AF059321	B	+	+		+	+	
sialyltransferase 8 (alpha-2,8-polysialyltransferase) D (SIAT8D)	1	L41680		+					
signal peptidase 25kDa subunit	1	L38950							
signal recognition particle 14kD (homologous Alu RNA-binding protein)	1	X73459	+	+	+	+	+	+	

(SRP14)										
signal recognition particle 54kD (SRP54)	1	U51920			+	+			+	
signal recognition particle 9kD (SRP9)	2	U20998		+	+	+	+	+		
signal recognition particle receptor ('docking protein') SRPR	5	X06272								
signal regulatory protein, beta, 1 (SIRP-BETA-1)	5	Y10376		+					+	
signal sequence receptor, alpha (translocon-associated protein alpha) (SSR1)	2	Z12830				+			+	
signal sequence receptor, beta (translocon-associated protein beta) (SSR2)	2	X74104	+	+	+	+			+	
signal transducer and activator of transcription (STAT5A)	4	L41142	+	+	+	+	+	+	+	
signal transducer and activator of transcription 2, 113KD (STAT2)	1	U18671							+	
signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3)	3	L29277								
signal transducer and activator of transcription 5A (STAT5A)	2	U48730	+	+	+	+	+	+	+	
signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 (STAM)	1	U43899								
silencing mediator of retinoid and thyroid hormone action (SMRT)	1	U37146								
similar to beta-transducin superfamily proteins (SAZD)	1	U02609	+	+	+				+	
similar to <i>S. cerevisiae</i> SSM4 (TEB4)	1	AB011169		+	+	+			+	

similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6	1	AF026031	+	+	+	+		+	
SIT protein	1	AJ010059.1							
Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro) (SSA1)	2	M62800						+	
Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro) (SSA1) (non-exact 63%) (match to zinc finger)	1	M62800							
SKAP55 homologue (SKAP-HOM)	1	AJ004886		+	+	+		+	
skb1 (S. pombe) homolog (SKB1)	2	AF015913	+	+	+	+		+	
skeletal muscle abundant protein	1	X87613	+	+	+	+		+	
SMA3 (SMA3)	1	X83300	+	+		+		+	
small acidic protein	3	U51678	+	+	+	+		+	
small EDRK-rich factor 2 (SERF2)	2	Y10351	+	+	+	+	+	+	high in fetal lung
small inducible cytokine A5 (RANTES) (SCYA5)	2	M21121	+	+	+	+	+	+	high in many libraries
small inducible cytokine subfamily C, member 2 (SCYC2)	1	D63789							
small nuclear ribonucleoprotein polypeptide B" (SNRPB2)	2	M15841		+	+	+		+	
small nuclear ribonucleoprotein polypeptide N (SNRPN)	4	J04615	+	+	+	+	+	+	
small nuclear ribonucleoprotein polypeptides B and B1 (SNRPB)	2	J04564	+	+	+	+		+	
small nuclear RNA activating complex,	1	AF093593	+	+	+	+		+	

polypeptide 5, 19kD (SNAPC5)									
smallest subunit of ubiquinol-cytochrome c reductase	1	D55636	+	+	+	+	+	+	high in fetal lung
SMC (mouse) homolog, X chromosome (SMCX)	1	L25270	+	+	+	+		+	
SMT3B protein (2)	2	X99585	+	+	+	+	+	+	
SNARE protein (YKT6) (low match)	1	U95735							
SNC19	1	U20428							
SNC73 protein (SNC73)	2	J00220	+	+		+	+	+	high in many libraries
solute carrier family 1 (neutral amino acid transporter), member 5 (SLC1A5)	2	U53347		+		+		+	
Solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1 (SLC11A1)	7	D50403	+						
solute carrier family 17 (sodium phosphate), member 3 (SLC17A3)	1	U90545				+			
solute carrier family 19 (folate transporter), member 1 (SLC19A1)	1	U17566	B, lymphoma	+			+		
solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1)	1	K03195	+	+	+	+	+	+	
solute carrier family 23 (nucleobase transporters), member 2 (SLC23A2)	3	D87075		+	+	+		+	
solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11 (SLC25A11)	1	AF070548	B, T	+	+		+	+	
solute carrier family 31 (copper transporters), member 2 (SLC31A2)	3	U83461		+		+			
solute carrier family 4, anion exchanger, member	1	X62137		+	+			+	

2 (erythrocyte membrane protein band 3-like 1) (SLC4A2)									
solute carrier family 4, sodium bicarbonate cotransporter, member 8 (SLC4A8)	1	AB018282		+					
solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 (SLC7A5)	2	M80244	T, W	+	+		+		
solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 (SLC7A6)	3	D87432	+	+	+			+	
solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 (SLC7A6) (non-exact 77%)	1	D87432							
solute carrier family 9 (sodium/hydrogen exchanger), isoform 6 (SLC9A6)	1	AF030409		+	+	+		+	
somatic cytochrome c (HCS)	2	M22877							
SON DNA binding protein (SON)	2	X63753		+	+	+		+	
son of sevenless (Drosophila) homolog 1 (SOS1)	1	L13858	+	+		+			
sorcin (SRI)	1	M32886							
sortilin 1 (SORT1)	2	X98248		+		+		+	
sortilin-related receptor, L (DLR class) A repeats-containing (SORL1)	6	Y08110							
sorting nexin 1 (SNX1)	3	U53225	+	+	+	+		+	
sorting nexin 2 (SNX2)	2	AF043453							
sorting nexin 6 (SNX6) (=U83194.1 TRAF4-associated factor 2)	1	AF121856.1							

Sp3 transcription factor (SP3)	1	X68560	+	+	+	+		+	
Sp3 transcription factor (SP3)	4	M97191	+	+	+	+		+	
special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's) (SATB1)	1	M97287							
speckle-type POZ protein (SPOP)	4	AJ000644							
speckle-type POZ protein (SPOP) (non-exact)	1	AJ000644							
spectrin SH3 domain binding protein 1 (SSH3BP1)	6	U87166	+	+	+	+			
Spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) (SPTAN1)	2	J05243		+	+			+	
spermidine/spermine N1-acetyltransferase (SAT)	11	M55580							
spermidine/spermine N1-acetyltransferase (SAT) (non-exact, 84%)	1	U40369							
spermine synthase (SMS)	1	AD001528	+	+	+	+		+	
SPF31' (SPF31)	1	AF083190	+	+	+	+		+	
sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase) (SMPD1)	1	X52679		+	+		+		
SPINDLIN HOMOLOG (PROTEIN DXF34)	1	Q99865							
spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) (SCA1)	3	X79204	B	+				+	
spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2) (SCA2)	1	U70323	B					+	

spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration) (SCA7)	2	AJ000517		+						
spliceosome associated protein (SAP 145)	3	U41371		+	+	+	+	+		
splicing factor (CC1.3) (CC1.3)	2	L10910	+	+	+	+	+	+		
splicing factor SRp40-1 (SRp40)	7	U30826	+	+	+	+	+	+		
splicing factor, arginine/serine-rich 11 (SFRS11)	3	M74002	B	+	+			+	+	
splicing factor, arginine/serine-rich 7 (35kD) (SFRS7)	4	L41887		+	+	+			+	
Src-like adapter protein (non-exact, 76%aa)	1	U30473								
Src-like-adapter (SLA)	6	D89077		+	+	+			+	
Src-like-adapter (SLA) (low match)	1	D89077								
Src-like-adapter (SLA) (low score)	1	U44403								
stannin (SNN)	2	AF030196	+	+	+	+			+	
STAT induced STAT inhibitor 3 (SSI-3)	1	AB004904				+				
STE20-like kinase 3 (MST- 3)	2	AF024636	+	+	+	+			+	
step II splicing factor SLU7 (SLU7)	1	AF101074		+		+	+	+		
steroid sulfatase	1	M17591								
steroid sulfatase (microsomal), arylsulfatase C, isozyme S (STS)	1	J04964		+	+	+				
sterol carrier protein 2 (SCP2)	1	M55421		+	+	+	+	+		
sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase)	1	AF059202						+		

1 (SOAT1)									
stimulated trans-acting factor (50 kDa) (STAF50)	6	X82200	+	+		+			
Striatin, calmodulin-binding protein (STRN) (low match, 71%aa)	1	U17989							
Stromal antigen 2 (STAG2)	2	Z75331			+	+	+	+	
stromal interaction molecule 1 (STIM1)	3	U52426	+	+	+	+		+	
structure specific recognition protein 1 (SSRP1)	1	M86737		+	+	+		+	
succinate dehydrogenase complex, subunit A, flavoprotein (Fp) (SDHA)	5	L21936			+				
succinate dehydrogenase complex, subunit B, iron sulfur (Ip) (SDHB)	1	U17248	+	+	+	+		+	
succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC)	1	U57877	+	+	+	+		+	
succinate dehydrogenase complex, subunit D, Integral membrane protein (SDHD)	3	AB006202		+	+		+		
succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2)	1	AF058954		+	+	+	+	+	
succinyl CoA synthetase	1	Z68204							
sudD (suppressor of bimD6, Aspergillus nidulans) homolog (SUDD)	2	AF013591		+			+	+	
sulfotransferase family 1A, phenol-preferring, member 1 (SULT1A1)	1	L19999		+			+	+	
sulfotransferase family 1A, phenol-preferring, member 3 (SULT1A3) (non-exact 67%)	1	U37686							
superoxide dismutase 1, soluble (amyotrophic lateral	4	X02317		+	+		+	+	

sclerosis 1 (adult)) (SOD1)									
superoxide dismutase 2, mitochondrial (SOD2)	5	Y00985		+	+	+	+	+	
supervillin (SVIL)	2	AF051851			+	+		+	
suppression of tumorigenicity 5 (ST5)	2	U15131		+		+		+	
suppression of tumorigenicity 5 (ST5) (non-exact 82%)	1	U15779							
suppressor of K+ transport defect 1 (SKD1)	1	AF038960			+	+			
suppressor of Ty (S.cerevisiae) 3 homolog (SUPT3H)	1	AF064804	+	+	+	+		+	
suppressor of Ty (S.cerevisiae) 4 homolog 1 (SUPT4H1)	2	U38817	+	+	+	+		+	
suppressor of Ty (S.cerevisiae) 5 homolog (SUPT5H)	2	U56402		+				+	
suppressor of Ty (S.cerevisiae) 6 homolog (SUPT6H)	2	U46691	+	+	+	+	+	+	
suppressor of variegation 3-9 (Drosophila) homolog-1 (SUV39H1)	1	AF019968		+	+	+			
survival of motor neuron 1, telomeric (SMN1)	1	U18423							
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SMARCA1) (non-exact, 75%)	1	M88163			+	+		+	
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2)	2	D26155		+					
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,	1	D26156	+	+	+	+	+	+	

member 4 (SMARCA4)									
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2 (SMARCC2)	4	U66616	+	+	+	+	+	+	
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 (SMARCE1)	2	AF035262	B, W	+	+		+	+	
synaptobrevin-like 1 (SYBL1)	1	X95803		+	+	+		+	
synaptosomal-associated protein, 23kD (SNAP23)	2	AJ011915		+	+	+		+	
syndecan binding protein (syntenin) (SDCBP)	15	AF006636	+	+	+	+		+	
synovial sarcoma, translocated to X chromosome (SSXT)	2	X79201		+					
syntaxin 16	1	AF038897							
syntaxin 3A (STX3A)	2	U32315		+		+		+	
syntaxin 6 (STX6)	1	AJ002078.1							
SYNTAXIN BINDING PROTEIN 3 (UNC-18 HOMOLOG 3) (UNC-18C)	1	O00186							
syntaxin-16C	1	AF008937							
SYT interacting protein (SIP)	1	AF080561		+	+	+		+	
T cell activation, increased late expression (TACTILE)	4	M88282				+			
T cell receptor V alpha gene segment V-alpha-7 (clone IGRa11)	2	X58744							
T cell receptor V alpha gene segment V-alpha-w27	1	X58740							
T3 receptor-associating cofactor-1	5	S83390	+	+	+	+	+	+	

tafazzin (cardiomyopathy, dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome) (TAZ)	1	X92763	+	+		+		+	
TAFII100 protein (non-exact 53%)	1	U80191							
tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS)	1	AF082556		+	+	+		+	
TAP1, TAP2, LMP2, LMP7 and DOB	1	X66401							
TAR DNA-binding protein-43	6	U23731	+	+	+	+		+	
Tat interactive protein (60kD) (TIP60)	2	U40989	+	+	+	+		+	
TATA box binding protein (TBP)-associated factor, RNA polymerase II, C1, 130kD (TAF2C1) (non-exact, 55%)	1	O00268							
TATA box binding protein (TBP)-associated factor, RNA polymerase II, F, 55kD (TAF2F)	4	X97999		+	+	+	+	+	
TATA box binding protein (TBP)-associated factor, RNA polymerase II, G, 32kD (TAF2G)	2	U21858		+	+	+	+	+	
TATA box binding protein (TBP)-associated factor, RNA polymerase II, I, 28kD (TAF2I)	1	D63705	+	+	+	+		+	
Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1)	1	U33821		+	+	+	+	+	
T-box 2 (TBX2) (non-exact 77%)	1	U28049			+	+		+	
TBP-associated factor 172 (TAF-172)	1	AJ001017		+		+		+	
T-cell death-associated gene 8 (TDAG8)	1	U95218				+			

T-cell leukemia/lymphoma 1A (TCL1A)	1	X82240	+							
T-cell leukemia/lymphoma 1A (TCL1A) (low match)	1	X82240								
T-cell receptor (delta D2-J1-region) (clone K3B)	1	M22197								
T-cell receptor (V beta 5.1, J beta 1.5, C beta 1) (low match)	1	M97705								
T-cell receptor alpha delta (=M94081)	2	AE000662								
T-cell receptor alpha enhancer-binding protein, short form (=X58636 Mouse LEF1 lymphoid enhancer binding factor 1 (=D16503))	1	B39625								
T-cell receptor delta gene D2-J1-region, clone K3B	1	M22197								
T-cell receptor germline beta chain gene V-region (V) V-beta-MT1-1	1	M11955								
T-cell receptor germline beta-chain gene J2.1 exon	1	M14159	+							only in blood
T-cell receptor germline delta-chain D-J region	2	M22152								
T-cell receptor interacting molecule (TRIM) protein	2	AJ224878							+	
T-cell receptor rearranged delta-chain, V-region (V-delta 3-J)	1	M21784								
T-cell receptor, alpha (V,D,J,C) (TCRA)	3	AE000660	+	+	+	+			+	
T-cell receptor, beta cluster (TCRB)	3	L34740	+	+	+	+	+	+	+	high in pancreas
T-cell receptor, delta (V,D,J,C) (TCRD)	2	X73617			+	+			+	
T-cell, immune regulator 1 (TCIRG1)	3	U45285								only found in tumor
TCF-1 mRNA for T cell	1	X59870								

factor 1									
TCF-1 mRNA for T cell factor 1 (splice form B) (low match)	1	X59870							
T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) (HIV-1 NEF INTERACTING PROTEIN)	1	Q99832							
T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) (CCT-THETA) (KIAA0002)	1	P50990							
TCR eta =T cell receptor(eta-exon)	1	S94421							
TCR V Beta 13.2	1	X75419							
TERA	1	AC004472							
testis enhanced gene transcript (TEGT)	33	X75861	+	+	+	+	+	+	
tetracycline transporter-like protein (TETRAN)	2	L11669		+	+	+		+	
tetratricopeptide repeat domain 1 (TTC1)	1	U46570	+	+	+	+		+	
tetratricopeptide repeat domain 2 (TTC2)	1	U46571		+		+		+	
tetratricopeptide repeat domain 3 (TTC3)	1	D84296	+	+	+	+		+	
TGFB1-induced anti-apoptotic factor 1 (TIAF1)	1	D86970	+	+	+	+		+	
thioredoxin reductase 1 (TXNRD1)	3	S79851		+	+	+		+	
THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE PRECURSOR, mitochondrial (ANTI-OXIDANT PROTEIN 1) (AOP-1)	1	P30048							
threonyl-tRNA synthetase (TARS)	1	M63180		+	+	+		+	

thrombin inhibitor	1	Z22658							
thrombospondin 1 (THBS1)	2	X04665		+	+	+	+	+	
thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V) (TBXAZ1)	1	M80647		+		+	+	+	
thymidine kinase 2, mitochondrial (TK2)	2	X76104		+	+		+		
thymidylate kinase (CDC8)	1	L16991		+	+	+		+	
thymine-DNA glycosylase (TDG)	2	U51166	+	+	+	+		+	
Thymosin, beta 10 (TMSB10)	2	M20259	+	+	+	+	+	+	
thymosin, beta 4, X chromosome (TMSB4X)	29	M17733		+	+	+		+	
thyroid autoantigen 70kD (Ku antigen) (G22P1)	7	J04611							
thyroid hormone receptor coactivating protein (SMAP)	1	AF016270		+		+		+	
thyroid hormone receptor interactor 7 (TRIP7)	2	L40357		+	+	+		+	
thyroid hormone receptor interactor 8r (TRIP8)	4	L40411		+					
thyroid hormone receptor- associated protein, 230 kDa subunit (TRAP230)	1	D83783							
thyroid receptor interacting protein 15 (TRIP15)	2	L40388	+	+	+	+			
TI-227H	1	D50525							
TIA1 cytotoxic granule- associated RNA-binding protein (TIA1)	1	M77142		+	+	+		+	
tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1)	1	X02598	+	+	+	+	+	+	
tissue inhibitor of metalloproteinase 2	1	M32304	+	+	+	+		+	high in placenta

(TIMP2)									
tissue specific transplantation antigen P35B (TSTA3)	1	U58766	+	+	+	+		+	
titin (TTN)	1	X64697	+	+	+	+		+	high in muscle
TNF receptor-associated factor 2 (TRAF2)	1	U12597		+	+	+		+	
TNF receptor-associated factor 3 (TRAF3)	1	AF110908.1		+					
TNF receptor-associated factor 6 (TRAF6) (low match)	1	U78798							
toll-like receptor 1 (TLR1)	1	U88540				+			
toll-like receptor 2 (TLR2)	1	U88878	+	+		+		+	
toll-like receptor 4 (TLR4)	1	U88880		+			+		
toll-like receptor 5 (TLR5)	1	AF051151		+		+			
topoisomerase (DNA) I (TOP1)	1	J03250		+	+	+			
topoisomerase (DNA) II beta (180kD) (TOP2B)	2	X68060	+	+	+	+		+	
topoisomerase (DNA) III beta (TOP3B)	3	D87012	+						
TR3beta	1	D85245		+					
TRAF family member-associated NF-kB activator (TANK)	3	U63830	+	+	+	+	+	+	
TRANSALDOLASE	1	P37837							
transaldolase 1 (TALDO1)	4	L19437		+	+	+	+	+	
transaldolase-related protein	1	AF010398							
transcobalamin II (TCII)	1	AF047576							
transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L)	2	Z47087	+	+	+	+		+	
transcription elongation factor B (SIII), polypeptide	1	L47345	+	+	+	+	+	+	

3 (110kD, elongin A) (TCEB3)									
transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12)	1	M83233	+	+	+	+		+	
transcription factor 17 (TCF17)	2	D89928		+		+			
transcription factor 4 (TCR4)	2	X52079		+	+	+		+	
transcription factor 6-like 1 (mitochondrial transcription factor 1-like) (TCF6L1)	2	M62810	+	+	+	+			
transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2)	1	Y11306		+	+	+		+	
transcription factor binding to IGHM enhancer 3 (TFE3)	1	X96717	+	+	+	+		+	
transcription factor IL-4 Stat	7	AF067575	+	+	+	+	+	+	
transcription factor IL-4 Stat (low match)	1	U16031							
transcription factor ISGF-3 (=M97936)	4	M97935							
transcription factor REST	1	A56138							
transcription factor TFIIID	1	Z22828							
transcriptional adaptor 2 (ADA2, yeast, homolog)- like (TADA2L)	1	AF064094							
transcriptional intermediary factor 1 (TIF1) (non-exact 72%)	1	AF009353							
transducin (beta)-like 1 (TBL1)	1	Y12781	+	+	+	+		+	
transducin-like enhancer of split 3, homolog of Drosophila E(sp1) (TLE3)	1	M99438	+	+					
Transformation/transcription domain-associated protein (TRRAP)	1	AF076974	+	+	+	+		+	

transformation-sensitive, similar to <i>Saccharomyces cerevisiae</i> STI1 (STI1L)	2	M86752		+	+	+		+	
transforming growth factor beta-activated kinase 1 (TAK1) (non-exact 78%)	1	AB009356							
transforming growth factor beta-stimulated protein TSC-22 (TSC22)	3	AJ222700	+	+	+	+		+	
transforming growth factor, beta receptor III (betaglycan, 300kD) (TGFB3)	1	L07594		+	+	+		+	
transforming growth factor, beta-induced, 68kD (TGFB1)	2	4507466	+	+	+	+	+	+	
TRANSFORMING GROWTH FACTOR-BETA INDUCED PROTEIN IG-H3 PRECURSOR (BETA IG-H3)	2	Q15582							
transforming, acidic coiled-coil containing protein 1 (TACC1) (non-exact 70%)	1	AF049910							
transgelin 2 (TAGLN2)	14	D21261	+	+	+	+	+	+	
transgelin 2 (TAGLN2) (non-exact)	1	D21261							
trans-Golgi network protein (46, 48, 51kD isoforms) (TGN51)	2	AF029316		+		+			
transient receptor potential channel 1 (TRPC1)	1	X89066		+	+	+		+	
transketolase (Wernicke-Korsakoff syndrome) (TKT)	7	L12711		+	+	+		+	
translation factor sui1 homolog (GC20)	1	AF064607		+	+	+	+	+	
translin (TSN)	3	X78627	+	+	+	+		+	
translin-associated factor X (TSNAX)	1	X95073		+	+	+		+	
transmembrane glycoprotein (A33)	1	U79725							

transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment (P63)	1	X69910	+	+	+	+		+	
transmembrane protein 1 (TMEM2)	1	AB001523		+		+		+	
TRANSMEMBRANE PROTEIN SEX PRECURSOR (non-exact 65%)	1	P51805							
transmembrane trafficking protein (TMP21)	2	X97442	+	+	+	+	+	+	
transporter 1, ABC (ATP binding cassette) (TAP1)	3	L21208	+	+	+	+		+	
Treacher Collins-Franceschetti syndrome 1 (TCOF1)	2	U40847	+	+	+	+		+	high in many libraries
triosephosphate isomerase 1 (TPI1)	2	X69723	+	+	+	+	+	+	
tropomyosin	2	X04201		+	+	+		+	
tropomyosin 4 (TPM4)	2	X05276	+	+	+	+		+	
TRPM-2 protein	2	M63376							
tryptase I precursor (non-exact 64%)(=P20231)	1	A35863							
tryptophan rich basic protein (WRB)	1	Y12478							
tryptophanyl-tRNA synthetase (WARS)	1	X59892	+	+	+	+	+	+	
Ts translation elongation factor, mitochondrial (TSFM)	1	L37936	+	+		+		+	
ttopoisomerase (DNA) II beta (180kD)	1	Z15115		+	+			+	
Tu translation elongation factor, mitochondrial (TUFM)	4	L38995							
tuberous sclerosis 1 (TSC1)	1	AF013168		+	+	+		+	

tuberous sclerosis 2 (TSC2)	1	X75621		+	+	+		+	
tubulin, alpha 1 (testis specific) (TUBA1)	1	X06956		+			+		
tubulin, alpha, ubiquitous (K-ALPHA-1)	11	K00558	+	+	+	+	+	+	high in many libraries
tubulin, alpha, ubiquitous (K-ALPHA-1) (low match)	1	K00558							
tubulin-specific chaperone c (TBCC)	1	U61234		+	+	+		+	
tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10)	7	U37518		+	+	+		+	
tumor necrosis factor (ligand) superfamily, member 13 (TNFSF13)	1	AF046888	+	+		+		+	
tumor necrosis factor (ligand) superfamily, member 14 (TNFSF14)	1	AF036581							
tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6)	1	D38122	+						Found only in library 386: T-cell lymphoma
tumor necrosis factor (ligand) superfamily, member 8 (TNFSF8)	1	L09753	B only						
tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains (FIP2)	1	AF061034		+	+	+		+	
Tumor necrosis factor receptor superfamily member 7 (TNFRSF7)	2	M63928		+				+	
tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B)	1	AF016266		+	+	+	+	+	
tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain (TNFRSF10C)	3	AF012629						+	
tumor necrosis factor receptor superfamily, member 10d, decoy with	1	AF023849							found only in prostate

truncated death domain (TNFRSF10D) (non-exact 84%)									
tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein) (TNFRSF12)	1	U94508	+	+	+	+		+	
tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator) (TNFRSF14)	1	U70321	+	+	+	+		+	
tumor necrosis factor receptor superfamily, member 1B (TNFRSF1B)	5	U52165	+	+	+	+		+	
tumor necrosis factor receptor superfamily, member 6 (TNFRSF6)	1	X63717	B, W					+	
tumor necrosis factor receptor superfamily, member 7 (TNFRSF7)	1	M63928	+	+					
tumor necrosis factor, alpha-induced protein 2 (TNFAIP2)	8	M92357		+	+		+		
tumor necrosis factor, alpha-induced protein 3 (TNFAIP3)	2	M59465							
tumor protein 53-binding protein, 1 (TP53BP1)	1	AF078776		+	+	+		+	
tumor protein p53 (Li-Fraumeni syndrome) (TP53)	1	M14695	+	+				+	
Tumor protein p53-binding protein (TP53BPL)	1	U82939	+			+		+	
tumor protein, translationally-controlled 1 (TPT1)	35	X16064							
tumor protein, translationally-controlled 1 (TPT1) (low score)	1	X16064							

tumor rejection antigen (gp96) 1 (TRA1)	9	X15187	+	+	+	+	+	+	
tumorous imaginal discs (Drosophila) homolog (TID1)	2	AF061749		+					
TXK tyrosine kinase (TXK)	2	L27071							
type II integral membrane protein (NKG2-E)	1	AJ001685					+		found only in fetal liver/spleen
TYRO protein tyrosine kinase binding protein (TYROBP)	3	AF019562			+				
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide (YWHAB)	1	X57346	+	+	+	+		+	high in ecnorm
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ)	1	M86400							
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ)	1	M86400							
Tyrosine kinase 2 (TYK2)	3	X54637		+	+	+		+	
TYROSINE-PROTEIN KINASE ZAP-70 (70 KD ZETA-ASSOCIATED PROTEIN) (SYK-RELATED TYROSINE KINASE)	2	P43403							
tyrosyl-tRNA synthetase (YARS)	1	U89436	+	+	+	+		+	
U1 small nuclear RNA	1	M14387							
U19H snoRNA (=M63485 R.norvegicus matrin 3)	1	AJ224166							
U2(RNU2) small nuclear RNA auxilliary factor 1 (non-standard symbol) (U2AF1)	1	M96982		+	+	+		+	

U22 snoRNA host gene (UHG)	2	U40580								
U4/U6-associated RNA splicing factor (HPRP3P)	4	AF016370		+	+	+			+	
U49 small nuclear RNA	1	X96649								
U5 snRNP-specific protein (220 kD), ortholog of <i>S. cerevisiae</i> Prp8p (PRP8)	1	AB007510	+	+	+	+			+	
U5 snRNP-specific protein, 116 kD (U5-116KD)	4	D21163	+	+	+	+			+	
U5 snRNP-specific protein, 200 kDa (DEXH RNA helicase family) (U5-200-KD)	3	Z70200								
Uba80 mRNA for ubiquitin	4	S79522	+	+	+	+	+	+		high in ovary
ubiquinol-cytochrome c reductase (6.4kD) subunit (UQCR)	1	D55636	+	+	+	+	+	+		high in fetal lung
UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) (low match)	1	P47985								
ubiquitin A-52 residue ribosomal protein fusion product 1 (UBA52)	2	X56999								
ubiquitin activating enzyme E1-like protein (GSA7)	1	AF094516		+	+				+	
ubiquitin C (UBC)	5	AB009010		+	+	+	+	+		high in ovary
ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) (UCHL3)	1	M30496	+	+	+	+			+	
ubiquitin fusion degradation 1-like (UFD1L)	1	U64444	+	+	+	+			+	
ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A)	1	U84404	B	+	+				+	

ubiquitin specific protease 10 (USP10)	4	D80012	+	+	+	+		+	
ubiquitin specific protease 11 (USP11)	1	U44839	+	+	+	+	+	+	
ubiquitin specific protease 15 (USP15)	3	AB011101	+	+	+	+		+	
ubiquitin specific protease 19 (USP19)	1	AB020698		+					
ubiquitin specific protease 4 (proto-oncogene) (USP4)	1	AF017305	B	+	+		+	+	
ubiquitin specific protease 4 (proto-oncogene) (USP4) (non-exact, 66%)	1	AF017306							
ubiquitin specific protease 7 (herpes virus-associated) (USP7)	1	Z72499		+	+	+		+	
ubiquitin specific protease 8 (USP8)	5	D29956		+	+	+		+	
UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN) (56%)	1	P22314							
ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing) (UBE1)	1	M58028	+	+	+	+		+	
ubiquitin-activating enzyme E1, like (UBE1L)	1	L34170	+	+		+		+	
UBIQUITIN-BINDING PROTEIN P62; phosphotyrosine independent ligand for the Lck SH2 domain p62 (P62)	1	U41806			+		+		
ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1)	2	U49278	+	+	+	+	+	+	
ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2)	1	X98091							
UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE)	1	Q16781							

ubiquitin-conjugating enzyme E2B (RAD6 homolog) (UBE2B)	1	M74525	+	+	+	+		+	
ubiquitin-conjugating enzyme E2G 2 (homologous to yeast UBC7) (UBE2G2)	1	AF032456	+	+	+	+		+	
ubiquitin-conjugating enzyme E2H (homologous to yeast UBC8) (UBE2H)	1	Z29328	+	+	+	+		+	
ubiquitin-conjugating enzyme E2L 1 (UBE2L1)	1	X92962		+	+			+	
ubiquitin-conjugating enzyme E2L 3 (UBE2L3)	3	AJ000519		+	+	+		+	
ubiquitin-conjugating enzyme E2L 6 (UBE2L6)	4	AF031141		+	+	+	+	+	
ubiquitin-like 1 (sentrin) (UBL1)	2	U61397	+	+	+	+		+	
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 2 (GalNAc-T2) (GALNT2)	2	X85019							
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 3 (GalNAc-T3) (GALNT3) (non-exact 65%)	1	X92689							
inactive progesterone receptor, 23 Kd (P23)	2	L24804		+	+	+		+	
unconventional myosin-ID (MYO1F)	3	U57053							
uncoupling protein homolog (UCPH)	1	U94592							
uncoupling protein homolog (UCPH) (low match 67%)	1	U94592							
Unknown gene product	1	AC002310							
unknown mRNA (clone 24514)	1	AF070542							

unknown protein (clone ICRFp507L0677)	2	Z70223							
unknown protein (Hs.93832)	1	AF070626	+	+	+	+	+	+	
unknown protein IT14	1	AF040966							
uppressor of Ty (S.cerevisiae) 6 homolog	1	D79984	+	+	+	+	+	+	
upregulated by 1,25-dihydroxyvitamin D-3 (VDUP1)	74	S73591	+	+	+	+		+	high in heart
upregulated by 1,25-dihydroxyvitamin D-3 (VDUP1) (low match)	1	S73591							
upregulated by 1,25-dihydroxyvitamin D-3 (VDUP1) (low match)	1	S73591							
upregulated by 1,25-dihydroxyvitamin D-3 (VDUP1) (low score)	1	S73591							
upstream binding factor (hUBF)	1	X53461	+	+		+		+	
UV radiation resistance associated gene (UVRAG)	2	X99050		+	+	+		+	
vacuolar proton-ATPase, subunit D; V-ATPase, subunit D (ATP6DV)	4	X71490		+	+	+	+	+	
v-akt murine thymoma viral oncogene homolog 1 (AKT1)	1	M63167	+	+	+	+		+	
Vanin 2 (VNN2)	3	AJ132100							
vasodilator-stimulated phosphoprotein (VASP)	3	Z46389	+		+	+		+	
vav 1 oncogene (VAV1)	1	M59834						+	
vav 2 oncogene (VAV2)	1	S76992	+	+					
v-crk avian sarcoma virus CT10 oncogene homolog (CRK)	1	D10656	W	+	+		+		
v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3	1	M29366						+	

(ERBB3)										
VERSICAN CORE PROTEIN PRECURSOR	1	P13611								
Vesicle-associated membrane protein 1 (synaptobrevin 1) (VAMP1)	1	M36196		+	+	+		+		
vesicle-associated membrane protein 3 (cellubrevin) (VAMP3)	1	U64520								
v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	26	K00650		+	+	+	+	+		high in aorta
v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS) (low match)	1	K00650								
villin 2 (ezrin) (VIL2)	1	X51521	+	+	+	+		+		
villin-like protein	1	D88154								
vimentin (VIM)	12	X56134		+	+	+	+	+		high in many libraries
vinculin (VCL)	4	M33308		+	+	+		+		
vitamin A responsive; cytoskeleton related (JWA)	6	AF070523		+	+	+		+		
v-jun avian sarcoma virus 17 oncogene homolog (JUN)	2	U65928	+	+	+	+		+		
v-myb avian myeloblastosis viral oncogene homolog (MYB)	1	M15024			+			+		
voltage-dependent anion channel 1 (VDAC1)	1	L06132	+	+	+	+		+		
voltage-dependent anion channel 3 (VDAC3)	4	U90943		+	+	+		+		
von Hippel-Lindau syndrome (VHL)	1	L15409		+	+	+		+		
von Willebrand factor (vWF) (low matched)	1	X06828								
v-raf murine sarcoma 3611 viral oncogene homolog 1	2	L24038	+	+	+	+				

(ARAF1)									
v-raf-1 murine leukemia viral oncogene homolog 1 (RAF1)	1	X03484	+	+	+	+		+	
v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein) (RALB)	3	M35416							
V-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA)	1	L19067		+	+	+		+	
v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN)	2	M16038	+	+		+		+	
WD repeat domain 1 (WDR1)	1	AB010427	+	+	+	+	+	+	
WDR1 (=AF020260)	1	AF020056							
WD-repeat protein (HAN11)	2	U94747		+	+			+	
Williams-Beuren syndrome chromosome region 1 (WBSCR1)	12	AF045555	+	+	+	+	+	+	
Wiskott-Aldrich syndrome protein interacting protein (WASPIP)	4	X86019	+	+	+			+	
X (inactive)-specific transcript (XIST)	2	M97168							
xeroderma pigmentosum, complementation group C (XPC)	3	D21089	+	+	+	+			
XIAP associated factor-1	2	X99699				+			
XIB	1	X90392		+	+		+	+	
X-linked anhidrotic ectodermal dysplasia	1	AF003528							
X-ray repair complementing defective repair in Chinese hamster cells 5 (double-	1	M30938	+	+	+	+		+	high in spleen

strand-break rejoining; Ku autoantigen, 80kD) (XRCC5)									
XRP2 protein	1	AJ007590							
yeloid differentiation primary response gene (88) (MYD88)	1	U84408		+	+	+		+	
zeta-chain (TCR) associated protein kinase (70kD) (ZAP70)	1	L05148	+			+			
zeta-chain (TCR) associated protein kinase (70kD) (ZAP70) (low match)	1	L05148							
zinc finger protein (Hs.47371)	2	U69274	+	+	+	+		+	
zinc finger protein (Hs.78765)	1	U69645	+	+	+	+		+	
zinc finger protein 10 (KOX 1) (ZNF10)	1	X78933						+	only
ZINC FINGER PROTEIN 124 (HZF-16) (non-exact 51%)	1	Q15973							
zinc finger protein 124 (HZF-16) (ZNF124) (non- exact, 78%)	1	S54641							
ZINC FINGER PROTEIN 133	1	P52736							
zinc finger protein 136 (clone pHZ-20) (ZNF136)	1	U09367			+	+			
zinc finger protein 140 (clone pHZ-39) (ZNF140)	1	U09368		+		+		+	
zinc finger protein 140 (clone pHZ-39) (ZNF140) (non-exact 59%)	1	AF060865							
zinc finger protein 140 (clone pHZ-39) (ZNF140) (non-exact 73%)	1	U09368							
zinc finger protein 140 (clone pHZ-39) (ZNF140)	1	S66508							

(non-exact 73%aa)										
zinc finger protein 140 (clone pHZ-39) (ZNF140) (non-exact, 80%)	1	U09368								
zinc finger protein 143 (clone pHZ-1) (ZNF143)	2	U09850	+	+	+	+	+	+		
zinc finger protein 143 (clone pHZ-1) (ZNF143) (low match)	1	U09850								
zinc finger protein 148 (pHZ-52) (ZNF148)	1	AF039019	+							
ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN) (low match)	1	Q13105								
zinc finger protein 173 (ZNF173)	1	U09825	B, T	+	+		+			
zinc finger protein 192 (ZNF192) (non-exact, 66%)	1	U57796								
zinc finger protein 198 (ZNF198)	1	AJ224901		+	+	+				
zinc finger protein 2 (ZNF2) (low match)	1	X60152								
zinc finger protein 200 (ZNF200)	1	AF060866		+		+				
zinc finger protein 207 (ZNF207)	6	AF046001	+	+	+	+	+	+		high in prostate
zinc finger protein 216 (ZNF216)	2	AF062072	+	+	+	+		+		
zinc finger protein 217 (ZNF217)	1	AF041259	T activated					+		
ZINC FINGER PROTEIN 22 (ZINC FINGER PROTEIN KOX15) (non- exact 58%)	1	P17026								
zinc finger protein 230 (ZNF230)	1	U95044		+						
Zinc finger protein 239 (ANF239)	1	L26914		+		+				

zinc finger protein 261 (ZNF261)	1	AB002383		+	+	+		+	
zinc finger protein 262 (ANF262)	1	AB007885		+	+	+		+	
zinc finger protein 263 (ZNF263)	1	D88827							
zinc finger protein 264 (ZNF264)	1	AB007872		+	+	+			
ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946)	1	Q06730							
zinc finger protein 42 (myeloid-specific retinoic acid- responsive) (ZNF42)	1	M58297	+	+	+	+		+	
zinc finger protein 43 (HTF6) (ZNF43) (low match)	1	X59244							
zinc finger protein 43 (HTF6) (ZNF43) (non-exact, 54%)	1	X59244							
zinc finger protein 43 (HTF6) (ZNF43) (non-exact, 71%)	1	X59244							
ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6) (non-exact 67%)	1	P28160							
zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide) (ZNF45)	1	L75847							only found in testis
ZINC FINGER PROTEIN 46 (ZINC FINGER PROTEIN KUP) (non-exact 62%)	1	P24278							
zinc finger protein 6 (CMPX1) (ZNF6)	1	X56465		+	+	+		+	
zinc finger protein 74 (Cos52) (ZNF74) (non-exact, 67%)	1	X71623							
zinc finger protein 76 (expressed in testis)	1	M91592		+	+	+		+	

(ZNF76)									
ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1) (non-exact 65%)	1	P51522							
zinc finger protein 84 (HPF2) (ZNF84)	1	M27878	T activated	+	+			+	
zinc finger protein 85 (ZNF85))	2	U35376		+	+	+			
zinc finger protein 9 (ZNF9)	5	M28372		+	+	+	+	+	
ZINC FINGER PROTEIN 93 (=ZINC FINGER PROTEIN HTF34) (non-exact 70%)	1	P35789							
zinc finger protein C2H2-25 (ZNF25)	3	U38904		+	+	+			
zinc finger protein clone L3-4	1	AF024706							
zinc finger protein homologous to Zfp-36 in mouse (ZFP36)	4	M92843	+						blood only
ZINC FINGER PROTEIN HRX (ALL-1) (71%a.a.)	1	Q03164							
zinc finger protein HZF4	1	X78927							
zinc finger protein RIZ	1	D45132	+	+	+	+		+	
zinc finger protein, subfamily 1A, 1 (Ikaros) (LYF1)	1	U40462	+						
zinc finger protein, subfamily 1A, 1 (Ikaros) (LYF1) (low match)	1	U40462							
zinc finger transcriptional regulator (GOS24)	1	M92844							
zinc-finger helicase (hZFH)	2	U91543	+	+	+	+		+	
Zn-15 related zinc finger protein (rlf)	1	U22377		+	+	+			
Zn-15 related zinc finger protein (rlf) (non-exact	1	U22377							

56%)										
ZNF80-linked ERV9 long terminal repeat	1	X83497								
ZW10 (Drosophila) homolog, centromere/kinetochore protein (ZW10)	2	U54996		+						
zyxin (ZYG)	4	X95735								

TABLE 3A					
Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	D scription	Gene Accession No.	Unig n Accession No.	Protein Accession No.
195	0.020318	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen; 80kDa) (XRCC5), mRNA /cds=(34,2232) /gb=NM_021141 /gi=12408650 /ug=Hs.84981 /len=3310	NM_021141	Hs.84981	NP_066964
248	0.004993	hemoglobin, beta (HBB), mRNA /cds=(51,494) /gb=NM_000518 /gi=28302128 /ug=Hs.155376 /len=626	NM_000518	Hs.155376	NP_000509
288	0.039781	phosphodiesterase 8B (PDE8B), mRNA /cds=(46,2703) /gb=NM_003719 /gi=26006850 /ug=Hs.78106 /len=3567	NM_003719	Hs.78106	NP_003710
310	0.037168	kinesin family member 13B (KIF13B), mRNA /cds=(38,5518) /gb=NM_015254 /gi=13194196 /ug=Hs.15711 /len=8743	NM_015254	Hs.15711	NP_056069
323	0.01661	associated molecule with the SH3 domain of STAM (AMSH), mRNA /cds=(188,1462) /gb=NM_006463 /gi=17738303 /ug=Hs.12479 /len=2107	NM_006463	Hs.12479	NP_006454
338	0.042541	chromosome 11 hypothetical protein ORF3 (LOC56851), mRNA /cds=(14,742) /gb=NM_020154 /gi=9910345 /ug=Hs.4245 /len=1072	NM_020154	Hs.4245	NP_064539
357	0.02428	deleted in pancreatic carcinoma (DPC4) gene, exon 3	AF045440		
362	0.039781	reversion-inducing-cysteine-rich protein with kazal motifs (RECK), mRNA /cds=(93,3008) /gb=NM_021111 /gi=11863155 /ug=Hs.29640 /len=4414	NM_021111	Hs.29640	NP_066934
367	0.037046	RNA (guanine-7-) methyltransferase (RNMT), mRNA /cds=(197,1627) /gb=NM_003799 /gi=4506566 /ug=Hs.8086 /len=6203	NM_003799	Hs.8086	NP_003790
394	0.006608	FLJ11874 fis, clone HEMBA1007073 /cds=UNKNOWN /gb=AK021936 /gi=10433239 /ug=Hs.367819 /len=2737	AK021936	Hs.367819	
434	0.032363	phosphoglycerate kinase 1 (PGK1), mRNA /cds=(70,1323) /gb=NM_000291 /gi=22095338 /ug=Hs.78771 /len=2338	NM_000291	Hs.78771	NP_000282
448	0.028082	laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=NM_002295 /gi=9845501 /ug=Hs.181357 /len=1039	NM_002295	Hs.181357	NP_002286
460	0.03016	sorting nexin 3 (SNX3), transcript variant 3, mRNA /cds=(326,667) /gb=NM_152828 /gi=23111042 /ug=Hs.12102 /len=1559	NM_152828	Hs.12102	NP_690041
462	0.048903	erg protein (ets-related gene)	M21535		NP_004440

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
475	0.039781	clone IMAGE:5303725, mRNA /gb=BC041987 /gi=27469480 /ug=Hs.434826 /len=2021	BC041987	Hs.434826	
589	0.039763	AGENCOURT_6640990 NIH_MGC_68 cDNA clone IMAGE:5735856 5', mRNA sequence /clone=IMAGE:5735856 /clone_end=5' /gb=BM907553 /gi=19357932 /ug=Hs.424427 /len=645	BM907553	Hs.424427	
599	0.022196	hypothetical protein similar to RNA-binding protein lark (MGC10871), mRNA /cds=(54,1133) /gb=NM_031492 /gi=13899353 /ug=Hs.49994 /len=1821	NM_031492	Hs.49994	NP_113680
600	0.024315	fascin 1, actin-bundling protein (Strongylocentrotus purpuratus) (FSCN1), mRNA /cds=(112,1593) /gb=NM_003088 /gi=4507114 /ug=Hs.118400 /len=2767	NM_003088	Hs.118400	NP_003079
626	0.020362	RTC domain containing 1 (RTCD1), mRNA /cds=(171,1271) /gb=NM_003729 /gi=4506588 /ug=Hs.27076 /len=1539	NM_003729	Hs.27076	NP_003720
627	0.047109	methionine-tRNA synthetase (MARS), mRNA /cds=(24,2726) /gb=NM_004990 /gi=14043021 /ug=Hs.279946 /len=2795	NM_004990	Hs.279946	NP_004981
633	0.014533	A kinase (PRKA) anchor protein 13 (AKAP13), transcript variant 2, mRNA /cds=(214,8655) /gb=NM_007200 /gi=21493028 /ug=Hs.301946 /len=10156	NM_007200	Hs.301946	NP_658913
652	0.042641	cDNA FLJ38331 fis, clone FCBBF3025285, moderately similar to Mus musculus peripheral benzodiazepine receptor associated protein (Pap7) mRNA. /gb=AK095650 /gi=21754954 /ug=Hs.9052 /len=3547	AK095650	Hs.9052	
657	0.015956	FLJ30577 fis, clone BRAWH2006760 /cds=UNKNOWN /gb=AK055139 /gi=16549803 /ug=Hs.324815 /len=2353	AK055139	Hs.324815	
658	0.01469	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 /len=1705	NM_006855	Hs.250696	NP_057839
662	0.007887	insulin-like growth factor binding protein 5 (IGFBP5), mRNA /cds=(752,1570) /gb=NM_000599 /gi=10834981 /ug=Hs.380833 /len=1722	NM_000599	Hs.380833	NP_000590
669	0.005341	putative zinc finger protein NY-REN-34 antigen (NY-REN-34), mRNA /cds=(129,704) /gb=NM_016119 /gi=7705832 /ug=Hs.279799 /len=1323	NM_016119	Hs.279799	NP_057203

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
691	0.034482	U5 snRNP-specific protein, 200-KD (U5-200KD), mRNA /cds=(189,5624) /gb=NM_014014 /gi=24307974 /ug=Hs.246112 /len=5898	NM_014014	Hs.246112	NP_054733
692	0.042541	chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1), mRNA /cds=(127,1278) /gb=NM_001276 /gi=4557017 /ug=Hs.75184 /len=1925	NM_001276	Hs.75184	NP_001267
697	0.048529	interferon, alpha-inducible protein (clone IFI-6-16) (G1P3), transcript variant 3, mRNA /cds=(108,524) /gb=NM_022873 /gi=13259549 /ug=Hs.265827 /len=841	NM_022873	Hs.265827	NP_075011
721	0.019388	mitochondrion, complete genome	NC_001807		
722	0.032363	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) (GOT1), mRNA /cds=(25,1266) /gb=NM_002079 /gi=4504066 /ug=Hs.597 /len=1941	NM_002079	Hs.597	NP_002070
726	0.005026	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747	NM_012479	Hs.25001	NP_036611
771	0.042541	zinc finger protein (ZFD25) (62% aa)	AB027251		NP_057304
772	0.007887	acid sphingomyelinase (ASM) gene, exons a, and alternative a (3' end), b and c (5' end)	M59917		
774	0.045456	BAF53 (BAF53A), mRNA /cds=(137,1426) /gb=NM_004301 /gi=4757717 /ug=Hs.274350 /len=1842	NM_004301	Hs.274350	NP_829888
807	0.037168	KIAA0102 gene product (KIAA0102), mRNA /cds=(308,679) /gb=NM_014752 /gi=7661907 /ug=Hs.77665 /len=1370	NM_014752	Hs.77665	NP_055567
808	0.017954	PIX1 mRNA (ORF)	AF037219		NP_570854
809	0.002077	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) (MCCC1), mRNA /cds=(133,2310) /gb=NM_020166 /gi=13518227 /ug=Hs.47649 /len=2528	NM_020166	Hs.47649	NP_064551
810	0.028082	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 /len=1705	NM_006855	Hs.250696	NP_057839
847	0.037168	peroxisomal biogenesis factor 3 (PEX3), mRNA /cds=(64,1185) /gb=NM_003630 /gi=4505726 /ug=Hs.7277 /len=1979	NM_003630	Hs.7277	NP_003621

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Prot in Accession No.
851	0.007223	of89c05.s1 NCI_CGAP_Li5 cDNA clone IMAGE:1437512 3' similar to contains Alu repetitive element,, mRNA sequence /clone=IMAGE:1437512 /clone_end=3' /gb=AA894384 /gi=3030785 /ug=Hs.432123 /len=296	AA894384	Hs.432123	
865	0.028082	mitochondrion, complete genome	NC_001807		
870	0.020917	KIAA0062 mRNA, partial cds /cds=(1,1598) /gb=D31887 /gi=505101 /ug=Hs.89868 /len=4573	D31887	Hs.89868	
877	0.013076	ring finger protein 11 (RNF11), mRNA /cds=(128,592) /gb=NM_014372 /gi=7657519 /ug=Hs.96334 /len=2529	NM_014372	Hs.96334	NP_055187
886	0.005026	hemoglobin, beta (HBB), mRNA /cds=(51,494) /gb=NM_000518 /gi=28302128 /ug=Hs.155376 /len=626	NM_000518	Hs.155376	NP_000509
887	0.01661	polyadenylate binding protein-interacting protein 1 (PAIP1), mRNA /cds=(188,1627) /gb=NM_006451 /gi=17511254 /ug=Hs.109643 /len=2764	NM_006451	Hs.109643	NP_006442
888	0.017954	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), transcript variant 4, mRNA /cds=(64,7536) /gb=NM_080685 /gi=18375649 /ug=Hs.211595 /len=8133	NM_080685	Hs.211595	NP_542416
918	0.015351	AGENCOURT_6456859 NIH_MGC_92 cDNA clone IMAGE:5576908 5', mRNA sequence /clone=IMAGE:5576908 /clone_end=5' /gb=BM466169 /gi=18515211 /ug=Hs.439148 /len=1150	BM466169	Hs.439148	
921	0.013076	mitochondrion, complete genome	NC_001807		
923	0.008602	eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa (EIF3S3), mRNA /cds=(6,1064) /gb=NM_003756 /gi=4503514 /ug=Hs.58189 /len=1280	NM_003756	Hs.58189	NP_003747
928	0.032363	apoptosis inhibitor 5 (API5), mRNA /cds=(133,1647) /gb=NM_006595 /gi=5729729 /ug=Hs.227913 /len=3739	NM_006595	Hs.227913	NP_006586
930	0.026124	FK506 binding protein 9, 63 kDa (FKBP9), mRNA /cds=(457,885) /gb=NM_007270 /gi=24307926 /ug=Hs.302749 /len=2517	NM_007270	Hs.302749	NP_009201
943	0.005512	XIST, coding sequence "a" mRNA (locus DXS399E): /gb=X56199 /gi=37987 /ug=Hs.352403 /len=1614	X56199	Hs.352403	
968	0.027649	translin (TSN), mRNA /cds=(236,922) /gb=NM_004622 /gi=20302160 /ug=Hs.75066 /len=3408	NM_004622	Hs.75066	NP_004613

Genes Corr sponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
991	0.03649	P311 protein (P311), mRNA /cds=(203,409) /gb=NM_004772 /gi=4758865 /ug=Hs.413760 /len=2036	NM_004772	Hs.413760	NP_004763
998	0.001683	down-regulator of transcription 1, TBP-binding (negative cofactor 2) (DR1), mRNA /cds=(548,1078) /gb=NM_001938 /gi=4503380 /ug=Hs.16697 /len=1375	NM_001938	Hs.16697	NP_001929
1008	0.005026	Alg5, <i>S. cerevisiae</i> , of (ALG5), mRNA /cds=(28,1002) /gb=NM_013338 /gi=9665250 /ug=Hs.227933 /len=1125	NM_013338	Hs.227933	NP_037470
1026	0.032363	methionine adenosyltransferase II, beta (MAT2B), mRNA /cds=(73,1077) /gb=NM_013283 /gi=20127525 /ug=Hs.54642 /len=2054	NM_013283	Hs.54642	NP_037415
1028	0.032363	ATP synthase, H transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=NM_006886 /gi=21327678 /ug=Hs.177530 /len=417	NM_006886	Hs.177530	NP_008817
1031	0.01661	decorin (DCN), transcript variant A1, mRNA /cds=(200,1279) /gb=NM_001920 /gi=19743844 /ug=Hs.433989 /len=1751	NM_001920	Hs.433989	NP_598014
1051	0.008602	HSPC133 protein (HSPC133), mRNA /cds=(83,481) /gb=NM_014168 /gi=7661791 /ug=Hs.273063 /len=963	NM_014168	Hs.273063	NP_054887
1099	0.03649	DKFZP586O0120 protein (DKFZP586O0120), mRNA /cds=(21,359) /gb=NM_014077 /gi=7661695 /ug=Hs.4766 /len=1465	NM_014077	Hs.4766	NP_054796
1104	0.028082	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
1121	0.045685	cDNA FLJ31399 fis, clone NT2NE1000181. /gb=AK055961 /gi=16550820 /ug=Hs.179833 /len=2159	AK055961	Hs.179833	
1163	0.022547	reticulon 4 (RTN4), mRNA /cds=(245,3823) /gb=NM_020532 /gi=24638438 /ug=Hs.65450 /len=4166	NM_020532	Hs.65450	NP_722550
1168	0.013076	thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556	NM_021109	Hs.75968	NP_066932
1170	0.020917	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_079425	Hs.77385	NP_524149

Genes Corresponding To Differentially Expressed Genes in Figure-8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1189	0.013587	mRNA; cDNA DKFZp451A142 (from clone DKFZp451A142) /cds=(39,1898) /gb=AL834245 /gi=21739785 /ug=Hs.124918 /len=4902	AL834245	Hs.124918	
1198	0.026124	hypothetical protein FLJ20729 (FLJ20729); mRNA /cds=(135,1547) /gb=NM_017953 /gi=20149642 /ug=Hs.5111 /len=2821	NM_017953	Hs.5111	NP_060423
1274	0.01205	HSJ1a (HSJ1) mRNA, complete cds; alternatively spliced. /cds=(26,859) /gb=S37375 /gi=250081 /ug=Hs.433237 /len=1760	S37375	Hs.433237	
1301	0.006608	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
1304	0.037168	eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=NM_001959 /gi=16519564 /ug=Hs.421608 /len=961	NM_001959	Hs.421608	NP_066944
1305	0.001683	cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA /cds=(90,281) /gb=NM_001867 /gi=18105039 /ug=Hs.430075 /len=448	NM_001867	Hs.430075	NP_001858
1306	0.019388	poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA /cds=(503,2404) /gb=NM_002568 /gi=4505574 /ug=Hs.172182 /len=2848	NM_002568	Hs.172182	NP_002559
1370	0.024342	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6 (SLC25A6), nuclear gene encoding mitochondrial protein, mRNA /cds=(93,989) /gb=NM_001636 /gi=27764862 /ug=Hs.407372 /len=1455	NM_001636	Hs.407372	NP_001627
1386	0.039164	AGENCOURT_6424254 NIH_MGC_67 cDNA clone IMAGE:5491531 5', mRNA sequence /clone=IMAGE:5491531 /clone_end=5' /gb=BM479954 /gi=18528996 /ug=Hs.381243 /len=1112	BM479954	Hs.381243	
1389	0.032363	heparan sulfate proteoglycan (HSPG2) mRNA, complete cds	M85289		NP_005520
1427	0.048529	small nuclear RNA activating complex, polypeptide 1, 43kDa (SNAPC1), mRNA /cds=(13,1119) /gb=NM_003082 /gi=19923159 /ug=Hs.179312 /len=2594	NM_003082	Hs.179312	NP_003073
1430	0.020917	synovial sarcoma, X breakpoint 2 interacting protein (SSX2IP), mRNA /cds=(265,2109) /gb=NM_014021 /gi=7662381 /ug=Hs.22587 /len=5835	NM_014021	Hs.22587	NP_054740

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gen Accession No.	Unigene Accession No.	Protein Accession No.
1431	0.02428	inhibitor of growth family, member 1 (ING1), mRNA /cds=(433,1701) /gb=NM_005537 /gi=19923770 /ug=Hs.46700 /len=2886	NM_005537	Hs.46700	NP_005528
1455	0.045456	CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA /cds=(260,2668) /gb=NM_001253 /gi=16357499 /ug=Hs.155174 /len=3012	NM_001253	Hs.155174	NP_001244
1456	0.026124	CGI-74 protein (CGI-59), mRNA /cds=(1,1209) /gb=NM_016019 /gi=7706309 /ug=Hs.7194 /len=2296	NM_016019	Hs.7194	NP_057103
1476	0.015351	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide (YWHAB), transcript variant 1, mRNA /cds=(277,1017) /gb=NM_003404 /gi=21328444 /ug=Hs.279920 /len=1117	NM_003404	Hs.279920	NP_647539
1482	0.048529	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=NM_006886 /gi=21327678 /ug=Hs.177530 /len=417	NM_006886	Hs.177530	NP_008817
1497	0.01661	hypothetical protein MGC45474 (MGC45474), mRNA /cds=(218,2035) /gb=NM_152369 /gi=22748794 /ug=Hs.234101 /len=2384	NM_152369	Hs.234101	
1506	0.017954	septin 2 (SEP2) mRNA, partial cds /cds=(1,1528) /gb=AF179995 /gi=9957543 /ug=Hs.80712 /len=4344	AF179995	Hs.80712	
1535	0.03016	mRNA for KIAA0752 protein, partial cds. /cds=(1,1006) /gb=AB018295 /gi=3882224 /ug=Hs.126779 /len=4332	AB018295	Hs.126779	NP_775934
1577	0.02428	POM121 membrane glycoprotein (rat) (POM121), mRNA /cds=(978,3932) /gb=NM_172020 /gi=26051277 /ug=Hs.295112 /len=6014	NM_172020	Hs.295112	NP_742017
1648	0.002819	mRNA; cDNA DKFZp564E193 (from clone DKFZp564E193) /gb=AL049259 /gi=4500005 /ug=Hs.333141 /len=1691	AL049259	Hs.333141	
1665	7.89E-04	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
1683	0.037168	mitochondrion, complete genome	NC_001807		
1720	0.013076	KIAA0971 protein (KIAA0971), mRNA /cds=(59,2005) /gb=NM_014929 /gi=7662421 /ug=Hs.84429 /len=4999	NM_014929	Hs.84429	NP_055744

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1723	0.02428	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) (CD59), mRNA /cds=(50,436) /gb=NM_000611 /gi=20127410 /ug=Hs.278573 /len=1946	NM_000611	Hs.278573	NP_000602
1724	0.034698	zinc finger RNA binding protein (ZFR), mRNA /cds=(44,1300) /gb=NM_016107 /gi=7706372 /ug=Hs.173518 /len=2734	NM_016107	Hs.173518	NP_057191
1749	0.004165	hypothetical protein MGC20781 (MGC20781), mRNA /cds=(366,1139) /gb=NM_052935 /gi=16418414 /ug=Hs.237536 /len=1476	NM_052935	Hs.237536	NP_443167
1751	0.007887	insulin induced protein 2 (LOC51141), mRNA /cds=(141,857) /gb=NM_016133 /gi=23821030 /ug=Hs.7089 /len=1358	NM_016133	Hs.7089	NP_057217
1756	0.039781	uronyl-2-sulfotransferase (UST), mRNA /cds=(104,1324) /gb=NM_005715 /gi=5032218 /ug=Hs.134015 /len=4196	NM_005715	Hs.134015	NP_005706
1790	0.034698	hypothetical protein FLJ21749 (FLJ21749), mRNA /cds=(102,689) /gb=NM_025124 /gi=13376700 /ug=Hs.288761 /len=961	NM_025124	Hs.288761	NP_079400
1799	0.019388	hypothetical protein MGC10911 (MGC10911), mRNA /cds=(234,602) /gb=NM_032302 /gi=14150059 /ug=Hs.85573 /len=985	NM_032302	Hs.85573	NP_115678
1830	6.88E-04	calmodulin-I (CALM1) mRNA, 3'UTR, partial sequence. /gb=U16850 /gi=576644 /ug=Hs.374441 /len=2383	U16850	Hs.374441	
1855	0.011093	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA /cds=(25,516) /gb=NM_006221 /gi=5453897 /ug=Hs.161362 /len=994	NM_006221	Hs.161362	NP_006212
1919	0.01661	cellular fibronectin (non-exact, 62%)	M10905		NP_473375
1946	0.02428	sphingolipid activator protein 1	J03015		NP_002769
1963	0.045456	Fanconi anemia, complementation group G (FANCG), mRNA /cds=(493,2361) /gb=NM_004629 /gi=4759335 /ug=Hs.8047 /len=2649	NM_004629	Hs.8047	NP_004620
1974	0.026124	CDC20 cell division cycle 20 (S. cerevisiae) (CDC20), mRNA /cds=(111,1610) /gb=NM_001255 /gi=4557436 /ug=Hs.82906 /len=1686	NM_001255	Hs.82906	NP_001246
1999	0.045456	chromosome 20 open reading frame 40 (C20orf40), mRNA /cds=(208,396) /gb=NM_014054 /gi=7661709 /ug=Hs.105379 /len=417	NM_014054	Hs.105379	NP_054773

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigen Accession No.	Protein Accession No.
2033	0.002819	calmodulin 1 (phosphorylase kinase, delta) (CALM1), mRNA /cds=(200,649) /gb=NM_006888 /gi=5901911 /ug=Hs.282410 /len=1526	NM_006888	Hs.282410	NP_008819
2041	0.039781	ribosomal protein L32 (RPL32), mRNA /cds=(51,458) /gb=NM_000994 /gi=15812220 /ug=Hs.169793 /len=521	NM_000994	Hs.169793	NP_000985
2070	0.020917	myotubular myopathy 1 (MTM1), mRNA /cds=(55,1866) /gb=NM_000252 /gi=4557895 /ug=Hs.75302 /len=3411	NM_000252	Hs.75302	NP_000243
2073	0.02428	transcription factor B1, mitochondrial (TFB1M), mRNA /cds=(73,1113) /gb=NM_016020 /gi=7705784 /ug=Hs.279908 /len=1290	NM_016020	Hs.279908	NP_057104
2075	0.01661	TRAF family member-associated NFKB activator (TANK), transcript variant 1, mRNA /cds=(159,1436) /gb=NM_004180 /gi=19743568 /ug=Hs.146847 /len=2089	NM_004180	Hs.146847	NP_597841
2105	0.042541	potassium channel, subfamily K, member 1 (KCNK1), mRNA /cds=(183,1193) /gb=NM_002245 /gi=15451900 /ug=Hs.79351 /len=1901	NM_002245	Hs.79351	NP_002236
2164	0.03016	KIAA1074 protein (KIAA1074), mRNA /cds=(151,5280) /gb=NM_014915 /gi=7662473 /ug=Hs.129218 /len=5360	NM_014915	Hs.129218	NP_055730
2181	0.019388	nucleobindin 2 (NUCB2), mRNA /cds=(220,1482) /gb=NM_005013 /gi=4826869 /ug=Hs.3164 /len=1586	NM_005013	Hs.3164	NP_005004
2194	0.039781	monocytic leukemia zinc finger protein-related factor (MORF), mRNA /cds=(316,6537) /gb=NM_012330 /gi=6912511 /ug=Hs.27590 /len=6537	NM_012330	Hs.27590	NP_036462
2234	0.048529	early endosome antigen 1, 162kD (EEA1), mRNA /cds=(137,4369) /gb=NM_003566 /gi=4503468 /ug=Hs.2864 /len=5028	NM_003566	Hs.2864	NP_003557
2241	0.022547	bone morphogenetic protein 6 (BMP6), mRNA /cds=(180,1721) /gb=NM_001718 /gi=4809281 /ug=Hs.285671 /len=2943	NM_001718	Hs.285671	NP_001709
2245	0.028082	ribosomal protein L15 (RPL15), mRNA /cds=(37,651) /gb=NM_002948 /gi=15431292 /ug=Hs.74267 /len=2018	NM_002948	Hs.74267	NP_002939
2252	0.028082	UI-CF-DU1-aag-k-05-0-UI.s1 UI-CF-DU1 cDNA clone UI-CF-DU1-aag-k-05-0-UI 3', mRNA sequence /clone=UI-CF-DU1-aag-k-05-0-UI /clone_end=3' /gb=BU676081 /gi=23520708 /ug=Hs.389894 /len=731	BU676081	Hs.389894	
2309	0.013076	GTPase-activating protein GAPIII	U20238		NP_033051

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2317	0.006039	mRNA for KIAA0570 protein, partial cds. /cds=(480,10718) /gb=AB011142 /gi=20521084 /ug=Hs.180948 /len=11269	AB011142	Hs.180948	
2318	0.006608	mRNA for KIAA0611 protein, partial cds. /cds=(1,2740) /gb=AB014511 /gi=3327035 /ug=Hs.406434 /len=7176	AB014511	Hs.406434	
2412	0.01205	guanine nucleotide binding protein (G protein), beta polypeptide 2 (GNB2), mRNA /cds=(259,1281) /gb=NM_005273 /gi=20357528 /ug=Hs.91299 /len=1666	NM_005273	Hs.91299	NP_005264
2480	0.032363	topoisomerase (DNA) I (TOP1), mRNA /cds=(247,2544) /gb=NM_003286 /gi=19913404 /ug=Hs.317 /len=3734	NM_003286	Hs.317	NP_003277
2520	0.037168	KIAA0164 gene product (KIAA0164), mRNA /cds=(254,3016) /gb=NM_014739 /gi=7661957 /ug=Hs.80338 /len=5538	NM_014739	Hs.80338	NP_055554
2527	0.045456	hypothetical protein FLJ12476 (FLJ12476), mRNA /cds=(564,2429) /gb=NM_022784 /gi=12232474 /ug=Hs.88144 /len=3623	NM_022784	Hs.88144	NP_073621
2557	0.009373	leucine-rich PPR-motif containing (LRPPRC), mRNA /cds=(46,3867) /gb=NM_133259 /gi=18959201 /ug=Hs.182490 /len=4782	NM_133259	Hs.182490	NP_573566
2678	0.032363	protein-L-isoaspartate (D-aspartate) O-methyltransferase (PCMT1), mRNA /cds=(74,757) /gb=NM_005389 /gi=4885538 /ug=Hs.79137 /len=1599	NM_005389	Hs.79137	NP_005380
2681	0.008602	HBS1-like (S. cerevisiae) (HBS1L), mRNA /cds=(194,2248) /gb=NM_006620 /gi=24431963 /ug=Hs.221040 /len=7163	NM_006620	Hs.221040	NP_006611
2786	0.039781	pogo transposable element with ZNF domain (POGZ), transcript variant 1, mRNA /cds=(6,4079) /gb=NM_015100 /gi=22027468 /ug=Hs.107088 /len=6157	NM_015100	Hs.107088	NP_665739
2797	0.026124	zinc finger homeobox 1b (ZFHX1B), mRNA /cds=(445,4089) /gb=NM_014795 /gi=7662183 /ug=Hs.34871 /len=5523	NM_014795	Hs.34871	NP_055610
2799	0.022547	glia maturation factor, beta (GMFB), mRNA /cds=(98,526) /gb=NM_004124 /gi=4758441 /ug=Hs.151413 /len=4131	NM_004124	Hs.151413	NP_004115
2801	0.048529	Rattus norvegicus mitochondrial genome	NC_001665		
2802	0.037168	HT001 protein (HT001), mRNA /cds=(242,1204) /gb=NM_014065 /gi=7661837 /ug=Hs.279040 /len=1402	NM_014065	Hs.279040	NP_054784

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2810	0.042541	ATP synthase, H transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), mRNA /cds=(255,683) /gb=NM_001689 /gi=4502300 /ug=Hs.429 /len=826	NM_001689	Hs.429	NP_001680
2813	0.003435	ribosomal protein L37a (RPL37A), mRNA /cds=(36,314) /gb=NM_000998 /gi=16306561 /ug=Hs.296290 /len=392	NM_000998	Hs.296290	NP_000989
2815	0.004165	proteasome (prosome, macropain) subunit, alpha type, 6 (PSMA6), mRNA /cds=(110,850) /gb=NM_002791 /gi=23110943 /ug=Hs.410276 /len=1035	NM_002791	Hs.410276	NP_002782
2821	0.037168	transcription factor forkhead-like 7 (FKHL7) gene, complete cds	AF048693		
2848	0.008602	BJ-HCC-24 tumor antigen mRNA, complete cds /cds=(2,1240) /gb=AY121805 /gi=22002585 /ug=Hs.433489 /len=1488	AY121805	Hs.433489	
2849	0.007223	chromosome 14 open reading frame 2 (C14orf2), mRNA /cds=(61,237) /gb=NM_004894 /gi=4758939 /ug=Hs.109052 /len=627	NM_004894	Hs.109052	NP_004885
2850	0.03016	helicase II (RAD54L) mRNA, complete cds. /cds=(54,4979) /gb=U09820 /gi=606832 /ug=Hs.96264 /len=6115	U09820	Hs.96264	NP_612115
2884	0.020917	mitochondrial ribosomal protein S30 (MRPS30), mRNA /cds=(39,1358) /gb=NM_016640 /gi=16950598 /ug=Hs.28555 /len=1482	NM_016640	Hs.28555	NP_057724
2885	0.048529	chromosome 1 specific transcript KIAA0491	AB007960		NP_057093
2910	0.045456	Sm protein F (LSM6), mRNA /cds=(82,324) /gb=NM_007080 /gi=5901997 /ug=Hs.42438 /len=596	NM_007080	Hs.42438	NP_009011
2913	0.005512	mortality factor 4 like 1 (MORF4L1), mRNA /cds=(132,1103) /gb=NM_006791 /gi=5803101 /ug=Hs.6353 /len=1766	NM_006791	Hs.6353	NP_006782
2928	0.042541	ligase IV, DNA, ATP-dependent (LIG4), mRNA /cds=(274,3009) /gb=NM_002312 /gi=23199992 /ug=Hs.166091 /len=3325	NM_002312	Hs.166091	NP_002303
2930	0.022547	vascular Rab-GAP/TBC-containing (VRP), mRNA /cds=(1118,3811) /gb=NM_007063 /gi=5902153 /ug=Hs.164170 /len=4404	NM_007063	Hs.164170	NP_008994
2931	0.048529	peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA /cds=(45,542) /gb=NM_021130 /gi=10863926 /ug=Hs.401787 /len=753	NM_021130	Hs.401787	NP_066953

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gen Accession No.	Unigene Accession No.	Protein Accession No.
2966	0.009373	RAB14, member RAS oncogene family (RAB14), mRNA /cds=(184,831) /gb=NM_016322 /gi=19923482 /ug=Hs.5807 /len=4106	NM_016322	Hs.5807	NP_057406
2967	0.020917	matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) (MMP2), mRNA /cds=(290,2272) /gb=NM_004530 /gi=11342665 /ug=Hs.111301 /len=3069	NM_004530	Hs.111301	NP_004521
2989	0.013076	hypothetical protein DKFZp434B195 (DKFZP434B195), mRNA /cds=(514,1290) /gb=NM_031284 /gi=21361960 /ug=Hs.10748 /len=2262	NM_031284	Hs.10748	NP_112574
2990	0.019388	cDNA FLJ31057 fis, clone HSYRA2000787. /gb=AK055619 /gi=16550395 /ug=Hs.296261 /len=2168	AK055619	Hs.296261	
2996	0.009373	ribosomal protein L12 (RPL12), mRNA /cds=(89,586) /gb=NM_000976 /gi=15431291 /ug=Hs.405042 /len=632	NM_000976	Hs.405042	NP_000967
3025	0.013076	FLJ30708 fis, clone FCBBF2001238 /cds=UNKNOWN /gb=AK055270 /gi=16549967 /ug=Hs.94812 /len=1965	AK055270	Hs.94812	
3029	2.91E-04	Yip1p-interacting factor (YIF1P), mRNA /cds=(116,997) /gb=NM_020470 /gi=9994168 /ug=Hs.406422 /len=1078	NM_020470	Hs.406422	NP_065203
3032	0.019388	golgi-specific brefeldin A resistance factor 1 (GBF1), mRNA /cds=(241,5820) /gb=NM_004193 /gi=4758415 /ug=Hs.155499 /len=6376	NM_004193	Hs.155499	NP_004184
3034	0.015351	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SERPINB6), mRNA /cds=(75,1205) /gb=NM_004568 /gi=28077084 /ug=Hs.41072 /len=1361	NM_004568	Hs.41072	NP_004559
3065	8.68E-04	KIAA0433 protein (KIAA0433), mRNA /cds=(510,4241) /gb=NM_015216 /gi=7662117 /ug=Hs.26179 /len=5814	NM_015216	Hs.26179	NP_056031
3070	0.006039	signal sequence receptor, beta (translocon-associated protein beta) (SSR2), mRNA /cds=(51,602) /gb=NM_003145 /gi=6552341 /ug=Hs.74564 /len=1093	NM_003145	Hs.74564	NP_003136
3108	0.01661	glycogen synthase 1 (muscle) (GYS1), mRNA /cds=(161,2374) /gb=NM_002103 /gi=4504232 /ug=Hs.772 /len=3531	NM_002103	Hs.772	NP_002094
3113	0.013076	phosphodiesterase 4D interacting protein (myomegalin) (PDE4DIP), mRNA /cds=(658,4056) /gb=NM_014644 /gi=11036643 /ug=Hs.265848 /len=5676	NM_014644	Hs.265848	NP_055459

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3137	0.03016	yp24c06.s1 Soares breast 3NbHBst cDNA clone IMAGE:188362 3' similar to gb:M10942_cds1 metallothionein-1e gene mRNA sequence /clone=IMAGE:188362 /clone_end=3' /gb=H43642 /gi=919694 /ug=Hs.418241 /len=452	H43642	Hs.418241	
3138	0.032363	NCAG1 (NCAG1), mRNA /cds=(1477,5145) /gb=NM_032160 /gi=23943786 /ug=Hs.124673 /len=9528	NM_032160	Hs.124673	NP_115536
3139	0.037168	mRNA for KIAA0530 protein, partial cds. /cds=(1,4693) /gb=AB011102 /gi=3043583 /ug=Hs.173081 /len=6578	AB011102	Hs.173081	
3141	0.034698	3-oxoacid CoA transferase (OXCT), nuclear gene encoding mitochondrial protein, mRNA /cds=(99,1661) /gb=NM_000436 /gi=4557816 /ug=Hs.177584 /len=3337	NM_000436	Hs.177584	NP_000427
3144	0.007887	solute carrier family 20 (phosphate transporter), member 1 (SLC20A1), mRNA /cds=(371,2410) /gb=NM_005415 /gi=7382462 /ug=Hs.78452 /len=3220	NM_005415	Hs.78452	NP_005406
3149	0.015351	thioredoxin domain-containing (TXNDC), mRNA /cds=(118,960) /gb=NM_030755 /gi=13559515 /ug=Hs.24766 /len=1112	NM_030755	Hs.24766	NP_110382
3165	0.026124	SOCS box-containing WD protein SWIP-1 (WSB1), transcript variant 3, mRNA /cds=(317,1051) /gb=NM_134264 /gi=20143909 /ug=Hs.187991 /len=4243	NM_134264	Hs.187991	NP_599027
3173	0.032363	hypothetical protein FLJ11730 (FLJ11730), mRNA /cds=(33,608) /gb=NM_022756 /gi=20149668 /ug=Hs.17118 /len=1558	NM_022756	Hs.17118	NP_073593
3174	1.72E-04	lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA /cds=(69,476) /gb=NM_002305 /gi=6006015 /ug=Hs.382367 /len=526	NM_002305	Hs.382367	NP_002296
3219	0.010202	actin, alpha, cardiac muscle (ACTC), mRNA /cds=(1,1134) /gb=NM_005159 /gi=10938011 /ug=Hs.118127 /len=1294	NM_005159	Hs.118127	NP_005150
3233	0.013076	uncharacterized hematopoietic stem/progenitor cells protein MDS027 (MDS027), mRNA /cds=(21,248) /gb=NM_018462 /gi=27544938 /ug=Hs.421654 /len=888	NM_018462	Hs.421654	NP_060932

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	D scription	G ne Accession No.	Unigene Accession No.	Protein Accession No.
3245	0.007289	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) (P4HB), mRNA /cds=(45,1571) /gb=NM_000918 /gi=20070124 /ug=Hs.410578 /len=2438	NM_000918	Hs.410578	NP_000909
3254	0.039781	splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(156,821) /gb=NM_003016 /gi=4506898 /ug=Hs.73965 /len=1879	NM_003016	Hs.73965	NP_003007
3266	0.03016	DKFZP564C186 protein (DKFZP564C186), mRNA /cds=(16,2265) /gb=NM_015658 /gi=7661605 /ug=Hs.134200 /len=2762	NM_015658	Hs.134200	NP_056473
3288	0.005026	cyclin G2 (CCNG2), mRNA /cds=(136,1170) /gb=NM_004354 /gi=4757935 /ug=Hs.79069 /len=2044	NM_004354	Hs.79069	NP_004345
3300	0.032363	3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMGCR), mRNA /cds=(51,2717) /gb=NM_000859 /gi=4557642 /ug=Hs.11899 /len=4471	NM_000859	Hs.11899	NP_000850
3302	0.048529	immature colon carcinoma transcript 1 (ICT1), mRNA /cds=(3,623) /gb=NM_001545 /gi=4557656 /ug=Hs.9078 /len=888	NM_001545	Hs.9078	NP_001536
3316	0.017954	glutathione S-transferase M3 (brain) (GSTM3), mRNA /cds=(311,988) /gb=NM_000849 /gi=23065551 /ug=Hs.2006 /len=1572	NM_000849	Hs.2006	NP_000840
3318	0.002302	endothelial protein C receptor	AB026584		
3322	0.045456	ribonuclease P (30kD) (RPP30), mRNA /cds=(295,1101) /gb=NM_006413 /gi=19923360 /ug=Hs.139120 /len=2643	NM_006413	Hs.139120	NP_006404
3354	0.001871	ribosomal protein L23 (RPL23), mRNA /cds=(27,449) /gb=NM_000978 /gi=14591907 /ug=Hs.234518 /len=493	NM_000978	Hs.234518	NP_000969
3355	0.020917	ets variant gene 5 (ets-related molecule) (ETV5), mRNA /cds=(224,1756) /gb=NM_004454 /gi=4758315 /ug=Hs.43697 /len=4071	NM_004454	Hs.43697	NP_004445
3390	0.011093	phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2), mRNA /cds=(212,1321) /gb=NM_002767 /gi=22538484 /ug=Hs.13339 /len=1890	NM_002767	Hs.13339	NP_002758

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3405	0.020917	lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA /cds=(69,476) /gb=NM_002305 /gi=6006015 /ug=Hs.382367 /len=526	NM_002305	Hs.382367	NP_002296
3433	0.048529	interferon induced transmembrane protein 3 (1-8U) (IFITM3), mRNA /cds=(238,639) /gb=NM_021034 /gi=11995467 /ug=Hs.381234 /len=808	NM_021034	Hs.381234	NP_066362
3440	0.010202	TERF1 (TRF1)-interacting nuclear factor 2 (TINF2), mRNA /cds=(263,1327) /gb=NM_012461 /gi=6912715 /ug=Hs.7797 /len=2095	NM_012461	Hs.7797	NP_036593
3444	0.037168	laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=NM_002295 /gi=9845501 /ug=Hs.181357 /len=1039	NM_002295	Hs.181357	NP_002286
3507	0.011093	UI-H-DT0-atx-l-07-0-UI.s1 NCI_CGAP_DT0 cDNA clone IMAGE:5865750 3', mRNA sequence /clone=IMAGE:5865750 /clone_end=3' /gb=BM994183 /gi=19719084 /ug=Hs.412022 /len=1284	BM994183	Hs.412022	
3512	0.011093	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
3548	0.005026	eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA /cds=(23,1360) /gb=NM_001568 /gi=4503520 /ug=Hs.106673 /len=1510	NM_001568	Hs.106673	NP_001559
3607	0.004578	mitochondrion, complete genome	NC_001807		
3609	0.039781	mortality factor 4 like 1 (MORF4L1), mRNA /cds=(132,1103) /gb=NM_006791 /gi=5803101 /ug=Hs.6353 /len=1766	NM_006791	Hs.6353	NP_006782
3619	0.01205	cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419 /len=802	NM_001861	Hs.433419	NP_001852
3641	0.004578	hypothetical protein CL25084 (CL25084), mRNA /cds=(132,1583) /gb=NM_015701 /gi=20070263 /ug=Hs.7100 /len=2412	NM_015701	Hs.7100	NP_056516
3642	0.004578	chromosome 1 open reading frame 22 (C1orf22), mRNA /cds=(54,2723) /gb=NM_025191 /gi=19923618 /ug=Hs.279951 /len=6298	NM_025191	Hs.279951	NP_079467

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3688	0.045456	isoleucine-tRNA synthetase (IARS), transcript variant long, mRNA /cds=(256,4044) /gb=NM_013417 /gi=7770071 /ug=Hs.172801 /len=4508	NM_013417	Hs.172801	NP_038203
3733	0.037168	MAGEF1 protein (MAGEF1), mRNA /cds=(177,1103) /gb=NM_022149 /gi=11545891 /ug=Hs.306123 /len=1615	NM_022149	Hs.306123	NP_071432
3755	0.009373	zinc finger protein 84 (HPF2) (ZNF84), mRNA /cds=(352,2568) /gb=NM_003428 /gi=4508036 /ug=Hs.9450 /len=3257	NM_003428	Hs.9450	NP_003419
3791	0.045456	TNF receptor-associated factor 4 (TRAF4), transcript variant 1, mRNA /cds=(86,1498) /gb=NM_004295 /gi=22027621 /ug=Hs.8375 /len=1999	NM_004295	Hs.8375	NP_665694
3800	0.011093	ribosomal protein, large, P0 (RPLP0), transcript variant 2, mRNA /cds=(111,1064) /gb=NM_053275 /gi=16933545 /ug=Hs.406511 /len=1148	NM_053275	Hs.406511	NP_444505
3801	0.048529	ribosomal protein S7 (RPS7), mRNA /cds=(91,675) /gb=NM_001011 /gi=15431308 /ug=Hs.301547 /len=729	NM_001011	Hs.301547	NP_001002
3830	0.015351	eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=NM_001959 /gi=16519564 /ug=Hs.421608 /len=961	NM_001959	Hs.421608	NP_066944
3844	0.02428	CGI-101 protein (F-LAN-1), mRNA /cds=(7,636) /gb=NM_016041 /gi=7705603 /ug=Hs.286131 /len=1123	NM_016041	Hs.286131	NP_057125
3861	0.03016	basigin (BSG), mRNA /cds=(58,867) /gb=NM_001728 /gi=4502458 /ug=Hs.74631 /len=1638	NM_001728	Hs.74631	NP_001719
3872	0.039781	6-phosphogluconolactonase (PGLS), mRNA /cds=(18,794) /gb=NM_012088 /gi=6912585 /ug=Hs.100071 /len=1010	NM_012088	Hs.100071	NP_036220
3888	0.01661	SAC2 suppressor of actin mutations 2-like (yeast) (SACM2L), transcript variant 1, mRNA /cds=(245,2416) /gb=NM_080564 /gi=18379336 /ug=Hs.169407 /len=2985	NM_080564	Hs.169407	NP_542131
3901	0.01205	estrogen receptor 1 (ESR1), mRNA /cds=(361,2148) /gb=NM_000125 /gi=4503602 /ug=Hs.1657 /len=6450	NM_000125	Hs.1657	NP_000116
3936	0.02428	hypothetical protein AF311304 (AF311304), mRNA /cds=(21,185) /gb=NM_031214 /gi=13654285 /ug=Hs.300624 /len=1138	NM_031214	Hs.300624	NP_112491

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3942	0.032363	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) (SPTAN1), mRNA /cds=(103,7521) /gb=NM_003127 /gi=4507190 /ug=Hs.77196 /len=7787	NM_003127	Hs.77196	NP_003118
3954	0.03016	esophageal cancer related gene 4 protein (ECRG4), mRNA /cds=(109,555) /gb=NM_032411 /gi=14165275 /ug=Hs.43125 /len=772	NM_032411	Hs.43125	NP_115787
3960	0.045456	RaIGDS-like gene (RGL), mRNA /cds=(450,2861) /gb=NM_015149 /gi=20127535 /ug=Hs.79219 /len=5111	NM_015149	Hs.79219	NP_055964
3968	0.019388	protein tyrosine phosphatase type IVA, member 2 (PTP4A2), transcript variant 1, mRNA /cds=(1011,1514) /gb=NM_003479 /gi=18104974 /ug=Hs.82911 /len=3925	NM_003479	Hs.82911	NP_536317
4007	0.037168	chondroitin sulfate proteoglycan 6 (bamacan) (CSPG6), mRNA /cds=(92,3745) /gb=NM_005445 /gi=24475891 /ug=Hs.24485 /len=4096	NM_005445	Hs.24485	NP_005436
4037	0.007223	coagulation factor VIII	AF062515		
4038	0.006608	multiple PDZ domain protein (MPDZ), mRNA /cds=(47,6175) /gb=NM_003829 /gi=4505230 /ug=Hs.169378 /len=6582	NM_003829	Hs.169378	NP_003820
4070	0.005026	ribosomal protein L26 (RPL26), mRNA /cds=(41,478) /gb=NM_000987 /gi=17017970 /ug=Hs.406682 /len=525	NM_000987	Hs.406682	NP_000978
4092	0.02428	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) (NDUFS3), mRNA /cds=(13,807) /gb=NM_004551 /gi=4758787 /ug=Hs.429506 /len=899	NM_004551	Hs.429506	NP_004542
4118	0.001513	HSPC154 protein (HSPC154), mRNA /cds=(200,946) /gb=NM_014177 /gi=7661809 /ug=Hs.7922 /len=1343	NM_014177	Hs.7922	NP_054896
4133	0.004578	vimentin (VIM), mRNA /cds=(123,1523) /gb=NM_003380 /gi=4507894 /ug=Hs.297753 /len=1851	NM_003380	Hs.297753	NP_000995
4146	0.048529	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SERPINB6), mRNA /cds=(75,1205) /gb=NM_004568 /gi=28077084 /ug=Hs.41072 /len=1361	NM_004568	Hs.41072	NP_004559
4152	0.048529	CG9469 gene product	AAF57414		
4159	0.02428	suppressor of Ty 3 (S. cerevisiae) (SUPT3H), mRNA /cds=(72,1025) /gb=NM_003599 /gi=4507308 /ug=Hs.304173 /len=1165	NM_003599	Hs.304173	NP_003590

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4176	0.03016	mitotic control protein dis3 (DIS3), mRNA /cds=(37,2913) /gb=NM_014953 /gi=19923415 /ug=Hs.323346 /len=7320	NM_014953	Hs.323346	NP_055768
4189	3.75E-04	fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4), transcript variant 2, mRNA /cds=(507,2642) /gb=NM_022977 /gi=12669908 /ug=Hs.81452 /len=5356	NM_022977	Hs.81452	NP_075266
4194	0.032363	peptidase D (PEPD), mRNA /cds=(17,1498) /gb=NM_000285 /gi=4557834 /ug=Hs.73947 /len=1888	NM_000285	Hs.73947	NP_000276
4197	0.048529	putative translation initiation factor (SUI1), mRNA /cds=(148,489) /gb=NM_005801 /gi=20070210 /ug=Hs.150580 /len=1324	NM_005801	Hs.150580	NP_005792
4200	0.037168	PTD013 protein (PTD013), mRNA /cds=(87,812) /gb=NM_015952 /gi=7706269 /ug=Hs.22679 /len=982	NM_015952	Hs.22679	NP_057036
4206	0.02428	ring finger protein 4 (RNF4), mRNA /cds=(271,843) /gb=NM_002938 /gi=4506560 /ug=Hs.66394 /len=2918	NM_002938	Hs.66394	NP_002929
4216	0.014175	KIAA0076 gene product (KIAA0076), mRNA /cds=(87,5183) /gb=NM_014780 /gi=7661893 /ug=Hs.51039 /len=5253	NM_014780	Hs.51039	NP_055595
4220	0.008602	ribosomal protein S2 (RPS2), mRNA /cds=(12,893) /gb=NM_002952 /gi=15055538 /ug=Hs.356360 /len=978	NM_002952	Hs.356360	NP_002943
4221	0.03016	ras inhibitor	M37190		NP_061866
4223	0.002819	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 (SLC25A20), mitochondrial protein encoded by nuclear gene, mRNA /cds=(37,942) /gb=NM_000387 /gi=6006040 /ug=Hs.13845 /len=1219	NM_000387	Hs.13845	NP_000378
4234	0.015351	ribosomal protein S4, Y-linked (RPS4Y), mRNA /cds=(13,804) /gb=NM_001008 /gi=17981706 /ug=Hs.180911 /len=931	NM_001008	Hs.180911	NP_000999
4274	0.020917	laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=NM_002295 /gi=9845501 /ug=Hs.181357 /len=1039	NM_002295	Hs.181357	NP_002286
4294	0.004578	hypothetical protein FLJ20729 (FLJ20729), mRNA /cds=(135,1547) /gb=NM_017953 /gi=20149642 /ug=Hs.5111 /len=2821	NM_017953	Hs.5111	NP_060423
4301	0.013076	mRNA for KIAA1404 protein, partial cds. /cds=(65,5842) /gb=AB037825 /gi=7243188 /ug=Hs.200317 /len=7204	AB037825	Hs.200317	NP_066363
4307	1.31E-04	HT015 protein (HT015)	AF223466		NP_061049

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4313	0.007223	chromosome 20 open reading frame 167 (C20orf167), mRNA /cds=(64,1053) /gb=NM_052951 /gi=16418440 /ug=Hs.26213 /len=1296	NM_052951	Hs.26213	NP_443183
4369	0.037168	ribosomal protein L36 (RPL36), transcript variant 2, mRNA /cds=(153,470) /gb=NM_015414 /gi=16117793 /ug=Hs.433411 /len=545	NM_015414	Hs.433411	NP_378669
4425	0.032363	gene amplified in squamous cell carcinoma 1 (GASC1), mRNA /cds=(151,3321) /gb=NM_015061 /gi=24307986 /ug=Hs.149918 /len=4239	NM_015061	Hs.149918	NP_055876
4435	0.045456	clone IMAGE:3633225, mRNA /gb=BC012758 /gi=15706478 /ug=Hs.356377 /len=1914	BC012758	Hs.356377	
4509	0.042541	likely ortholog of mouse deleted in polyposis 1 (DP1), mRNA /cds=(38,595) /gb=NM_005669 /gi=24307896 /ug=Hs.178112 /len=3000	NM_005669	Hs.178112	NP_005660
4530	0.009373	I factor (complement) (IF), mRNA /cds=(15,1766) /gb=NM_000204 /gi=4504578 /ug=Hs.36602 /len=1963	NM_000204	Hs.36602	NP_000195
4584	0.042541	Rho-associated, coiled-coil containing protein kinase 1 (ROCK1), mRNA /cds=(1,4065) /gb=NM_005406 /gi=4885582 /ug=Hs.17820 /len=4065	NM_005406	Hs.17820	NP_005397
4657	0.032363	PR domain containing 4 (PRDM4), mRNA /cds=(123,2528) /gb=NM_012406 /gi=9055315 /ug=Hs.21807 /len=3901	NM_012406	Hs.21807	NP_036538
4672	0.01205	coronin, actin binding protein, 1C (CORO1C), mRNA /cds=(97,1521) /gb=NM_014325 /gi=27477119 /ug=Hs.17377 /len=3828	NM_014325	Hs.17377	NP_055140
4678	0.009373	hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA /cds=(49,2259) /gb=NM_000414 /gi=4504504 /ug=Hs.75441 /len=2593	NM_000414	Hs.75441	NP_000405
4687	0.039781	CREBBP/EP300 inhibitory protein 1 (CRI1), mRNA /cds=(63,626) /gb=NM_014335 /gi=7656937 /ug=Hs.381137 /len=1719	NM_014335	Hs.381137	NP_055150
4703	0.03016	leukotriene A4 hydrolase (LTA4H), mRNA /cds=(69,1904) /gb=NM_000895 /gi=4505028 /ug=Hs.81118 /len=2060	NM_000895	Hs.81118	NP_000886
4720	0.010202	heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA /cds=(91,1992) /gb=NM_005826 /gi=14141188 /ug=Hs.15265 /len=2663	NM_005826	Hs.15265	NP_005817

Genes Corr sponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4724	0.020917	Niemann-Pick disease, type C1 (NPC1), mRNA /cds=(124,3960) /gb=NM_000271 /gi=4557802 /ug=Hs.76918 /len=4673	NM_000271	Hs.76918	NP_000262
4741	0.048529	hypothetical protein MGC21981 (MGC21981), mRNA /cds=(66,764) /gb=NM_153267 /gi=23397567 /ug=Hs.131987 /len=1727	NM_153267	Hs.131987	NP_694999
4758	0.015351	inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA /cds=(86,1366) /gb=NM_002192 /gi=4504698 /ug=Hs.727 /len=1840	NM_002192	Hs.727	NP_002183
4774	0.003113	ribosomal protein S19 (RPS19), mRNA /cds=(70,507) /gb=NM_001022 /gi=14591914 /ug=Hs.298262 /len=569	NM_001022	Hs.298262	NP_001013
4778	0.015351	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994
4782	0.022547	CDC-like kinase1 (CLK1), mRNA /cds=(156,1610) /gb=NM_004071 /gi=4758007 /ug=Hs.2083 /len=1834	NM_004071	Hs.2083	NP_004062
4794	0.008602	mitochondrion, complete genome	NC_001807		
4805	0.010202	high-mobility group box 1 (HMGB1), mRNA /cds=(77,724) /gb=NM_002128 /gi=20149538 /ug=Hs.6727 /len=1207	NM_002128	Hs.6727	NP_002119
4810	0.028082	mRNA; cDNA DKFZp7271051 (from clone DKFZp7271051); partial cds /cds=(1,2099) /gb=AL117478 /gi=5911952 /ug=Hs.239370 /len=2480	AL117478	Hs.239370	NP_056412
4814	0.045456	ribosomal protein L10a (RPL10A), mRNA /cds=(16,669) /gb=NM_007104 /gi=15431287 /ug=Hs.425293 /len=700	NM_007104	Hs.425293	NP_009035
4819	0.005026	ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500	NM_000991	Hs.356371	NP_000982
4821	0.034698	eukaryotic translation termination factor 1 (ETF1), mRNA /cds=(136,1449) /gb=NM_004730 /gi=4759033 /ug=Hs.77324 /len=3653	NM_004730	Hs.77324	NP_004721
4833	0.022547	ATP synthase, H transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), mRNA /cds=(98,868) /gb=NM_001688 /gi=21361564 /ug=Hs.81634 /len=1230	NM_001688	Hs.81634	NP_001679
4837	0.039781	UI-H-BW1-amj-g-07-0-UI.s1 NCI_CGAP_Sub7 cDNA clone IMAGE:3070261 3', mRNA sequence /clone=IMAGE:3070261 /clone_end=3' /gb=BF513214 /gi=11598393 /ug=Hs.445888 /len=620	BF513214	Hs.445888	

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	UniGene Accession No.	Protein Accession No.
4848	0.045456	aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 2, mRNA /cds=(61,7308) /gb=NM_013227 /gi=6995993 /ug=Hs.2159 /len=7434	NM_013227	Hs.2159	NP_037359
4861	0.013076	protein serine kinase H1 (PSKH1), mRNA /cds=(131,1405) /gb=NM_006742 /gi=27901802 /ug=Hs.150601 /len=3460	NM_006742	Hs.150601	NP_006733
4862	0.005512	mRNA for FLJ00005 protein, partial cds. /cds=(1,338) /gb=AK000005 /gi=7209310 /ug=Hs.367690 /len=4706	AK000005	Hs.367690	
4863	0.026124	FLJ14819 fis, clone OVARC1000241, moderately similar to HYPOXIA-INDUCIBLE FACTOR 1 ALPHA	AK027725		NP_690009
4874	0.048529	ankyrin repeat domain 10 (ANKRD10), mRNA /cds=(136,1398) /gb=NM_017664 /gi=8923103 /ug=Hs.172572 /len=2509	NM_017664	Hs.172572	NP_060134
4877	0.007223	chromosome 20 open reading frame 31 (C20orf31), mRNA /cds=(83,1819) /gb=NM_018217 /gi=8922666 /ug=Hs.93871 /len=1885	NM_018217	Hs.93871	NP_060687
4878	0.042541	ribosomal protein L35a (RPL35A), mRNA /cds=(74,406) /gb=NM_000996 /gi=16117790 /ug=Hs.288544 /len=511	NM_000996	Hs.288544	NP_000987
4898	0.022547	cDNA FLJ12024 fis, clone HEMBB1001797. /gb=AK022086 /gi=10433407 /ug=Hs.8958 /len=1672	AK022086	Hs.8958	
4900	0.020917	hypothetical protein FLJ10702 (FLJ10702), mRNA /cds=(175,735) /gb=NM_018184 /gi=8922600 /ug=Hs.104222 /len=2944	NM_018184	Hs.104222	NP_060654
4916	0.01205	collagen, type X, alpha 1 (Schmid metaphyseal chondrodysplasia) (COL10A1), mRNA /cds=(97,2139) /gb=NM_000493 /gi=18105031 /ug=Hs.179729 /len=3285	NM_000493	Hs.179729	NP_000484
4939	0.03016	UI-H-DH0-aui-p-19-0-UI.s1 NCI_CGAP_DH0 cDNA clone IMAGE:5871234 3', mRNA sequence /clone=IMAGE:5871234 /clone_end=3' /gb=BM994422 /gi=19719323 /ug=Hs.289721 /len=2081	BM994422	Hs.289721	
4942	0.005512	AF034176 mRNA (Tripodis and Ragoussis) cDNA clone ntcon5 contig /gb=AF034176 /gi=2707738 /ug=Hs.188882 /len=7232	AF034176	Hs.188882	

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Acc ssion No.	Unigene Accession No.	Protein Accession No.
4944	0.039781	hypothetical protein FLJ20452 (FLJ20452), mRNA /cds=(15,614) /gb=NM_017828 /gi=21361660 /ug=Hs.351327 /len=1948	NM_017828	Hs.351327	NP_060298
4956	0.011093	hypothetical protein FLJ20671 (FLJ20671), mRNA /cds=(43,465) /gb=NM_017924 /gi=19923511 /ug=Hs.180201 /len=2855	NM_017924	Hs.180201	NP_060394
4958	0.045456	cDNA FLJ10235 fis, clone HEMBB1000339. /gb=AK001097 /gi=7022149 /ug=Hs.406774 /len=2530	AK001097	Hs.406774	
4960	0.03016	hypothetical protein FLJ20958 (FLJ20958), mRNA /cds=(141,914) /gb=NM_022102 /gi=13430855 /ug=Hs.261023 /len=1842	NM_022102	Hs.261023	NP_071385
4970	0.013076	decorin (DCN), transcript variant A1, mRNA /cds=(200,1279) /gb=NM_001920 /gi=19743844 /ug=Hs.433989 /len=1751	NM_001920	Hs.433989	NP_598014
4978	0.042541	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 24 (DDX24), mRNA /cds=(100,2679) /gb=NM_020414 /gi=14251213 /ug=Hs.155986 /len=2967	NM_020414	Hs.155986	NP_065147
4979	0.004165	ribosomal protein L6 (RPL6), mRNA /cds=(32,898) /gb=NM_000970 /gi=16753226 /ug=Hs.409045 /len=950	NM_000970	Hs.409045	NP_000961
4992	0.03016	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) (TFPI), mRNA /cds=(1,915) /gb=NM_006287 /gi=6715569 /ug=Hs.170279 /len=915	NM_006287	Hs.170279	NP_006278
4994	0.01205	Nedd4 binding protein 2 (N4BP2), mRNA /cds=(339,5600) /gb=NM_018177 /gi=20357506 /ug=Hs.18685 /len=6760	NM_018177	Hs.18685	NP_060647
4995	0.013076	S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) (S100A10), mRNA /cds=(112,405) /gb=NM_002966 /gi=4506760 /ug=Hs.400250 /len=649	NM_002966	Hs.400250	NP_002957
5016	0.007223	ribosomal protein L17 (RPL17), mRNA /cds=(287,841) /gb=NM_000985 /gi=14591906 /ug=Hs.82202 /len=898	NM_000985	Hs.82202	NP_000976
5021	0.032363	hypothetical protein MGC4368 (MGC4368), mRNA /cds=(728,1411) /gb=NM_024510 /gi=21362053 /ug=Hs.9732 /len=2250	NM_024510	Hs.9732	NP_078786
5060	0.020917	HIF-1 responsive RTP801 (RTP801), mRNA /cds=(198,896) /gb=NM_019058 /gi=9506686 /ug=Hs.111244 /len=1760	NM_019058	Hs.111244	NP_061931

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5069	0.020917	hsp70-interacting protein (HSPBP1), mRNA /cds=(312,1400) /gb=NM_012267 /gi=21361406 /ug=Hs.53066 /len=1795	NM_012267	Hs.53066	NP_036399
5098	0.015351	hypothetical protein, clone MGC:12969 IMAGE:3343683, mRNA, complete cds /cds=(931,1614) /gb=BC006428 /gi=13623618 /ug=Hs.15093 /len=2632	BC006428	Hs.15093	NP_057547
5102	0.003113	cofilin 1 (non-muscle) (CFL1), mRNA /cds=(52,552) /gb=NM_005507 /gi=5031634 /ug=Hs.180370 /len=1059	NM_005507	Hs.180370	NP_005498
5138	0.02428	exostoses (multiple) 2 (EXT2), mRNA /cds=(488,2644) /gb=NM_000401 /gi=4557572 /ug=Hs.75334 /len=3781	NM_000401	Hs.75334	NP_000392
5155	0.011093	phosphoglycerate kinase 1 (PGK1), mRNA /cds=(70,1323) /gb=NM_000291 /gi=22095338 /ug=Hs.78771 /len=2338	NM_000291	Hs.78771	NP_000282
5161	0.004578	basic transcription factor 3 (BTF3), mRNA /cds=(240,728) /gb=NM_001207 /gi=20070129 /ug=Hs.101025 /len=952	NM_001207	Hs.101025	NP_001198
5195	0.01661	angiopoietin-like 4 (ANGPTL4), transcript variant 1, mRNA /cds=(196,1416) /gb=NM_139314 /gi=21536397 /ug=Hs.9613 /len=1967	NM_139314	Hs.9613	NP_647475
5200	0.039781	thrombospondin 1 (THBS1), mRNA /cds=(112,3624) /gb=NM_003246 /gi=4507484 /ug=Hs.87409 /len=5722	NM_003246	Hs.87409	NP_003237
5226	0.034698	mRNA; cDNA DKFZp564L2416 (from clone DKFZp564L2416) /gb=AL050385 /gi=4914588 /ug=Hs.48332 /len=5511	AL050385	Hs.48332	
5230	0.042541	CDC28 protein kinase regulatory subunit 2 (CKS2), mRNA /cds=(96,335) /gb=NM_001827 /gi=4502858 /ug=Hs.83758 /len=627	NM_001827	Hs.83758	NP_001818
5238	0.048529	NRAS-related gene (D1S155E), mRNA /cds=(428,2824) /gb=NM_007158 /gi=20070240 /ug=Hs.69855 /len=4076	NM_007158	Hs.69855	NP_009089
5261	0.011093	replication factor C (activator 1) 4, 37kDa (RFC4), mRNA /cds=(284,1375) /gb=NM_002916 /gi=4506490 /ug=Hs.35120 /len=1446	NM_002916	Hs.35120	NP_002907
5262	0.010202	ALL1-fused gene from chromosome 1q (AF1Q), mRNA /cds=(353,625) /gb=NM_006818 /gi=21626459 /ug=Hs.75823 /len=1653	NM_006818	Hs.75823	NP_006809
5264	0.045456	small GTP-binding protein RAB1A	AF226873		NP_033022

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5318	0.048529	603021120F1 NIH_MGC_114 cDNA clone IMAGE:5191733 5', mRNA sequence /clone=IMAGE:5191733 /clone_end=5' /gb=BI488592 /gi=15327820 /ug=Hs.380956 /len=988	BI488592	Hs.380956	
5329	0.032363	dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST), mRNA /cds=(60,1430) /gb=NM_005216 /gi=20070196 /ug=Hs.34789 /len=2045	NM_005216	Hs.34789	NP_005207
5367	0.026124	hypothetical protein MGC4415 (MGC4415), mRNA /cds=(154,675) /gb=NM_031484 /gi=13899343 /ug=Hs.209614 /len=3243	NM_031484	Hs.209614	NP_113672
5384	0.028082	Hypothetical protein(cDNA FLJ11422 fis, clone HEMBA1001008)	AK021484		
5400	0.004165	dUTP pyrophosphatase (DUT), mRNA /cds=(20,514) /gb=NM_001948 /gi=21361335 /ug=Hs.367676 /len=1816	NM_001948	Hs.367676	NP_001939
5402	0.039781	brain cDNA, clone:QnpA-21421	AB050422		
5411	0.045456	DKFZp566J2446 (from clone DKFZp566J2446)	AL050082		NP_008944
5420	0.002302	matrilin 3 (MATN3) precursor, mRNA /cds=(64,1524) /gb=NM_002381 /gi=13518040 /ug=Hs.278461 /len=2599	NM_002381	Hs.278461	NP_002372
5438	0.005026	mitochondrion, complete genome	NC_001807		
5477	0.007223	lectin, galactoside-binding, soluble, 3 (galectin 3) (LGALS3), mRNA /cds=(19,771) /gb=NM_002306 /gi=4504982 /ug=Hs.621 /len=914	NM_002306	Hs.621	NP_002297
5497	0.028082	zinc finger, DHHC domain containing 4 (ZDHHC4), mRNA /cds=(222,1256) /gb=NM_018106 /gi=21361700 /ug=Hs.5268 /len=1704	NM_018106	Hs.5268	NP_060576
5498	4.81E-04	polymerase (RNA) II (DNA directed) polypeptide G (POLR2G), mRNA /cds=(107,625) /gb=NM_002696 /gi=4505946 /ug=Hs.14839 /len=828	NM_002696	Hs.14839	NP_002687
5551	0.011093	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit (HADHA), mRNA /cds=(35,2326) /gb=NM_000182 /gi=20127407 /ug=Hs.75860 /len=2972	NM_000182	Hs.75860	NP_000173
5594	0.03016	hypothetical gene supported by U81006; NM_004800 (LOC121929), mRNA	XM_071779		
5640	0.002819	nonhistone protein HMG1	M21683		

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5644	0.048529	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700	NM_002211	Hs.287797	NP_596867
5671	0.003784	EPC-1 (=M76979 PEDF;U29953;M90493)	U57446		
5672	0.006039	clone IMAGE:5265581, mRNA /gb=BC035165 /gi=23272508 /ug=Hs.400548 /len=2237	BC035165	Hs.400548	
5717	0.039781	MLL septin-like fusion (MSF), mRNA /cds=(258,1964) /gb=NM_006640 /gi=19923366 /ug=Hs.181002 /len=3929	NM_006640	Hs.181002	NP_006631
5747	0.048529	chromosome 20 open reading frame 14 (C20orf14), mRNA /cds=(100,2925) /gb=NM_012469 /gi=6912731 /ug=Hs.31334 /len=3060	NM_012469	Hs.31334	NP_036601
5754	0.037168	KIAA1360	AB037781		NP_060458
5784	0.037168	suppressor of cytokine signaling 2 (SOCS2), mRNA /cds=(591,1187) /gb=NM_003877 /gi=21536304 /ug=Hs.405946 /len=2210	NM_003877	Hs.405946	NP_003868
5789	0.015351	ribosomal protein L31 (RPL31), mRNA /cds=(28,405) /gb=NM_000993 /gi=15812219 /ug=Hs.184014 /len=442	NM_000993	Hs.184014	NP_000984
5814	0.001216	ribosomal protein L36a-like (RPL36AL), mRNA /cds=(95,415) /gb=NM_001001 /gi=16306559 /ug=Hs.419465 /len=537	NM_001001	Hs.419465	NP_000992
5821	0.007223	ribosomal protein L11 (RPL11), mRNA /cds=(21,557) /gb=NM_000975 /gi=15431289 /ug=Hs.388664 /len=609	NM_000975	Hs.388664	NP_000966
5826	0.017954	ribosomal protein L13a (RPL13A), mRNA /cds=(23,634) /gb=NM_012423 /gi=14591905 /ug=Hs.389335 /len=1142	NM_012423	Hs.389335	NP_036555
5870	0.014175	Similar to cyclin K, clone MGC:9113 IMAGE:3907416, mRNA, complete cds /cds=(110,1174) /gb=BC015935 /gi=16198507 /ug=Hs.375192 /len=1925	BC015935	Hs.375192	
5893	0.003113	golgi phosphoprotein 2 (GOLPH2), mRNA /cds=(151,1353) /gb=NM_016548 /gi=7706084 /ug=Hs.182793 /len=3042	NM_016548	Hs.182793	NP_808800
5899	0.006039	Fas (TNFRSF6) associated factor 1 (FAF1), transcript variant 1, mRNA /cds=(454,2406) /gb=NM_007051 /gi=19528653 /ug=Hs.25821 /len=2610	NM_007051	Hs.25821	NP_572051
5914	0.042541	ribosomal protein S20 (RPS20), mRNA /cds=(128,487) /gb=NM_001023 /gi=14591915 /ug=Hs.8102 /len=539	NM_001023	Hs.8102	NP_001014

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5918	0.026124	Mus musculus mitochondrion, complete genome	NC_001569		
5934	0.020917	enthoprotin (ENTH), mRNA /cds=(102,1979) /gb=NM_014666 /gi=7661967 /ug=Hs.132853 /len=3336	NM_014666	Hs.132853	NP_055481
5938	0.039781	chaperonin containing TCP1, subunit 3 (gamma) (CCT3), mRNA /cds=(1,1635) /gb=NM_005998 /gi=5174726 /ug=Hs.1708 /len=1901	NM_005998	Hs.1708	NP_005989
5959	0.01661	germline T-cell receptor beta chain	U66061		
5974	0.01205	KIAA0266 gene product (KIAA0266), mRNA /cds=(734,3034) /gb=NM_021645 /gi=11063982 /ug=Hs.127376 /len=5585	NM_021645	Hs.127376	NP_067677
5989	0.026124	CDA02 protein (CDA02), mRNA /cds=(3,1832) /gb=NM_032025 /gi=14042940 /ug=Hs.332404 /len=2179	NM_032025	Hs.332404	NP_114414
6006	0.003435	ribosomal protein L23a (RPL23A), mRNA /cds=(22,492) /gb=NM_000984 /gi=17105393 /ug=Hs.419463 /len=546	NM_000984	Hs.419463	NP_000975
6009	0.026124	methylmalonyl Coenzyme A mutase (MUT), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,2329) /gb=NM_000255 /gi=4557766 /ug=Hs.155212 /len=2798	NM_000255	Hs.155212	NP_000246
6013	0.039781	Similar to hect domain and RLD 2, clone IMAGE:4830978, mRNA /gb=BC033888 /gi=21706785 /ug=Hs.429904 /len=4297	BC033888	Hs.429904	
6027	0.002549	mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA /cds=(182,1093) /gb=NM_005924 /gi=21396478 /ug=Hs.77858 /len=2284	NM_005924	Hs.77858	NP_005915
6034	0.037168	NRAS-related gene (D1S155E), mRNA /cds=(428,2824) /gb=NM_007158 /gi=20070240 /ug=Hs.69855 /len=4076	NM_007158	Hs.69855	NP_009089
6037	0.028082	splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(156,821) /gb=NM_003016 /gi=4506898 /ug=Hs.73965 /len=1879	NM_003016	Hs.73965	NP_003007
6042	0.028082	laminin, gamma 1 (formerly LAMB2) (LAMC1), mRNA /cds=(300,5129) /gb=NM_002293 /gi=9845497 /ug=Hs.432855 /len=7923	NM_002293	Hs.432855	NP_002284
6065	0.045456	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa (NDUFC2), mRNA /cds=(151,510) /gb=NM_004549 /gi=19923255 /ug=Hs.193313 /len=2168	NM_004549	Hs.193313	NP_004540

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6068	0.03016	mitochondrial ribosomal protein L27 (MRPL27), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA /cds=(32,316) /gb=NM_148571 /gi=22547130 /ug=Hs.7736 /len=2472	NM_148571	Hs.7736	NP_683412
6072	0.002819	mRNA for KIAA0530 protein, partial cds. /cds=(1,4693) /gb=AB011102 /gi=3043583 /ug=Hs.173081 /len=6578	AB011102	Hs.173081	
6083	0.011093	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA /cds=(9,536) /gb=NM_002495 /gi=4505368 /ug=Hs.10758 /len=668	NM_002495	Hs.10758	NP_002486
6102	0.022547	homer 2 (Drosophila) (HOMER2), mRNA /cds=(1,1065) /gb=NM_004839 /gi=4758547 /ug=Hs.93564 /len=1800	NM_004839	Hs.93564	NP_004830
6106	0.003435	EST (ym17h04.s1 clone 48282 3')	H11657		
6139	0.011093	cofilin 1 (non-muscle) (CFL1), mRNA /cds=(52,552) /gb=NM_005507 /gi=5031634 /ug=Hs.180370 /len=1059	NM_005507	Hs.180370	NP_005498
6144	0.013076	CSE1 chromosome segregation 1-like (yeast) (CSE1L), mRNA /cds=(124,3039) /gb=NM_001316 /gi=4503072 /ug=Hs.90073 /len=3147	NM_001316	Hs.90073	NP_803185
6164	0.01205	antigen NY-CO-33 (NY-CO-33)	AF039698		NP_005777
6166	0.028082	ribosomal protein L10 (RPL10), mRNA /cds=(42,686) /gb=NM_006013 /gi=15718685 /ug=Hs.412900 /len=2188	NM_006013	Hs.412900	NP_006004
6182	0.045456	signal sequence receptor, gamma (translocon-associated protein gamma) (SSR3), mRNA /cds=(57,614) /gb=NM_007107 /gi=6005883 /ug=Hs.28707 /len=3061	NM_007107	Hs.28707	NP_009038
6188	0.02428	phosphodiesterase 10A(PDE10A) mRNA	NM_006661		NP_006652
6191	0.017954	calsyntenin 3 (CLSTN3), mRNA /cds=(539,3445) /gb=NM_014718 /gi=7662267 /ug=Hs.107809 /len=4300	NM_014718	Hs.107809	NP_055533
6200	0.037168	KIAA0922 protein (KIAA0922), mRNA /cds=(123,3842) /gb=NM_015196 /gi=14149672 /ug=Hs.37892 /len=3906	NM_015196	Hs.37892	NP_056011
6205	0.020917	jumping translocation breakpoint (JTB), mRNA /cds=(433,873) /gb=NM_006694 /gi=5729888 /ug=Hs.6396 /len=1040	NM_006694	Hs.6396	NP_006685
6268	0.007197	cDNA: FLJ22008 fis, clone HEP06934. /gb=AK025661 /gi=10438250 /ug=Hs.193700 /len=2207	AK025661	Hs.193700	
6286	0.042541	ribosomal protein S13 (RPS13), mRNA /cds=(33,488) /gb=NM_001017 /gi=14591910 /ug=Hs.165590 /len=529	NM_001017	Hs.165590	NP_001008

Genes Corresponding T Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6309	0.027243	WW domain binding protein 11 (WBP11), mRNA /cds=(162,2087) /gb=NM_016312 /gi=18375679 /ug=Hs.334811 /len=2690	NM_016312	Hs.334811	NP_057396
6322	0.015351	ubiquitin specific protease 9 (USP9Y)	XM_000563		
6337	0.034698	adaptor-related protein complex 2, mu 1 subunit (AP2M1), mRNA /cds=(136,1443) /gb=NM_004068 /gi=14917108 /ug=Hs.152936 /len=1936	NM_004068	Hs.152936	NP_004059
6341	0.004165	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 (ADAMTS1), mRNA /cds=(294,3146) /gb=NM_006988 /gi=11038653 /ug=Hs.8230 /len=4459	NM_006988	Hs.8230	NP_008919
6346	0.002819	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (B3GNT6), mRNA /cds=(80,1327) /gb=NM_006876 /gi=5802983 /ug=Hs.8526 /len=2011	NM_006876	Hs.8526	NP_006867
6352	0.020028	ILK-1 gene for integrin-linked kinase 1, exons 1-13	AJ404847		
6359	0.007887	lysyl oxidase-like 2 (LOXL2), mRNA /cds=(248,2572) /gb=NM_002318 /gi=4505010 /ug=Hs.83354 /len=3432	NM_002318	Hs.83354	NP_002309
6374	0.045456	alcohol dehydrogenase beta-1-subunit (ADH1-2 allele)	X03350		NP_000659
6402	0.009373	actin, gamma 1 (ACTG1), mRNA /cds=(75,1202) /gb=NM_001614 /gi=11038618 /ug=Hs.14376 /len=1919	NM_001614	Hs.14376	NP_001605
6425	0.02428	insulin receptor substrate-2 (IRS2) mRNA, complete cds	AF073310		NP_003740
6516	0.004578	ribosomal protein S27-like (RPS27L), mRNA /cds=(73,327) /gb=NM_015920 /gi=18490988 /ug=Hs.108957 /len=523	NM_015920	Hs.108957	NP_057004
6546	0.034698	hypothetical protein (KIAA0594)	AB011166		NP_055925
6554	0.008602	mitochondrial ribosomal protein L13 (MRPL13), nuclear gene encoding mitochondrial protein, mRNA /cds=(287,823) /gb=NM_014078 /gi=21265072 /ug=Hs.333823 /len=1086	NM_014078	Hs.333823	NP_054797
6565	0.032363	PTK9 protein tyrosine kinase 9 (PTK9), mRNA /cds=(61,1113) /gb=NM_002822 /gi=4506274 /ug=Hs.82643 /len=3000	NM_002822	Hs.82643	NP_002813
6577	0.034698	ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=NM_004152 /gi=9845504 /ug=Hs.281960 /len=986	NM_004152	Hs.281960	NP_004143

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6592	0.003113	methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,1111) /gb=NM_006636 /gi=13699869 /ug=Hs.154672 /len=2154	NM_006636	Hs.154672	NP_006627
6593	0.045456	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae) (NHP2L1), mRNA /cds=(95,481) /gb=NM_005008 /gi=4826859 /ug=Hs.182255 /len=1475	NM_005008	Hs.182255	NP_004999
6603	0.002549	tm68a09.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2163256 3', mRNA sequence /clone=IMAGE:2163256 /clone_end=3' /gb=AI498805 /gi=4390787 /ug=Hs.436349 /len=460	AI498805	Hs.436349	
6604	0.042541	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) (SFRS1), mRNA /cds=(36,782) /gb=NM_006924 /gi=19923382 /ug=Hs.73737 /len=2708	NM_006924	Hs.73737	NP_008855
6622	0.017954	aquaporin 1 (channel-forming integral protein, 28kDa) (AQP1), mRNA /cds=(39,848) /gb=NM_000385 /gi=4755121 /ug=Hs.76152 /len=1662	NM_000385	Hs.76152	NP_000376
6623	0.005026	atractin (ATRN), transcript variant 1, mRNA /cds=(80,4369) /gb=NM_139321 /gi=21450860 /ug=Hs.194019 /len=8645	NM_139321	Hs.194019	NP_647538
6626	0.022547	tumor antigen SLP-8p (HCC8), mRNA /cds=(21,2921) /gb=NM_016516 /gi=7705396 /ug=Hs.48499 /len=3480	NM_016516	Hs.48499	NP_057600
6633	0.02428	HSPCO34 protein (LOC51668), mRNA /cds=(58,402) /gb=NM_016126 /gi=7706382 /ug=Hs.46967 /len=598	NM_016126	Hs.46967	NP_057210
6634	0.010202	surfeit 4 (SURF4), mRNA /cds=(131,940) /gb=NM_033161 /gi=19593984 /ug=Hs.284296 /len=2985	NM_033161	Hs.284296	NP_149351
6646	5.42E-04	protein phosphatase 1, regulatory (inhibitor) subunit 12A (PPP1R12A), mRNA /cds=(1,3093) /gb=NM_002480 /gi=4505316 /ug=Hs.16533 /len=4613	NM_002480	Hs.16533	NP_002471
6647	0.01205	sterol carrier protein 2 (SCP2), mRNA /cds=(22,1665) /gb=NM_002979 /gi=19923232 /ug=Hs.75760 /len=2572	NM_002979	Hs.75760	NP_002970
6650	0.034698	tetratricopeptide repeat domain 1 (TTC1), mRNA /cds=(51,929) /gb=NM_003314 /gi=4507710 /ug=Hs.7733 /len=1407	NM_003314	Hs.7733	NP_003305

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6654	0.009373	pM5 protein (PM5), mRNA /cds=(1,3669) /gb=NM_014287 /gi=10947030 /ug=Hs.439182 /len=4182	NM_014287	Hs.439182	NP_055102
6659	0.042541	heat shock 70kDa protein 8 (HSPA8), transcript variant 1, mRNA /cds=(79,2019) /gb=NM_006597 /gi=24234684 /ug=Hs.180414 /len=2276	NM_006597	Hs.180414	NP_694881
6661	0.020917	stromal antigen 1 (STAG1), mRNA /cds=(401,4177) /gb=NM_005862 /gi=5032062 /ug=Hs.286148 /len=4337	NM_005862	Hs.286148	NP_005853
6666	0.034698	tigger transposable element derived 1 (TIGD1), mRNA /cds=(635,2410) /gb=NM_145702 /gi=22209000 /ug=Hs.351348 /len=2448	NM_145702	Hs.351348	NP_663748
6677	0.007223	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA /cds=(69,965) /gb=NM_001152 /gi=4502098 /ug=Hs.79172 /len=1225	NM_001152	Hs.79172	NP_001143
6682	0.004578	hypothetical protein FLJ12442 (FLJ12442), mRNA /cds=(412,1974) /gb=NM_022908 /gi=12597652 /ug=Hs.84753 /len=2057	NM_022908	Hs.84753	NP_075059
6683	2.24E-04	lamin A/C (LMNA), transcript variant 1, mRNA /cds=(213,2207) /gb=NM_170707 /gi=27436945 /ug=Hs.377973 /len=3181	NM_170707	Hs.377973	NP_733822
6717	0.008602	fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 1, mRNA /cds=(89,6274) /gb=NM_013451 /gi=19718757 /ug=Hs.234680 /len=6829	NM_013451	Hs.234680	NP_579899
6722	0.037168	syndecan 1 (SDC1), mRNA /cds=(253,1185) /gb=NM_002997 /gi=21359855 /ug=Hs.82109 /len=2484	NM_002997	Hs.82109	NP_002988
6734	1.72E-04	PAI-1 mRNA-binding protein (PAI-RBP1), mRNA /cds=(86,1249) /gb=NM_015640 /gi=7661625 /ug=Hs.165998 /len=2201	NM_015640	Hs.165998	NP_056455
6735	0.007223	DKFZp586J021 (from clone DKFZp586J021) /cds=UNKNOWN /gb=AL110197 /gi=5817115 /ug=Hs.6441 /len=1896	AL110197	Hs.6441	NP_003246
6744	0.026124	ribosomal protein, large, P0 (RPLP0), transcript variant 2, mRNA /cds=(111,1064) /gb=NM_053275 /gi=16933545 /ug=Hs.406511 /len=1148	NM_053275	Hs.406511	NP_444505
6745	0.019388	mRNA; cDNA DKFZp434A163 (from clone DKFZp434A163); partial cds /cds=(1,4964) /gb=AL110218 /gi=5817150 /ug=Hs.127401 /len=5084	AL110218	Hs.127401	

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6749	0.034698	histidyl-tRNA synthetase 2 (HARS2), mRNA /cds=(111,752) /gb=NM_080820 /gi=21361784 /ug=Hs.352419 /len=2396	NM_080820	Hs.352419	NP_543010
6750	0.004165	ADP-ribosylation-like factor 6 interacting protein 4 (ARL6IP4), mRNA /cds=(63,719) /gb=NM_016638 /gi=7706183 /ug=Hs.103561 /len=952	NM_016638	Hs.103561	NP_061164
6752	2.56E-04	tumor endothelial marker 6 (TEM6), mRNA /cds=(93,3710) /gb=NM_022748 /gi=17511208 /ug=Hs.12210 /len=6702	NM_022748	Hs.12210	NP_073585
6770	0.009373	FK506 binding protein 1A, 12kDa (FKBP1A), transcript variant 12B, mRNA /cds=(104,430) /gb=NM_000801 /gi=17149837 /ug=Hs.380080 /len=1578	NM_000801	Hs.380080	NP_463460
6771	0.014175	surfeit 6 (SURF6), mRNA /cds=(56,1141) /gb=NM_006753 /gi=19557701 /ug=Hs.274430 /len=2329	NM_006753	Hs.274430	NP_006744
6772	0.003435	hypothetical protein FLJ22301 (FLJ22301), mRNA /cds=(696,2054) /gb=NM_024836 /gi=13376246 /ug=Hs.181406 /len=2952	NM_024836	Hs.181406	NP_079112
6773	0.003784	hypothetical protein FLJ14834 (FLJ14834), mRNA /cds=(326,1237) /gb=NM_032849 /gi=21361885 /ug=Hs.62905 /len=2342	NM_032849	Hs.62905	NP_116238
6861	0.02428	mRNA; cDNA DKFZp434A012 (from clone DKFZp434A012) /gb=AL096752 /gi=5419888 /ug=Hs.306327 /len=2248	AL096752	Hs.306327	
6863	0.034698	Sm protein F (LSM6), mRNA /cds=(82,324) /gb=NM_007080 /gi=5901997 /ug=Hs.42438 /len=596	NM_007080	Hs.42438	NP_009011
6865	0.003435	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), mRNA /cds=(91,336) /gb=NM_002489 /gi=4505356 /ug=Hs.50098 /len=518	NM_002489	Hs.50098	NP_002480
6881	0.020917	uncharacterized hematopoietic stem/progenitor cells protein MDS029 (MDS029), mRNA /cds=(112,438) /gb=NM_018464 /gi=8923929 /ug=Hs.43549 /len=636	NM_018464	Hs.43549	NP_060934
6888	0.017954	enolase 1, (alpha) (ENO1), mRNA /cds=(152,1456) /gb=NM_001428 /gi=16507965 /ug=Hs.254105 /len=1812	NM_001428	Hs.254105	NP_001419
6930	0.003113	HMT1 hnRNP methyltransferase-like 1 (S. cerevisiae) (HRMT1L1), mRNA /cds=(166,1467) /gb=NM_001535 /gi=4504494 /ug=Hs.235887 /len=2093	NM_001535	Hs.235887	NP_001526

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6935	0.037168	FtsJ 3 (E. coli) (FTSJ3), mRNA /cds=(72,2615) /gb=NM_017647 /gi=17017990 /ug=Hs.257486 /len=2999	NM_017647	Hs.257486	NP_060117
6942	0.003435	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
6948	0.048529	putative DNA binding protein (M96), mRNA /cds=(244,2025) /gb=NM_007358 /gi=6678763 /ug=Hs.31016 /len=2648	NM_007358	Hs.31016	NP_031384
6950	0.039781	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) (SFPQ), mRNA /cds=(86,2209) /gb=NM_005066 /gi=4826997 /ug=Hs.180610 /len=3071	NM_005066	Hs.180610	NP_005057
6957	0.003435	ATP synthase, H transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O), mRNA /cds=(37,678) /gb=NM_001697 /gi=4502302 /ug=Hs.433960 /len=772	NM_001697	Hs.433960	NP_001688
6959	0.005026	HLCS gene for holocarboxylase synthetase, complete cds	AB063285		
6969	0.004578	oligophrenin 1 (OPHN1), mRNA /cds=(638,3046) /gb=NM_002547 /gi=4505506 /ug=Hs.128824 /len=7350 (=FLJ11206)	NM_002547	Hs.128824	NP_002538
6970	0.007223	neuroblastoma apoptosis-related RNA-binding protein (CUGBP2) gene, exons 10, 11a, 11b, 12, 13a, 13b, 14, and complete cds, alternatively spliced	AF295068		
7005	5.42E-04	clone MGC:24133 IMAGE:4693393, mRNA, complete cds /cds=(61,528) /gb=BC017973 /gi=22450811 /ug=Hs.288010 /len=946	BC017973	Hs.288010	NP_777556
7022	0.048529	ribosomal protein S29 (RPS29), mRNA /cds=(31,201) /gb=NM_001032 /gi=13904868 /ug=Hs.539 /len=346	NM_001032	Hs.539	NP_001023
7048	0.007887	twisted gastrulation 1 (Drosophila) (TWSG1), mRNA /cds=(106,777) /gb=NM_020648 /gi=21314788 /ug=Hs.247302 /len=3693	NM_020648	Hs.247302	NP_065699
7049	0.045456	C3HC4-like zinc finger protein (ZFP26), mRNA /cds=(144,836) /gb=NM_016422 /gi=21361492 /ug=Hs.44685 /len=1108	NM_016422	Hs.44685	NP_057506

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7067	0.03016	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 (GNB2L1), mRNA /cds=(96,1049) /gb=NM_006098 /gi=24475893 /ug=Hs.5662 /len=1093	NM_006098	Hs.5662	NP_006089
7082	0.032363	NCK-associated protein 1 (NCKAP1), mRNA /cds=(272,3658) /gb=NM_013436 /gi=20127530 /ug=Hs.278411 /len=4487	NM_013436	Hs.278411	NP_038464
7090	0.02428	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
7098	0.006039	inactive progesterone receptor, 23 kD (TEBP), mRNA /cds=(107,589) /gb=NM_006601 /gi=23308578 /ug=Hs.278270 /len=1490	NM_006601	Hs.278270	NP_006592
7102	0.003784	survival of motor neuron protein interacting protein 1 (SIP1), mRNA /cds=(84,926) /gb=NM_003616 /gi=4506960 /ug=Hs.102456 /len=1285	NM_003616	Hs.102456	NP_003607
7123	0.007887	KIAA0857 protein (KIAA0857), mRNA /cds=(241,2202) /gb=NM_015470 /gi=24308074 /ug=Hs.24557 /len=4340	NM_015470	Hs.24557	NP_056285
7126	0.015351	ribosomal protein S18 (RPS18), mRNA /cds=(46,504) /gb=NM_022551 /gi=14165467 /ug=Hs.275865 /len=549	NM_022551	Hs.275865	NP_072045
7127	0.014175	actin-related protein 10 (S. cerevisiae) (ACTR10), mRNA /cds=(81,1334) /gb=NM_018477 /gi=8923711 /ug=Hs.274369 /len=1621	NM_018477	Hs.274369	NP_060947
7149	0.017954	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 (SLC25A3), nuclear gene encoding mitochondrial protein, transcript variant 1b, mRNA /cds=(49,1134) /gb=NM_002635 /gi=4505774 /ug=Hs.78713 /len=1330	NM_002635	Hs.78713	NP_005879
7150	0.034698	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
7187	0.037168	collagen, type V, alpha 1 (COL5A1), mRNA /cds=(383,5899) /gb=NM_000093 /gi=16554578 /ug=Hs.146428 /len=6496	NM_000093	Hs.146428	NP_000084
7224	0.028082	hypothetical protein FLJ20312 (FLJ20312), mRNA /cds=(384,803) /gb=NM_017761 /gi=20127576 /ug=Hs.7862 /len=2382	NM_017761	Hs.7862	NP_060231

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7236	0.037168	eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA /cds=(23,1360) /gb=NM_001568 /gi=4503520 /ug=Hs.106673 /len=1510	NM_001568	Hs.106673	NP_001559
7238	0.011093	pp11741 mRNA, complete cds /cds=(1126,2058) /gb=AF318323 /gi=18027737 /ug=Hs.382867 /len=3222	AF318323	Hs.382867	
7241	0.032363	likely ortholog of mouse guanine nucleotide releasing protein x (GNRPX), mRNA /cds=(82,531) /gb=NM_018049 /gi=8922332 /ug=Hs.173739 /len=1215	NM_018049	Hs.173739	NP_060519
7243	0.002302	calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2), transcript variant 1, mRNA /cds=(830,2596) /gb=NM_006549 /gi=27437014 /ug=Hs.108708 /len=5620	NM_006549	Hs.108708	NP_757380
7272	0.037168	hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4 (FLJ11021), mRNA /cds=(767,1375) /gb=NM_023012 /gi=20127619 /ug=Hs.81648 /len=1878	NM_023012	Hs.81648	NP_075388
7285	0.045456	MR4-ET0140-070501-014-g01 ET0140 cDNA, mRNA sequence /gb=BQ331564 /gi=20972721 /ug=Hs.442329 /len=219	BQ331564	Hs.442329	
7310	0.006608	UI-H-BI2-agp-f-12-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2725031 3', mRNA sequence /clone=IMAGE:2725031 /clone_end=3' /gb=AW292456 /gi=6699092 /ug=Hs.437793 /len=745	AW292456	Hs.437793	
7319	0.020917	mRNA for KIAA0276 gene, partial cds. /cds=(1,932) /gb=D87466 /gi=1665816 /ug=Hs.240112 /len=4185	D87466	Hs.240112	
7361	0.042541	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 (SMARCA4), mRNA /cds=(277,5220) /gb=NM_003072 /gi=21071055 /ug=Hs.78202 /len=5681	NM_003072	Hs.78202	NP_003063
7414	0.004165	tetraspanin similar to TM4SF9 (DC-TM4F2), mRNA /cds=(79,891) /gb=NM_030927 /gi=13569888 /ug=Hs.101395 /len=2556	NM_030927	Hs.101395	NP_112189
7437	0.045456	similar to endothelial cell-selective adhesion molecule (ESAM), mRNA /cds=(139,1311) /gb=NM_138961 /gi=20452463 /ug=Hs.173840 /len=1838	NM_138961	Hs.173840	NP_620411
7450	0.048529	KIAA0097 gene product (KIAA0097), mRNA /cds=(27,5945) /gb=NM_014756 /gi=24307972 /ug=Hs.76989 /len=6449	NM_014756	Hs.76989	NP_055571

Genes Corrsponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7475	0.048529	mRNA; cDNA DKFZp451F056 (from clone DKFZp451F056) /gb=AL832357 /gi=21732919 /ug=Hs.118837 /len=4901	AL832357	Hs.118837	
7482	0.019388	kinesin family member 1C (KIF1C), mRNA /cds=(114,3425) /gb=NM_006612 /gi=5729896 /ug=Hs.139648 /len=4082	NM_006612	Hs.139648	NP_006603
7491	0.034698	chromosome 20 open reading frame 149 (C20orf149), mRNA /cds=(150,494) /gb=NM_024299 /gi=13236523 /ug=Hs.79625 /len=803	NM_024299	Hs.79625	NP_077275
7497	2.56E-04	mRNA for KIAA1266 protein, partial cds. /cds=(131,1936) /gb=AB033092 /gi=6331198 /ug=Hs.58598 /len=5484	AB033092	Hs.58598	
7508	0.002819	mRNA for RCC1-like protein (TD-60 gene) /cds=(236,1804) /gb=AJ421269 /gi=27526612 /ug=Hs.284146 /len=4114	AJ421269	Hs.284146	NP_061185
7520	0.042541	hypothetical protein FLJ10350 (FLJ10350), mRNA /cds=(676,2340) /gb=NM_018067 /gi=21361780 /ug=Hs.177596 /len=2811	NM_018067	Hs.177596	NP_060537
7543	0.039781	hypothetical protein FLJ20255 (FLJ20255), mRNA /cds=(146,1090) /gb=NM_017728 /gi=8923229 /ug=Hs.15797 /len=1769	NM_017728	Hs.15797	NP_060198
7548	0.026124	methionine adenosyltransferase II, beta (MAT2B), mRNA /cds=(73,1077) /gb=NM_013283 /gi=20127525 /ug=Hs.54642 /len=2054	NM_013283	Hs.54642	NP_037415
7569	0.011093	KIAA1601 protein, partial cds /cds=UNKNOWN /gb=AB046821 /gi=10047276 /ug=Hs.4007 /len=3851	AB046821	Hs.4007	NP_009090
7574	0.028082	ubiquitin-conjugating enzyme E2N (UBC13 yeast) (UBE2N), mRNA /cds=(64,522) /gb=NM_003348 /gi=4507792 /ug=Hs.75355 /len=1203	NM_003348	Hs.75355	NP_003339
7576	0.001513	cytochrome P450, family 1, subfamily B, polypeptide 1 (CYP1B1), mRNA /cds=(373,2004) /gb=NM_000104 /gi=13325059 /ug=Hs.154654 /len=5128	NM_000104	Hs.154654	NP_000095
7587	0.006608	XPA binding protein 1; putative ATP(GTP)-binding protein (NTPBP), mRNA /cds=(25,1149) /gb=NM_007266 /gi=14149628 /ug=Hs.18259 /len=1829	NM_007266	Hs.18259	NP_009197
7599	0.01205	fibrinogen, B beta polypeptide (FGB), mRNA /cds=(9,1484) /gb=NM_005141 /gi=11761630 /ug=Hs.7645 /len=1918	NM_005141	Hs.7645	NP_005132

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7618	0.026124	hypothetical protein FLJ11240 (FLJ11240), mRNA /cds=(26,1648) /gb=NM_018368 /gi=8922955 /ug=Hs.339833 /len=1947	NM_018368	Hs.339833	NP_060838
7629	0.039781	spermidine/spermine N1-acetyltransferase (SAT), mRNA /cds=(166,681) /gb=NM_002970 /gi=4506788 /ug=Hs.28491 /len=1060	NM_002970	Hs.28491	NP_002961
7637	0.001216	serum response factor (c-fos serum response element-binding transcription factor) (SRF), mRNA /cds=(359,1885) /gb=NM_003131 /gi=4507204 /ug=Hs.155321 /len=4201	NM_003131	Hs.155321	NP_003122
7660	0.015351	bladder cancer overexpressed protein (BLOV1), mRNA /cds=(72,1136) /gb=NM_018656 /gi=8922084 /ug=Hs.125830 /len=2324	NM_018656	Hs.125830	NP_061126
7692	0.007887	ribosomal protein, L41 (RPL41), mRNA /cds=(84,161) /gb=NM_021104 /gi=10863874 /ug=Hs.356795 /len=478	NM_021104	Hs.356795	NP_066927
7694	0.002549	cDNA FLJ25013 fis, clone CBL01365. /gb=AK057742 /gi=16553667 /ug=Hs.380091 /len=2200	AK057742	Hs.380091	
7711	0.017954	death inducer with SAP domain DIS mRNA, complete cds /cds=(120,3572) /gb=AF465616 /gi=27497117 /ug=Hs.183779 /len=3856	AF465616	Hs.183779	NP_060707
7719	0.011093	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 (EDG2), transcript variant 2, mRNA /cds=(394,1488) /gb=NM_057159 /gi=16950637 /ug=Hs.75794 /len=2732	NM_057159	Hs.75794	NP_476500
7724	0.003784	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), mRNA /cds=(252,1457) /gb=NM_002546 /gi=22547122 /ug=Hs.81791 /len=2291	NM_002546	Hs.81791	NP_002537
7728	0.007887	Down syndrome critical region gene 5 (DSCR5), transcript variant 3, mRNA /cds=(342,668) /gb=NM_016430 /gi=24497594 /ug=Hs.408790 /len=875	NM_016430	Hs.408790	NP_710149
7749	0.039781	mRNA; cDNA DKFZp666E058 (from clone DKFZp666E058) /gb=AL833023 /gi=21733613 /ug=Hs.379886 /len=1761	AL833023	Hs.379886	
7750	0.048529	period 2 (Drosophila) (PER2), transcript variant 1, mRNA /cds=(123,3890) /gb=NM_022817 /gi=12707561 /ug=Hs.153405 /len=6219	NM_022817	Hs.153405	NP_073728

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7962	0.039781	hypothetical protein MGC2941 (MGC2941), mRNA /cds=(172,969) /gb=NM_024297 /gi=13236519 /ug=Hs.288217 /len=2005	NM_024297	Hs.288217	NP_077273
7964	0.022547	CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), mRNA /cds=(969,1733) /gb=NM_006449 /gi=19923355 /ug=Hs.260024 /len=2768	NM_006449	Hs.260024	NP_006440
8020	0.020917	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART), mRNA /cds=(79,3111) /gb=NM_000819 /gi=24475881 /ug=Hs.82285 /len=3291	NM_000819	Hs.82285	NP_780294
8053	0.01661	centromere protein C 1 (CENPC1), mRNA /cds=(157,2988) /gb=NM_001812 /gi=4502778 /ug=Hs.154207 /len=3132	NM_001812	Hs.154207	NP_001803
8054	4.81E-04	pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence /cds=UNKNOWN/gb=AF334710 /gi=12658438 /ug=Hs.8364 /len=1819	AF334710	Hs.8364	NP_002603
8056	0.039781	ADP-ribosyltransferase (NAD ; poly (ADP-ribose) polymerase) (ADPRT), mRNA /cds=(160,3204) /gb=NM_001618 /gi=11496989 /ug=Hs.177766 /len=3859	NM_001618	Hs.177766	NP_001609
8097	0.010441	mRNA for KIAA1915 protein, partial cds. /cds=(356,2536) /gb=AB067502 /gi=15620888 /ug=Hs.12915 /len=7801	AB067502	Hs.12915	
8151	0.006608	cDNA: FLJ23115 fis, clone LNG07933. /gb=AK026768 /gi=10439696 /ug=Hs.98728 /len=1917	AK026768	Hs.98728	
8179	0.01205	karyopherin (importin) beta 3 (KPNB3), mRNA /cds=(139,3486) /gb=NM_002271 /gi=24797085 /ug=Hs.113503 /len=5977	NM_002271	Hs.113503	NP_002262
8180	0.039781	wn97f10.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2453803 3' similar to TR:O76003 O76003 THIOREDOXIN-LIKE PROTEIN. ; mRNA sequence /clone=IMAGE:2453803 /clone_end=3' /gb=AI934154 /gi=5673024 /ug=Hs.215019 /len=425	AI934154	Hs.215019	
8341	0.015351	EST(we27d09.x1 NCI_CGAP_Lu24 clone IMAGE:2342321 3')	AI797144		NP_002877
8355	0.03016	hypothetical protein FLJ12716 (FLJ12716), mRNA /cds=(66,2513) /gb=NM_021942 /gi=21361577 /ug=Hs.5354 /len=3522	NM_021942	Hs.5354	NP_068761

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8380	0.02428	yy31a11.s1 Soares melanocyte 2NbHM cDNA clone IMAGE:272828 3', mRNA sequence /clone=IMAGE:272828 /clone_end=3' /gb=N32993 /gi=1153392 /ug=Hs.149690 /len=478	N32993	Hs.149690	
8381	0.007887	Tho2 mRNA, complete cds /cds=(1,4437) /gb=AF441770 /gi=20799317 /ug=Hs.16411 /len=4452	AF441770	Hs.16411	
8389	0.042541	EST ov31h03.x1 Soares_testis_NHT cDNA clone IMAGE:1638965 3'	AI017329		
8438	0.032363	mRNA sequence /gb=L26969 /gi=16905391 /ug=Hs.362852 /len=1738	L26969	Hs.362852	
8472	0.039781	cDNA FLJ14188 fis, clone NT2RP2005980. /gb=AK024250 /gi=10436579 /ug=Hs.288671 /len=2289	AK024250	Hs.288671	
8477	0.037168	EST(EST36627 Embryo, 8 week I 5' monoamine oxidase B)	AA332652		NP_694587
8480	0.017954	ribosomal protein L37a (RPL37A), mRNA /cds=(36,314) /gb=NM_000998 /gi=16306561 /ug=Hs.296290 /len=392	NM_000998	Hs.296290	NP_000989
8492	0.020917	EST CM2-BT0857-021100-470-g06 BT0857 Homo sapiens cDNA	BF745663		
8508	0.01661	602384282F1 NIH_MGC_93 cDNA clone IMAGE:4513125 5', mRNA sequence /clone=IMAGE:4513125 /clone_end=5' /gb=BG289274 /gi=13044952 /ug=Hs.202537 /len=776	BG289274	Hs.202537	
8514	0.007887	mRNA; cDNA DKFZp451B1818 (from clone DKFZp451B1818) /gb=AL832623 /gi=21733198 /ug=Hs.77554 /len=6240	AL832623	Hs.77554	
8516	0.011093	EST (MR1-SN0033-100400-001-a10 SN0033)	AW867013		
8549	0.034698	EST(am82e07.s1 Stratagene schizo brain S11 cDNA clone IMAGE:1629636 3')	AA984215		NP_003109
8557	0.028082	UI-H-ED0-awy-a-01-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5825160 3', mRNA sequence /clone=IMAGE:5825160 /clone_end=3' /gb=BQ017647 /gi=19752924 /ug=Hs.124747 /len=1445	BQ017647	Hs.124747	
8560	0.001357	ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500	NM_000991	Hs.356371	NP_000982
8595	0.01661	ribosomal protein L3 (RPL3), mRNA /cds=(27,1238) /gb=NM_000967 /gi=16507968 /ug=Hs.119598 /len=1311	NM_000967	Hs.119598	NP_000958

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8639	0.039781	clone IMAGE:4391536, mRNA/cds=UNKNOWN /gb=BC017742 /gi=17389403 /ug=Hs.334534 /len=2651	BC017742	Hs.334534	NP_002067
8668	0.020917	AGENCOURT_6461316 NIH_MGC_88 cDNA clone IMAGE:5559480 5', mRNA sequence /clone=IMAGE:5559480 /clone_end=5' /gb=BM802105 /gi=19118928 /ug=Hs.48376 /len=1152	BM802105	Hs.48376	
8669	0.01661	cDNA FLJ10190 fis, clone HEMBA1004753. /gb=AK001052 /gi=7022081 /ug=Hs.274546 /len=1318	AK001052	Hs.274546	
8675	0.001357	UI-H-EI0-ayo-a-20-0-UI.s1 NCI_CGAP_EI0 cDNA clone IMAGE:5841307 3', mRNA sequence /clone=IMAGE:5841307 /clone_end=3' /gb=BQ004581 /gi=19729481 /ug=Hs.412459 /len=1095	BQ004581	Hs.412459	
8708	0.01661	BX111624 NCI_CGAP_Lu5 cDNA clone IMAGp998D244068, mRNA sequence /clone=IMAGp998D244068; IMAGE:1604327 /gb=BX111624 /gi=27837123 /ug=Hs.184840 /len=808	BX111624	Hs.184840	
8714	0.02428	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
8746	0.045456	tg02e02.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2107610 3', mRNA sequence /clone=IMAGE:2107610 /clone_end=3' /gb=AI380429 /gi=4190282 /ug=Hs.172445 /len=478	AI380429	Hs.172445	
8771	0.042541	mitochondrion, complete genome	NC_001807		
8782	0.020917	mitochondrion, complete genome	NC_001807		
8788	0.032363	ESTs, cDNA /gb=AW978555 /gi=8169822 /ug=Hs.92448 /len=754	AW978555	Hs.92448	
8796	0.002819	ESTs, cDNA, 3' end /clone=UI-E-EJ0-aii-I-19-0-UI /clone_end=3' /gb=BM681301 /gi=18991197 /ug=Hs.355029 /len=591	BM681301	Hs.355029	
8801	0.002549	cDNA, 5' end /clone=IMAGE:5185850 /clone_end=5' /gb=BI759660 /gi=15751238 /ug=Hs.250691 /len=866	BI759660	Hs.250691	
8837	0.005026	no significant match	SEQ.ID.No.39		
8840	0.014175	No significant match	SEQ.ID.No.54		
8850	0.037168	chromosome 15 clone RP11-215M5 map 15, WORKING DRAFT SEQUENCE, 6 unordered pieces	AC027467		
8856	0.008602	control			

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8915	0.044991	EST qh51c12.x1 Soares_fetal_liver_spleen_1NFLS_S1 H.sapiens cDNA clone IMAGE:1848214 3'	AI242874		
8929	0.014175	EST(EST92395 Skin tumor I cDNA 5' end)	AA379393		
8931	0.03016	chromosome 21 open reading frame 6 (C21orf6), mRNA /cds=(92,1051) /gb=NM_016940 /gi=8393017 /ug=Hs.34136 /len=1729	NM_016940	Hs.34136	NP_058636
8942	0.045456	mRNA for Sec24 protein (Sec24A isoform), partial /cds=(1,3237) /gb=AJ131244 /gi=3947687 /ug=Hs.211612 /len=5967	AJ131244	Hs.211612	
8946	0.042541	hypothetical protein FLJ33282 (FLJ33282), mRNA /cds=(225,1523) /gb=NM_152388 /gi=22748830 /ug=Hs.346509 /len=2078	NM_152388	Hs.346509	
8949	0.008602	tx18g05.x1 NCI_CGAP_Ut4 cDNA clone IMAGE:2269592 3', mRNA sequence /clone=IMAGE:2269592 /clone_end=3' /gb=AI612954 /gi=4622121 /ug=Hs.187303 /len=205	AI612954	Hs.187303	
8970	0.03016	on43h10.y5 NCI_CGAP_Co8 cDNA clone IMAGE:1559491 5', mRNA sequence /clone=IMAGE:1559491 /clone_end=5' /gb=AI793153 /gi=5340869 /ug=Hs.58262 /len=521	AI793153	Hs.58262	
8981	0.002549	AV737351 CB cDNA clone CBLALE11 5', mRNA sequence /clone=CBLALE11 /clone_end=5' /gb=AV737351 /gi=10854932 /ug=Hs.444989 /len=511	AV737351	Hs.444989	
8983	0.022547	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
8990	0.011093	hypothetical protein FLJ39514 (FLJ39514), mRNA /cds=(121,2040) /gb=NM_152540 /gi=22749126 /ug=Hs.48565 /len=2221	NM_152540	Hs.48565	NP_689753
9010	0.015351	602129918F1 NIH_MGC_56 cDNA clone IMAGE:4286549 5', mRNA sequence /clone=IMAGE:4286549 /clone_end=5' /gb=BF697934 /gi=11983259 /ug=Hs.162812 /len=820	BF697934	Hs.162812	
9020	0.034698	Similar to hypothetical protein FLJ31322, clone IMAGE:5296647, mRNA /gb=BC045189 /gi=28277118 /ug=Hs.350001 /len=2971	BC045189	Hs.350001	NP_787112

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9021	0.028082	EST (zs08a07.r1 NCI_CGAP_GCB1 cDNA clone IMAGE:684564 5')	AA251433		
9036	0.045456	BX115055 Soares infant brain 1NIB cDNA clone IMAGp998A16174, mRNA sequence /clone=IMAGp998A16174_ IMAGE:41580 /gb=BX115055 /gi=27839210 /ug=Hs.443738 /len=490	BX115055	Hs.443738	
9057	0.015351	glycosyltransferase (LOC83468), mRNA /cds=(408,1457) /gb=NM_031302 /gi=21314737 /ug=Hs.159993 /len=1908	NM_031302	Hs.159993	NP_112592
9061	0.03016	cDNA FLJ33960 fis, clone CTONG2018843. /gb=AK091279 /gi=21749612 /ug=Hs.126465 /len=2849	AK091279	Hs.126465	
9072	0.001683	clone MGC:20469 IMAGE:4554554, mRNA, complete cds /cds=(208,1149) /gb=BC012182 /gi=15082546 /ug=Hs.82508 /len=1862	BC012182	Hs.82508	
9087	0.026124	EST370944 MAGE resequences, MAGE cDNA, mRNA sequence /gb=AW958874 /gi=8148558 /ug=Hs.403977 /len=504	AW958874	Hs.403977	
9096	0.03016	C1q and tumor necrosis factor related protein 7 (C1QTNF7), mRNA /cds=(234,1103) /gb=NM_031911 /gi=21314748 /ug=Hs.153714 /len=3959	NM_031911	Hs.153714	NP_114117
9108	0.005512	UI-H-EI0-aye-c-17-0-UI.s1 NCI_CGAP_EI0 cDNA clone UI-H-EI0-aye-c-17-0-UI 3', mRNA sequence /clone=UI-H-EI0-aye-c-17-0-UI /clone_end=3' /gb=CA447385 /gi=24811805 /ug=Hs.420740 /len=812	CA447385	Hs.420740	
9110	0.045456	UI-E-CR1-adz-a-04-0-UI.r1 UI-E-CR1 cDNA clone UI-E-CR1-adz-a-04-0-UI 5', mRNA sequence /clone=UI-E-CR1-adz-a-04-0-UI /clone_end=5' /gb=BM706524 /gi=19019782 /ug=Hs.421063 /len=1149	BM706524	Hs.421063	
9124	0.019388	UI-H-EZ1-bbf-l-14-0-UI.s1 NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-bbf-l-14-0-UI 3', mRNA sequence /clone=UI-H-EZ1-bbf-l-14-0-UI /clone_end=3' /gb=BQ575680 /gi=21478997 /ug=Hs.257044 /len=1036	BQ575680	Hs.257044	
9138	0.022547	mRNA full length insert cDNA clone EUROIMAGE 1287006 /cds=UNKNOWN /gb=AJ420423 /gi=17066287 /ug=Hs.23703 /len=1742	AJ420423	Hs.23703	NP_003349

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigen Accession No.	Protein Accession No.
9200	0.011093	602387746F1 NIH_MGC_93 cDNA clone IMAGE:4516739 5', mRNA sequence /clone=IMAGE:4516739 /clone_end=5' /gb=BG287971 /gi=13042340 /ug=Hs.303110 /len=749	BG287971	Hs.303110	
9244	0.009373	Mus musculus mitochondrion, complete genome	NC_001569		
9253	0.007223	603390782F1 NIH_MGC_87 cDNA clone IMAGE:5399756 5', mRNA sequence /clone=IMAGE:5399756 /clone_end=5' /gb=BI860842 /gi=16001577 /ug=Hs.112472 /len=917	BI860842	Hs.112472	
9274	5.42E-04	mRNA; cDNA DKFZp586G2120 (from clone DKFZp586G2120); complete cds /cds=(19,2604) /gb=AL136924/gi=12053342 /ug=Hs.62349 /len=4137	AL136924	Hs.62349	NP_061866
9275	0.037168	ESTs, cDNA, 5' end /clone=IMAGE:3857750 /clone_end=5' /gb=BF035134 /gi=10742846 /ug=Hs.195789 /len=847	BF035134	Hs.195789	
9310	0.001683	No significant match	SEQ.ID.No.71		
9317	0.042541	No significant match, ORF+1(37~252,298~399)	SEQ.ID.No.95		
9383	0.048529	phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta) (PIK3R2), mRNA /cds=(242,2428) /gb=NM_005027 /gi=4826907 /ug=Hs.211586 /len=3201	NM_005027	Hs.211586	NP_005018
9440	0.042541	ATP citrate lyase (ACLY), mRNA /cds=(85,3402) /gb=NM_001096 /gi=4501864 /ug=Hs.174140 /len=4297	NM_001096	Hs.174140	NP_001087
9446	0.037168	hypothetical protein RP1-317E23 (LOC56181), mRNA /cds=(311,1189) /gb=NM_019557 /gi=24475811 /ug=Hs.323396 /len=2119	NM_019557	Hs.323396	NP_062457
9459	0.01205	ubiquinol-cytochrome c reductase binding protein (UQCRB), mRNA /cds=(54,389) /gb=NM_006294 /gi=20070231 /ug=Hs.131255 /len=965	NM_006294	Hs.131255	NP_006285
9461	0.005512	thioredoxin-like protein p19 (TLP19), mRNA /cds=(280,798) /gb=NM_015913 /gi=23943808 /ug=Hs.241489 /len=1616	NM_015913	Hs.241489	NP_056997
9468	0.005026	hypothetical protein MGC13159 (MGC13159), mRNA /cds=(592,1017) /gb=NM_032927 /gi=14249719 /ug=Hs.12845 /len=1759	NM_032927	Hs.12845	NP_116316

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9473	0.037168	mRNA; cDNA DKFZp564D152 (from clone DKFZp564D152); complete cds /cds=(99,1415) /gb=AL136629 /gi=12052783 /ug=Hs.278479 /len=3229	AL136629	Hs.278479	
9489	0.001216	similar to putative (H. sapiens) (LOC129641), mRNA	XM_059369		
9498	0.032363	PFTAIRe protein kinase 1 (PFTK1), mRNA /cds=(145,1500) /gb=NM_012395 /gi=6912583 /ug=Hs.57856 /len=4957	NM_012395	Hs.57856	NP_036527
9513	0.042541	hypothetical gene supported by AY007122 (LOC92719), mRNA	XM_046853		
9530	0.002302	hypothetical protein FLJ10856 (FLJ10856), mRNA /cds=(148,1233) /gb=NM_018247 /gi=8922719 /ug=Hs.108530 /len=3720	NM_018247	Hs.108530	NP_060717
9541	0.037168	alcohol dehydrogenase IB (class I), beta polypeptide (ADH1B), mRNA /cds=(71,1198) /gb=NM_000668 /gi=11496887 /ug=Hs.4 /len=2534	NM_000668	Hs.4	NP_000659
9545	0.01205	mRNA; cDNA DKFZp686C117 (from clone DKFZp686C117) /gb=AL832773 /gi=21733355 /ug=Hs.433512 /len=5984	AL832773	Hs.433512	
9595	0.013076	hypothetical protein MGC4701 (MGC4701), mRNA /cds=(149,1585) /gb=NM_024511 /gi=24308290 /ug=Hs.421054 /len=1686	NM_024511	Hs.421054	NP_078787
9596	0.003113	vimentin (VIM), mRNA /cds=(123,1523) /gb=NM_003380 /gi=4507894 /ug=Hs.297753 /len=1851	NM_003380	Hs.297753	NP_000995
9610	0.048529	nuclear DNA-binding protein (C1D), transcript variant 1, mRNA /cds=(64,489) /gb=NM_006333 /gi=27894371 /ug=Hs.15164 /len=1200	NM_006333	Hs.15164	NP_775269
9627	0.019388	hypothetical protein DKFZp564B1162 (DKFZp564B1162), mRNA /cds=(661,2628) /gb=NM_031305 /gi=13775229 /ug=Hs.93589 /len=4593	NM_031305	Hs.93589	NP_112595
9632	0.03016	clone MGC:9947 IMAGE:3876105, mRNA, complete cds /cds=(51,2216) /gb=BC013590 /gi=15488925 /ug=Hs.2437 /len=2651	BC013590	Hs.2437	
9648	0.002549	Similar to RIKEN cDNA 1500009M05 gene, clone MGC:40370 IMAGE:5105935, mRNA, complete cds /cds=(45,452) /gb=BC032300 /gi=21619026 /ug=Hs.295953 /len=1617	BC032300	Hs.295953	

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9682	0.007887	BX091044 Soares retina N2b4HR cDNA clone IMAGp998D18828 ; IMAGE:360161, mRNA sequence /clone=IMAGp998D18828 ; IMAGE:360161 /gb=BX091044 /gi=27826224 /ug=Hs.435655 /len=644	BX091044	Hs.435655	
9741	0.032363	EST UI-H-BI0p-aau-a-05-0-UI.s1 NCI_CGAP_Sub2 Human sapiens cDNA clone IMAGE:2710544 3'	AW015507		NP_037442
9758	0.022547	UI-E-DX0-agr-j-18-0-UI.s1 UI-E-DX0 cDNA clone UI-E-DX0-agr-j-18-0-UI 3', mRNA sequence /clone=UI-E-DX0-agr-j-18-0-UI /clone_end=3' /gb=BM667357 /gi=18975188 /ug=Hs.436172 /len=983	BM667357	Hs.436172	
9774	0.039781	cDNA FLJ36605 fis, clone TRACH2015316, highly similar to VIMENTIN. /cds=(631,1317) /gb=AK093924 /gi=21752883 /ug=Hs.379100 /len=2665	AK093924	Hs.379100	
9886	0.004165	mRNA; cDNA DKFZp451F1910 (from clone DKFZp451F1910) /gb=AL833265 /gi=21733898 /ug=Hs.332030 /len=5254	AL833265	Hs.332030	
9972	0.005026	caldesmon 1 (CALD1), transcript variant 1, mRNA /cds=(230,2611) /gb=NM_033138 /gi=15149460 /ug=Hs.325474 /len=3610	NM_033138	Hs.325474	NP_149347
9985	0.026124	mRNA from chromosome 5q21-22, clone:843Ex. /gb=AB002449 /gi=2943812 /ug=Hs.182723 /len=1228	AB002449	Hs.182723	
10002	0.022547	synaptotagmin-like 4 (granuphilin-a) (SYTL4), mRNA /cds=(333,2348) /gb=NM_080737 /gi=18152766 /ug=Hs.247525 /len=3914	NM_080737	Hs.247525	NP_542775
10041	0.01661	COP9 constitutive photomorphogenic subunit 4 (Arabidopsis) (COPS4), mRNA /cds=(7,1224) /gb=NM_016129 /gi=7705844 /ug=Hs.6671 /len=1613	NM_016129	Hs.6671	NP_057213
10060	0.048529	roundabout, axon guidance receptor, 1 (Drosophila) (ROBO1), transcript variant 2, mRNA /cds=(964,5802) /gb=NM_133631 /gi=19743805 /ug=Hs.301198 /len=7475	NM_133631	Hs.301198	NP_598334
10092	0.039781	hypothetical protein MGC14376 (MGC14376), mRNA /cds=(185,256) /gb=NM_032895 /gi=14249657 /ug=Hs.417157 /len=1263	NM_032895	Hs.417157	NP_116284
10146	0.042541	EST qz90a06.x1 Soares_pregnant_uterus_NbHPU cDNA clone IMAGE:2041810 3'	AI493872		NP_008878

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10151	0.003784	cDNA FLJ36605 fis, clone TRACH2015316, highly similar to VIMENTIN. /cds=(631,1317) /gb=AK093924 /gi=21752883 /ug=Hs.379100 /len=2665	AK093924	Hs.379100	
10192	0.019388	hypothetical protein clone 25242 mRNA	AF131854		
10205	0.011093	EST (ol74f05.s1 NCI_CGAP_Kid3 cDNA clone IMAGE:1535361 3')	AA919165		
10208	0.007887	cDNA FLJ33503 fis, clone BRAMY2004521. /cds=(367,750) /gb=AK090822 /gi=21749052 /ug=Hs.356719 /len=2339	AK090822	Hs.356719	NP_787089
10228	0.028082	hypothetical protein FLJ10342 (FLJ10342), mRNA /cds=(534,1145) /gb=NM_018064 /gi=14149717 /ug=Hs.101514 /len=1506	NM_018064	Hs.101514	NP_060534
10247	6.88E-04	vimentin (VIM) gene	M18895		
10277	0.037168	likely ortholog of mouse embryonic epithelial gene 1 (EEG1), mRNA /cds=(319,1794) /gb=NM_017611 /gi=18252046 /ug=Hs.274453 /len=2630	NM_017611	Hs.274453	NP_060081
10293	0.037168	BX102130 NCI_CGAP_Pr3 cDNA clone IMAGp998P072795, mRNA sequence /clone=IMAGp998P072795; IMAGE:1115766 /gb=BX102130 /gi=27831621 /ug=Hs.433046 /len=450	BX102130	Hs.433046	
10323	0.03016	mRNA; cDNA DKFZp434K1115 (from clone DKFZp434K1115); complete cds /cds=(97,2877) /gb=AL136764 /gi=12053044 /ug=Hs.42676 /len=4868	AL136764	Hs.42676	
10342	0.048529	hypothetical protein FLJ38725 (FLJ38725), mRNA /cds=(322,1614) /gb=NM_153218 /gi=23397476 /ug=Hs.210586 /len=2468	NM_153218	Hs.210586	NP_694950
10358	0.006039	cDNA, 5' end /clone=IMAGE:4148900 /clone_end=5' /gb=BF342391 /gi=11289392 /ug=Hs.30469 /len=803	BF342391	Hs.30469	NP_055313
10385	0.042541	chondroitin sulfate GalNAcT-2 (GALNACT-2), mRNA /cds=(336,1964) /gb=NM_018590 /gi=24429591 /ug=Hs.180758 /len=3745	NM_018590	Hs.180758	NP_061060
10392	0.006608	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10432	0.02428	UI-H-BW0-ajd-b-12-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2731343 3', mRNA sequence /clone=IMAGE:2731343 /clone_end=3' /gb=AW297162 /gi=6703808 /ug=Hs.438076 /len=690	AW297162	Hs.438076	
10438	0.045456	we90c07.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2348364 3', mRNA sequence /clone=IMAGE:2348364 /clone_end=3' /gb=AI797677 /gi=5363149 /ug=Hs.199882 /len=554	AI797677	Hs.199882	
10456	0.037168	mRNA; cDNA DKFZp451D112 (from clone DKFZp451D112); complete cds /cds=(316,4719) /gb=AL831962 /gi=21732493 /ug=Hs.202949 /len=5391	AL831962	Hs.202949	
10475	0.013076	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1 (SLC25A1), mRNA /cds=(100,1035) /gb=NM_005984 /gi=21389314 /ug=Hs.111024 /len=1619	NM_005984	Hs.111024	NP_005975
10485	0.013076	cDNA FLJ36429 fis, clone THYMU2011573. /gb=AK093748 /gi=21752675 /ug=Hs.378821 /len=1901	AK093748	Hs.378821	
10527	0.03016	clone MGC:26123 IMAGE:4823171, mRNA, complete cds /cds=(279,1991) /gb=BC030580 /gi=21040474 /ug=Hs.374951 /len=2464	BC030580	Hs.374951	
10531	0.042541	mRNA; cDNA DKFZp686J172 (from clone DKFZp686J172) /gb=AL832206 /gi=21732751 /ug=Hs.56896 /len=6055	AL832206	Hs.56896	
10536	0.001254	nascent-polypeptide-associated complex alpha polypeptide (NACA), mRNA /cds=(26,673) /gb=NM_005594 /gi=5031930 /ug=Hs.32916 /len=797	NM_005594	Hs.32916	NP_005585
10559	0.042541	UI-E-CL1-afg-c-18-0-UI.r1 UI-E-CL1 cDNA clone UI-E-CL1-afg-c-18-0-UI 5', mRNA sequence /clone=UI-E-CL1-afg-c-18-0-UI /clone_end=5' /gb=BM691757 /gi=19005015 /ug=Hs.11355 /len=1234	BM691757	Hs.11355	
10565	0.019388	clone IMAGE:5284350, mRNA /gb=BC037924 /gi=23138690 /ug=Hs.143061 /len=2659	BC037924	Hs.143061	
10601	0.009373	EST(cDNA clone IMAGE:3566688 3')	BF110315		NP_002154
10603	0.028082	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10612	0.048529	cDNA FLJ39382 fis, clone PERIC2000473 /gb=AK096701 /gi=21756253 /ug=Hs.293799 /len=2425	AK096701	Hs.293799	
10632	0.009373	UI-H-EI1-aze-g-21-0-UI.s1 NCI_CGAP_EI1 cDNA clone IMAGE:5847596 3', mRNA sequence /clone=IMAGE:5847596 /clone_end=3' /gb=BQ003542 /gi=19728442 /ug=Hs.190642 /len=1086	BQ003542	Hs.190642	
10779	0.026124	EST (ADB cDNA clone ADBAKA02 5')	AV704531		
10780	0.048529	hypothetical protein FLJ10300 (FLJ10300), mRNA /cds=(1710,3359) /gb=NM_018051 /gi=21361686 /ug=Hs.42233 /len=3785	NM_018051	Hs.42233	NP_060521
10788	0.028082	yg45f12.s1 Soares infant brain 1NIB cDNA clone IMAGE:35625 3', mRNA sequence /clone=IMAGE:35625 /clone_end=3' /gb=R45691 /gi=822137 /ug=Hs.268774 /len=574	R45691	Hs.268774	
10789	0.017954	cDNA FLJ14374 fis, clone HEMBA1001635, weakly similar to TESTIS SPECIFIC PROTEIN A. /cds=(185,1464) /gb=AK027280 /gi=14041858 /ug=Hs.400618 /len=1464	AK027280	Hs.400618	
10794	0.004578	FSHD region gene 1 (FRG1), mRNA /cds=(192,968) /gb=NM_004477 /gi=4758403 /ug=Hs.203772 /len=1042	NM_004477	Hs.203772	NP_004468
10853	0.001088	EST(zf89c05.r1 Soares testis NHT clone 729512 5')	AA398038		NP_004632
10862	0.006608	mitochondrion, complete genome	NC_001807		
10888	1.14E-04	UI-H-DH0-aui-j-10-0-UI.s1 NCI_CGAP_DH0 cDNA clone IMAGE:5871081 3', mRNA sequence /clone=IMAGE:5871081 /clone_end=3' /gb=BM994461 /gi=19719362 /ug=Hs.434057 /len=2059	BM994461	Hs.434057	
10906	0.034698	cDNA FLJ39740 fis, clone SMINT2016477. /gb=AK097059 /gi=21756705 /ug=Hs.432907 /len=1987	AK097059	Hs.432907	NP_444269
10972	0.042541	fetal liver cDNA library Human cDNA	AI132941		
10975	0.034698	FLJ30021 fis, clone 3NB692000973	AK054583		
10991	0.042541	ribosomal protein L12 (RPL12), mRNA /cds=(89,586) /gb=NM_000976 /gi=15431291 /ug=Hs.405042 /len=632	NM_000976	Hs.405042	NP_000967

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10996	0.010202	BX118052 Soares breast 2NbHBst cDNA clone IMAGp998C21252, mRNA sequence /clone=IMAGp998C21252_ IMAGE:158156 /gb=BX118052 /gi=27840946 /ug=Hs.32250 /len=612	BX118052	Hs.32250	
11003	0.007887	cDNA FLJ14832 fis, clone OVARC1001169. /gb=AK027738 /gi=14042638 /ug=Hs.235860 /len=2350	AK027738	Hs.235860	
11011	0.028082	EST(cDNA clone IMAGE:2686869 3')	AW197394		
11016	0.014175	mitochondrion, complete genome	NC_001807		
11026	0.022547	EST(cDNA clone IMAGE:4663252 5')	BG534476		
11032	0.037168	nj38c05.s1 NCI_CGAP_AA1 cDNA clone IMAGE:994760 3' similar to gb:M62424 THROMBIN RECEPTOR PRECURSOR mRNA sequence /clone=IMAGE:994760 /clone_end=3' /gb=AA548630 /gi=2318912 /ug=Hs.105848 /len=555	AA548630	Hs.105848	
11085	0.013076	EST(cDNA clone IMAGE:2126419 3')	AI435109		
11115	0.032363	basic transcription factor 3 (BTF3), mRNA /cds=(240,728) /gb=NM_001207 /gi=20070129 /ug=Hs.101025 /len=952	NM_001207	Hs.101025	NP_001198
11136	0.01661	clone IMAGE:3138608, mRNA /cds=UNKNOWN /gb=BC007266 /gi=13938277 /ug=Hs.334566 /len=1635	BC007266	Hs.334566	
11148	0.02428	ij23g01.x1 Melton Normalized Islet 4 N4-HIS 1 cDNA clone IMAGE:6135721 3', mRNA sequence /clone=IMAGE:6135721 /clone_end=3' /gb=BQ100789 /gi=20133773 /ug=Hs.372964 /len=568	BQ100789	Hs.372964	
11161	0.037168	ESTs, cDNA /gb=AW975851 /gi=8167072 /ug=Hs.361171 /len=684	AW975851	Hs.361171	
11167	0.037168	cDNA FLJ31063 fis, clone HSYRA2001105	AK055625		
11237	0.004165	vesicle-associated membrane protein 2 (synaptobrevin 2) (VAMP2), mRNA /cds=(95,445) /gb=NM_014232 /gi=7657674 /ug=Hs.25348 /len=2159	NM_014232	Hs.25348	NP_055047
11243	0.014175	apoA polymorphism Kringle IV gene, exons 1 and 2	L14005		
11257	0.032363	mRNA for FLJ00086 protein, partial cds. /cds=(1951,3150) /gb=AK024487 /gi=10440487 /ug=Hs.343828 /len=4456	AK024487	Hs.343828	NP_835461
11266	0.004165	B-cell translocation gene 1, anti-proliferative (BTG1), mRNA /cds=(309,824) /gb=NM_001731 /gi=4502472 /ug=Hs.77054 /len=1783	NM_001731	Hs.77054	NP_001722

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigen Accession No.	Protein Accession No.
11293	0.042541	hypothetical protein (FLJ20485), mRNA /cds=(112,729) /gb=NM_019042 /gi=9506680 /ug=Hs.98806 /len=2021	NM_019042	Hs.98806	NP_061915
11305	0.007223	tousled-like kinase 2 (TLK2), mRNA /cds=(147,2396) /gb=NM_006852 /gi=11140818 /ug=Hs.57553 /len=3327	NM_006852	Hs.57553	NP_006843
11321	0.020917	transient receptor potential cation channel, subfamily C, member 1 (TRPC1), mRNA /cds=(138,2417) /gb=NM_003304 /gi=27545448 /ug=Hs.250687 /len=4085	NM_003304	Hs.250687	NP_003295
11329	0.023405	similar to CG9578 gene product (MGC3794), mRNA /cds=(146,964) /gb=NM_152902 /gi=23097249 /ug=Hs.137576 /len=1314	NM_152902	Hs.137576	NP_690866
11332	0.026124	polyadenylate binding protein-interacting protein 1 (PAIP1), mRNA /cds=(188,1627) /gb=NM_006451 /gi=17511254 /ug=Hs.109643 /len=2764	NM_006451	Hs.109643	NP_006442
11334	0.022547	clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992	AF001542	Hs.356442	
11355	0.034698	chondroitin sulfate proteoglycan 6 (bamacan) (CSPG6), mRNA /cds=(92,3745) /gb=NM_005445 /gi=24475891 /ug=Hs.24485 /len=4096	NM_005445	Hs.24485	NP_005436
11362	0.034698	mitochondrial ribosomal protein L35 (MRPL35), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA /cds=(35,601) /gb=NM_016622 /gi=22035591 /ug=Hs.93814 /len=2805	NM_016622	Hs.93814	NP_663619
11364	0.01661	NAD(P)H dehydrogenase, quinone 1 (NQO1), mRNA /cds=(51,875) /gb=NM_000903 /gi=4505414 /ug=Hs.406515 /len=2447	NM_000903	Hs.406515	NP_000894
11365	0.027243	Rho-specific guanine-nucleotide exchange factor 164 kDa (P164RHOGF), mRNA /cds=(16,6207) /gb=NM_014786 /gi=21361457 /ug=Hs.45180 /len=7540	NM_014786	Hs.45180	NP_055601
11382	0.039781	GTP cyclohydrolase 1 (dopa-responsive dystonia) (GCH1), mRNA /cds=(149,901) /gb=NM_000161 /gi=4503948 /ug=Hs.86724 /len=2921	NM_000161	Hs.86724	NP_000152
11398	0.022547	CGI-147 protein (CGI-147), mRNA /cds=(128,667) /gb=NM_016077 /gi=7706350 /ug=Hs.12677 /len=806	NM_016077	Hs.12677	NP_057161

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	UniGene Accession No.	Protein Accession No.
11402	0.037168	cytochrome c, somatic (CYCS), mRNA /cds=(61,378) /gb=NM_018947 /gi=21361707 /ug=Hs.169248 /len=3990	NM_018947	Hs.169248	NP_061820
11446	0.006039	ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=NM_004152 /gi=9845504 /ug=Hs.281960 /len=986	NM_004152	Hs.281960	NP_004143
11454	0.01205	similar to protein tyrosine phosphatase, receptor type, E; Protein tyrosine phosphatase, receptor type, epsilon; protein tyrosine phosphatase, receptor type, epsilon polypeptide (H. sapiens) (LOC119466), mRNA	XM_005781		
11466	0.034698	chemokine (C-C motif) ligand 13 (CCL13), mRNA /cds=(76,372) /gb=NM_005408 /gi=22538799 /ug=Hs.11383 /len=861	NM_005408	Hs.11383	NP_005399
11475	0.02428	mitogen-activated protein kinase kinase kinase 8 (MAP3K8), mRNA /cds=(697,2100) /gb=NM_005204 /gi=22035597 /ug=Hs.248 /len=3096	NM_005204	Hs.248	NP_005195
11479	0.042541	B lymphocyte activation-related protein BC-2048	AAL26788		
11482	0.005026	clone IMAGE:5271722, mRNA /gb=BC038786 /gi=24270905 /ug=Hs.190456 /len=1535	BC038786	Hs.190456	
11501	0.019388	RAB34, member RAS oncogene family (RAB34), mRNA /cds=(206,985) /gb=NM_031934 /gi=21361998 /ug=Hs.301853 /len=1340	NM_031934	Hs.301853	NP_114140
11519	0.045456	mRNA; cDNA DKFZp761O0611 (from clone DKFZp761O0611) /gb=AL834155 /gi=21739631 /ug=Hs.22969 /len=4502	AL834155	Hs.22969	
11536	0.011093	EST(yh89e10.r1 cDNA clone 136938 5') 8e06 match	R38461		NP_001002
11543	0.037168	UI-H-BI1-adj-f-10-0-UI.s1 NCI_CGAP_Sub3 cDNA clone IMAGE:2716963 3', mRNA sequence /clone=IMAGE:2716963 /clone_end=3' /gb=AW137857 /gi=6142175 /ug=Hs.437502 /len=612	AW137857	Hs.437502	
11545	0.003784	UI-H-CO0-aqn-g-08-0-UI.s1 NCI_CGAP_Sub9 cDNA clone IMAGE:3104798 3', mRNA sequence /clone=IMAGE:3104798 /clone_end=3' /gb=BM987319 /gi=19706708 /ug=Hs.445870 /len=655	BM987319	Hs.445870	
11553	0.034698	EST(yv89b04.s1 clone 249871 3')	H96982		NP_775876

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hyp rtension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11596	0.019388	hypothetical protein cDNA DKFZp761K1115 (from clone DKFZp761K1115); partial cds	AL162046		NP_060717
11597	0.03016	EST HUM517A08B Clontech human placenta polyA mRNA (#6572) Human sapiens cDNA clone GEN-517A08 5'	D63277		
11608	0.009373	EST(MR0-HT0407-140300-013-h01 HT0407)	BE159552		NP_003751
11616	0.044991	EST qz49d11.x1 NCI_CGAP_Kid11 IMAGE:2030229 3'	AI493076		
11634	0.003113	hypothetical protein FLJ12118 (FLJ12118), mRNA /cds=(24,1718) /gb=NM_024537 /gi=13375694 /ug=Hs.381043 /len=1843	NM_024537	Hs.381043	NP_078813
11643	0.010441	cDNA FLJ14388 fis, clone HEMBA1002716. /gb=AK027294 /gi=14041878 /ug=Hs.9812 /len=1673	AK027294	Hs.9812	
11646	0.004578	df117a11.w1 Morton Fetal Cochlea cDNA clone IMAGE:2539676 3', mRNA sequence /clone=IMAGE:2539676 /clone_end=3' /gb=BI495331 /gi=15334675 /ug=Hs.347861 /len=405	BI495331	Hs.347861	
11650	0.010202	EST IL3-CT0214-040400-108-C01 CT0214 H.sapiens cDNA	AW849070		
11691	2.24E-04	cDNA sequence cDNA sequence DKFZp434D0935 (from clone cDNA sequence DKFZp434D0935)	AL117502		NP_149107
11692	0.007887	KIAA0874 protein (KIAA0874), mRNA /cds=(1,6189) /gb=NM_015208 /gi=14140237 /ug=Hs.27973 /len=6189	NM_015208	Hs.27973	NP_056023
11706	0.034698	KIAA1887 protein (KIAA1887), mRNA /cds=(259,3270) /gb=NM_052897 /gi=24308373 /ug=Hs.348428 /len=3592	NM_052897	Hs.348428	NP_443129
11710	0.039781	translocase of outer mitochondrial membrane 20 (yeast) (KIAA0016), mRNA /cds=(102,539) /gb=NM_014765 /gi=7657256 /ug=Hs.75187 /len=3259	NM_014765	Hs.75187	NP_055580
11721	0.042541	Wolf-Hirschhorn syndrome candidate 1 (WHSC1), transcript variant 4, mRNA /cds=(495,2903) /gb=NM_014919 /gi=19913345 /ug=Hs.110457 /len=8458	NM_014919	Hs.110457	NP_579891
11724	0.037168	chromosome 14 open reading frame 2 (C14orf2), mRNA /cds=(61,237) /gb=NM_004894 /gi=4758939 /ug=Hs.109052 /len=627	NM_004894	Hs.109052	NP_004885
11732	0.007223	hypothetical protein FLJ20699 (FLJ20699), mRNA /cds=(33,1043) /gb=NM_017931 /gi=8923627 /ug=Hs.15125 /len=2594	NM_017931	Hs.15125	NP_060401

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11742	0.048529	prolactin regulatory element binding (PREB), mRNA /cds=(132,1385) /gb=NM_013388 /gi=7019502 /ug=Hs.279784 /len=2059	NM_013388	Hs.279784	NP_037520
11765	0.03016	ribosomal protein L12 (RPL12), mRNA /cds=(89,586) /gb=NM_000976 /gi=15431291 /ug=Hs.405042 /len=632	NM_000976	Hs.405042	NP_000967
11775	0.01661	UI-E-CQ1-acq-f-05-0-UI.r1 UI-E-CQ1 cDNA clone UI-E-CQ1-acq-f-05-0-UI 5', mRNA sequence /clone=UI-E-CQ1-acq-f-05-0-UI /clone_end=5' /gb=BM688680 /gi=19001938 /ug=Hs.406520 /len=934	BM688680	Hs.406520	
11781	0.01661	serum/glucocorticoid regulated kinase-like (SGKL), transcript variant 1, mRNA /cds=(416,1705) /gb=NM_013257 /gi=25168264 /ug=Hs.380877 /len=4155	NM_013257	Hs.380877	NP_733827
11783	0.011093	cDNA FLJ20709 fis, clone KAIA1124, highly similar to D86324 mRNA for CMP-N-acetylneuraminic acid. /gb=AK000716 /gi=7020978 /ug=Hs.24697 /len=3488	AK000716	Hs.24697	
11784	0.001683	sperm associated antigen 9 (SPAG9), transcript variant 1, mRNA /cds=(79,4002) /gb=NM_003971 /gi=27436919 /ug=Hs.129872 /len=4663	NM_003971	Hs.129872	NP_758853
11788	0.032363	Bardet-Biedl syndrome 2 (BBS2), mRNA /cds=(422,2587) /gb=NM_031885 /gi=22208996 /ug=Hs.332633 /len=2978	NM_031885	Hs.332633	NP_114091
11805	0.03016	tryptophanyl-tRNA synthetase (WARS), mRNA /cds=(188,1603) /gb=NM_004184 /gi=7710155 /ug=Hs.82030 /len=2693	NM_004184	Hs.82030	NP_004175
11811	2.91E-04	FLJ11481 fis, clone HEMBA1001803 /cds=UNKNOWN /gb=AK021543 /gi=10432744 /ug=Hs.135159 /len=1539	AK021543	Hs.135159	
11816	0.020917	likely ortholog of rat V-1 protein (V-1), mRNA /cds=(229,585) /gb=NM_145808 /gi=21956644 /ug=Hs.21321 /len=3770	NM_145808	Hs.21321	NP_665807
11822	0.037168	protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C), mRNA /cds=(89,1633) /gb=NM_002719 /gi=4506022 /ug=Hs.171734 /len=4064	NM_002719	Hs.171734	NP_848703
11830	0.014175	DKFZp564P2064_s1 564 (synonym: hfbr2) cDNA clone DKFZp564P2064 3', mRNA sequence /clone=DKFZp564P2064 /clone_end=3' /gb=AL037172 /gi=5406623 /ug=Hs.328612 /len=682	AL037172	Hs.328612	
11851	0.037168	mitochondrion, complete genome	NC_001807		

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11897	0.007887	hypothetical protein FLJ20701 (FLJ20701), mRNA /cds=(39,938) /gb=NM_017933 /gi=8923631 /ug=Hs.424598 /len=2284	NM_017933	Hs.424598	NP_060403
11927	0.009373	CCR4-NOT transcription complex, subunit 8 (CNOT8), mRNA /cds=(245,1123) /gb=NM_004779 /gi=24496777 /ug=Hs.26703 /len=2489	NM_004779	Hs.26703	NP_004770
11958	0.03016	mRNA; cDNA DKFZp686D143 (from clone DKFZp686D143) /gb=AL833539 /gi=21734184 /ug=Hs.56340 /len=8318	AL833539	Hs.56340	
11967	0.034698	TNF receptor-associated factor 5 (TRAF5), transcript variant 1, mRNA /cds=(194,1867) /gb=NM_004619 /gi=22027625 /ug=Hs.29736 /len=4132	NM_004619	Hs.29736	NP_665702
12041	0.034698	kelch-like protein C3IP1 (C3IP1), mRNA /cds=(201,1907) /gb=NM_021633 /gi=21361889 /ug=Hs.3826 /len=3338	NM_021633	Hs.3826	NP_067646
12066	0.037168	chromosome 1 open reading frame 19 (C1orf19), mRNA /cds=(51,566) /gb=NM_052965 /gi=24308389 /ug=Hs.32058 /len=1943	NM_052965	Hs.32058	NP_443197
12072	0.015351	EST(ta04f03.x1 Soares_pregnant_uterus_NbHPU clone IMAGE:2043101 3')	AI580773		
12080	0.019388	AGENCOURT_8899857 NIH_MGC_142 cDNA clone IMAGE:6451082 5', mRNA sequence /clone=IMAGE:6451082 /clone_end=5' /gb=BU595281 /gi=23247040 /ug=Hs.5250 /len=1163	BU595281	Hs.5250	
12083	0.044991	EST on95c11.s1 Soares_NFL_T_GBC_S1 IMAGE:1564436 3'	AA934121		NP_057174
12085	0.008602	retinoic acid induced 14 (RAI14), mRNA /cds=(112,3054) /gb=NM_015577 /gi=13470085 /ug=Hs.15165 /len=4925	NM_015577	Hs.15165	NP_056392
12117	0.045456	EST(tj90g04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone	AI470101		
12123	0.028082	UI-H-BI0-aaa-f-10-0-UI.s1 NCI_CGAP_Sub1 cDNA clone IMAGE:2708874 3', mRNA sequence /clone=IMAGE:2708874 /clone_end=3' /gb=AW014102 /gi=5862859 /ug=Hs.304671 /len=654	AW014102	Hs.304671	
12200	0.026124	hypothetical protein FLJ10159 (FLJ10159), mRNA /cds=(1,807) /gb=NM_018013 /gi=8922262 /ug=Hs.22505 /len=2070	NM_018013	Hs.22505	NP_060483

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12210	0.026124	cDNA FLJ38039 fis, clone CTONG2013934. /gb=AK095358 /gi=21754600 /ug=Hs.46506 /len=2956	AK095358	Hs.46506	
12222	0.007887	GRB2-associated binding protein 3 (GAB3), mRNA /cds=(33,1793) /gb=NM_080612 /gi=18079322 /ug=Hs.102630 /len=4731	NM_080612	Hs.102630	NP_542179
12252	0.045456	UI-E-CL1-afb-k-21-0-UI.s1 UI-E-CL1.cDNA clone UI-E-CL1-afb-k-21-0-UI 3', mRNA sequence /clone=UI-E-CL1-afb-k-21-0-UI /clone_end=3' /gb=BM665519 /gi=18972482 /ug=Hs.159501 /len=1100	BM665519	Hs.159501	
12257	0.01661	EST390958 MAGE resequences, MAGP cDNA, mRNA sequence /gb=AW978849 /gi=8170126 /ug=Hs.124977 /len=678	AW978849	Hs.124977	
12271	0.048529	EST(ne86c04.s1 NCI_CGAP_Kid1 clone IMAGE:911142 contains L1.t1 L1 repeat)	AA480776		
12310	0.007887	602644358F1 NIH_MGC_61 cDNA clone IMAGE:4775006 5', mRNA sequence /clone=IMAGE:4775006 /clone_end=5' /gb=BG615069 /gi=13666440 /ug=Hs.190422 /len=770	BG615069	Hs.190422	
12313	0.02428	EST ya88e03.r1 Stratagene placenta(#937225) cDNA clone IMAGE:68764 5'	T53373		
12320	0.037168	EST(EST178403 Colon carcinoma (HCC) cell line cDNA 5' end similar to similar to ribosomal protein L30)	AA307521		NP_000980
12346	0.005512	selenoprotein H (SEIH), mRNA /cds=(243,611) /gb=NM_170746 /gi=25014108 /ug=Hs.290874 /len=834	NM_170746	Hs.290874	NP_734467
12399	0.017954	UI-E-CK1-afb-b-14-0-UI.r1 UI-E-CK1 cDNA clone UI-E-CK1-afb-b-14-0-UI 5', mRNA sequence /clone=UI-E-CK1-afb-b-14-0-UI /clone_end=5' /gb=BM702699 /gi=19015957 /ug=Hs.446508 /len=1088	BM702699	Hs.446508	
12403	0.042541	mRNA; cDNA DKFZp564D2071 (from clone DKFZp564D2071) /gb=AL110232 /gi=5817171 /ug=Hs.279243 /len=1077	AL110232	Hs.279243	
12412	0.001357	cDNA / IL3-NT0294-060401-533-D04 NT0294	BI041924		
12440	0.048529	clone IMAGE:5286019, mRNA /gb=BC042960 /gi=27693187 /ug=Hs.5724 /len=3174	BC042960	Hs.5724	
12465	0.006039	ESTs, cDNA, 5' end /clone=IMAGE:3922401 /clone_end=5' /gb=BE894201 /gi=10356330 /ug=Hs.176376 /len=916	BE894201	Hs.176376	

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12470	0.034698	cDNA: FLJ22930 fis, clone KAT07255. /gb=AK026583 /gi=10439467 /ug=Hs.90790 /len=1600	AK026583	Hs.90790	
12500	0.039781	EST(cDNA clone IMAGE:2974964 3')	AW628675		NP_006274
12501	0.032363	EST(cDNA clone IMAGE:4693130 5')	BG539987		NP_005397
12510	0.011093	hypothetical protein DKFZp564F013 (DKFZP564F013), mRNA /cds=(107,2194) /gb=NM_020432 /gi=24308192 /ug=Hs.128653 /len=4572	NM_020432	Hs.128653	NP_065165
12571	0.009373	EST, clone IMAGE:4127796, mRNA	BC007799		NP_443107
12574	0.002077	UI-H-ED0-awx-b-15-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5824814 3', mRNA sequence /clone=IMAGE:5824814 /clone_end=3' /gb=BQ020068 /gi=19755345 /ug=Hs.396278 /len=1351	BQ020068	Hs.396278	
12580	0.009373	No significant match	SEQ.ID.No.34		
12604	2.91E-04	EST(IL3-HT0618-120500-138-D11 HT0618 cDNA, MRNA sequence)	BE179957		
12608	0.034698	mRNA; cDNA DKFZp586L081 (from clone DKFZp586L081) /gb=AL080234 /gi=5262727 /ug=Hs.432862 /len=2159	AL080234	Hs.432862	
12609	0.019388	Similar to hypothetical protein FLJ31322, clone IMAGE:5296647, mRNA /gb=BC045189 /gi=28277118 /ug=Hs.350001 /len=2971	BC045189	Hs.350001	NP_787112
12626	0.032363	Novel	SEQ.ID.No.85		
12676	0.034698	UI-E-EJ0-aij-i-12-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-aij-i-12-0-UI 5', mRNA sequence /clone=UI-E-EJ0-aij-i-12-0-UI /clone_end=5' /gb=BM726397 /gi=19047730 /ug=Hs.232059 /len=973	BM726397	Hs.232059	
12688	0.039781	myxoid liposarcoma associated protein 4 (MLAT4), mRNA /cds=(199,2325) /gb=NM_018192 /gi=27764881 /ug=Hs.42824 /len=3396	NM_018192	Hs.42824	NP_060662
12689	0.045456	hypothetical protein MGC3077 (MGC3077), mRNA /cds=(137,703) /gb=NM_024051 /gi=13129017 /ug=Hs.433404 /len=1195	NM_024051	Hs.433404	NP_076956
12696	0.026124	cDNA, 3' end /clone=IMAGE:2369618 /clone_end=3' /gb=AI819052 /gi=5438216 /ug=Hs.50918 /len=540	AI819052	Hs.50918	
12705	0.032363	hypothetical protein FLJ31121 (FLJ31121), mRNA /cds=(15,614) /gb=NM_144723 /gi=21389510 /ug=Hs.350194 /len=1512	NM_144723	Hs.350194	NP_653324

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12708	0.042541	nz86f07.s1 NCI_CGAP_GCB1 cDNA clone IMAGE:1302373 3', mRNA sequence /clone=IMAGE:1302373 /clone_end=3' /gb=AA731386 /gi=2753542 /ug=Hs.120251 /len=295	AA731386	Hs.120251	
12715	0.026124	cDNA FLJ31753 fis, clone NT2RI2007468. /gb=AK056315 /gi=16551681 /ug=Hs.349283 /len=2361	AK056315	Hs.349283	
12720	0.034698	mRNA; cDNA DKFZp667O1616 (from clone DKFZp667O1616) /gb=AL713722 /gi=19584452 /ug=Hs.365655 /len=1773	AL713722	Hs.365655	
12725	1.31E-04	EST(CM3-BN0151-130400-146-f01_1 BN0151)	BE008220		
12726	0.03016	aldehyde dehydrogenase 6 family, member A1 (ALDH6A1), nuclear gene encoding mitochondrial protein, mRNA /cds=(100,1707) /gb=NM_005589 /gi=25777737 /ug=Hs.293970 /len=2183	NM_005589	Hs.293970	NP_005580
12743	0.013076	EST (RC3-BN0036-090200-011-h11 BN0036 cDNA)	AW994082		
12762	0.034698	wd19h11.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2328645 3', mRNA sequence /clone=IMAGE:2328645 /clone_end=3' /gb=AI674745 /gi=4875225 /ug=Hs.377373 /len=347	AI674745	Hs.377373	
12765	0.042541	EST (RC5-BT0663-050400-012-H04 BT0663 cDNA)	BE085097		
12776	0.01205	EST(cDNA clone IMAGE:4780057 5')	BG743394		NP_004087
12778	0.005512	cDNA FLJ33834 fis, clone CTONG2004264, moderately similar to NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK. /cds=(6,2381) /gb=AK091153 /gi=21749455 /ug=Hs.378738 /len=2712	AK091153	Hs.378738	
12797	0.034698	EST(xu17f02.x1 NCI_CGAP_Co14 cDNA clone IMAGE:2800443 3')	AW272306		NP_002201
12798	0.008602	UI-H-DF0-bem-a-10-0-UI.s1 NCI_CGAP_DF0 cDNA clone UI-H-DF0-bem-a-10-0-UI 3', mRNA sequence /clone=UI-H-DF0-bem-a-10-0-UI /clone_end=3' /gb=CA425521 /gi=24788247 /ug=Hs.411829 /len=1131	CA425521	Hs.411829	
12811	0.048529	EST(UI-CF-EC1-aec-j-17-0-UI.s1 UI-CF-EC1 cDNA clone UI-CF-EC1-aec-j-17-0-UI 3')	BM977996		
12843	0.028082	cDNA clone IMAGE:123789 3' similar to contains Alu repetitive element; contains THR repetitive element ; Soares fetal liver spleen 1NFLS	R01434		

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	D scription	Gene Accession No.	Unigene Acc ssion No.	Protein Accession No.
12847	0.019388	EST(cDNA clone IMAGE:4472298 5')	BG251774		NP_598001
12848	0.014175	cDNA: FLJ23165 fis, clone LNG09846. /gb=AK026818 /gi=10439763 /ug=Hs.279898 /len=2117	AK026818	Hs.279898	
12851	0.009373	FLJ11311 fis, clone PLACE1010102/cds=UNKNOWN /gb=AK002173 /gi=7023889 /ug=Hs.5518 /len=1839	AK002173	Hs.5518	NP_689971
12871	0.034698	wg97c03.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2379172 3' similar to contains L1.b1 L1 repetitive element ;, mRNA sequence /clone=IMAGE:2379172 /clone_end=3' /gb=AI762342 /gi=5178009 /ug=Hs.304298 /len=531	AI762342	Hs.304298	
12878	0.039781	cDNA PSEC0152 fis, clone PLACE1007885. /cds=(20,1144) /gb=AK075459 /gi=22761560 /ug=Hs.350475 /len=2130	AK075459	Hs.350475	
12892	8.68E-04	ESTs, cDNA, 5' end /clone=IMAGE:1554245 /clone_end=5' /gb=AI792925 /gi=5340641 /ug=Hs.137097 /len=585	AI792925	Hs.137097	
12905	0.031589	UI-H-BI3-ako-d-10-0-UI.s1 NCI_CGAP_Sub5 cDNA clone IMAGE:2734914 3', mRNA sequence /clone=IMAGE:2734914 /clone_end=3' /gb=AW450461 /gi=6991237 /ug=Hs.440730 /len=755	AW450461	Hs.440730	
13007	0.014175	EST(cDNA clone GKCAHD03 5')	AV696986		NP_072179
13042	0.010202	EST(cDNA clone IMAGE:4717063 5')	BG569807		
13065	0.045456	control			
13079	0.03649	DKFZp686H0168_r1 686 (synonym: hlcc3) cDNA clone DKFZp686H0168 5', mRNA sequence /clone=DKFZp686H0168 /clone_end=5' /gb=AL710266 /gi=19693621 /ug=Hs.123224 /len=839	AL710266	Hs.123224	
13109	0.026124	cDNA FLJ13752 fis, clone PLACE3000352. /gb=AK023814 /gi=10435863 /ug=Hs.144871 /len=3904	AK023814	Hs.144871	
13110	7.74E-04	hypothetical protein P1 p373c6 (P1P373C6), mRNA /cds=(254,1891) /gb=NM_019110 /gi=17738284 /ug=Hs.44720 /len=2316	NM_019110	Hs.44720	NP_061983
13134	0.007887	sine oculis homeobox 2 (Drosophila) (SIX2), mRNA /cds=(283,1158) /gb=NM_016932 /gi=21314676 /ug=Hs.101937 /len=2141	NM_016932	Hs.101937	NP_058628

Genes Corresponding To Differentially Expressed Genes in Figur 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigen Accession No.	Protein Accession No.
13139	0.002077	chromosome 1 open reading frame 8 (C1orf8), mRNA /cds=(251,1222) /gb=NM_004872 /gi=27545320 /ug=Hs.416495 /len=1709	NM_004872	Hs.416495	NP_004863
13151	0.034698	cell division cycle associated 4 (CDCA4), transcript variant 1, mRNA /cds=(164,889) /gb=NM_017955 /gi=22027508 /ug=Hs.34045 /len=2171	NM_017955	Hs.34045	NP_663747
13152	0.003435	cDNA FLJ13545 fis, clone PLACE1006867. /gb=AK023607 /gi=10435587 /ug=Hs.421529 /len=1887	AK023607	Hs.421529	
13159	0.034698	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial (ECHS1), nuclear gene encoding mitochondrial protein, mRNA /cds=(72,944) /gb=NM_004092 /gi=12707569 /ug=Hs.76394 /len=1326	NM_004092	Hs.76394	NP_004083
13180	0.005512	F-box only protein 7 (FBXO7), mRNA /cds=(281,1849) /gb=NM_012179 /gi=15812192 /ug=Hs.5912 /len=2165	NM_012179	Hs.5912	NP_036311
13182	0.037168	mRNA for KIAA1564 protein, partial cds. /cds=(1,6016) /gb=AB046784 /gi=20521943 /ug=Hs.173421 /len=6143	AB046784	Hs.173421	
13184	0.017954	KIAA1903 protein, partial cds /cds=UNKNOWN /gb=AB067490 /gi=15620864 /ug=Hs.89278 /len=4382	AB067490	Hs.89278	NP_060823
13188	2.14E-05	hypothetical protein PRO2013 (PRO2013), mRNA /cds=(136,381) /gb=NM_021243 /gi=24308272 /ug=Hs.238205 /len=876	NM_021243	Hs.238205	
13190	0.020917	membrane-spanning 4-domains, subfamily A, member 6A (MS4A6A), transcript variant 1, mRNA /cds=(239,985) /gb=NM_152852 /gi=23238237 /ug=Hs.17914 /len=1564	NM_152852	Hs.17914	NP_690591
13199	0.02428	HSKM-B protein (HSKM-B), mRNA /cds=(23,1324) /gb=NM_020197 /gi=9910273 /ug=Hs.66170 /len=1694	NM_020197	Hs.66170	NP_064582
13200	0.017954	FLJ12726 fis, clone NT2RP2000001, highly similar to Human mRNA for KIAA1111 protein	AK022788		
13206	0.009373	spinal cord-derived growth factor-B (SCDGF-B), transcript variant 1, mRNA /cds=(176,1288) /gb=NM_025208 /gi=15451919 /ug=Hs.112885 /len=3808	NM_025208	Hs.112885	NP_149126
13207	0.006039	ARP8 actin-related protein 8 (yeast) (ACTR8), mRNA /cds=(5,1129) /gb=NM_022899 /gi=12597636 /ug=Hs.124219 /len=2797	NM_022899	Hs.124219	NP_075050

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13210	0.034698	hypothetical protein FLJ13188 (FLJ13188), mRNA /cds=(247,948) /gb=NM_022063 /gi=11545770 /ug=Hs.11859 /len=2746	NM_022063	Hs.11859	NP_071346
13212	0.01661	hypothetical protein FLJ20060 (FLJ20060), mRNA /cds=(72,2078) /gb=NM_017645 /gi=24431978 /ug=Hs.54617 /len=2884	NM_017645	Hs.54617	NP_060115
13222	0.039781	yf95a11.s1 Soares infant brain 1NIB cDNA clone IMAGE:30037 3', mRNA sequence /clone=IMAGE:30037 /clone_end=3' /gb=R41424 /gi=816727 /ug=Hs.387904 /len=396	R41424	Hs.387904	
13227	0.028082	cysteine dioxygenase, type I (CDO1), mRNA /cds=(255,857) /gb=NM_001801 /gi=4502754 /ug=Hs.3229 /len=1556	NM_001801	Hs.3229	NP_001792
13233	0.002453	synovial sarcoma translocation gene on chromosome 18-like 2 (SS18L2), mRNA /cds=(99,332) /gb=NM_016305 /gi=10047103 /ug=Hs.9774 /len=817	NM_016305	Hs.9774	NP_057389
13291	0.014175	actin related protein 2/3 complex, subunit 5, 16kDa (ARPC5), mRNA /cds=(192,647) /gb=NM_005717 /gi=23238212 /ug=Hs.82425 /len=2000	NM_005717	Hs.82425	NP_005708
13304	0.010202	wl27d01.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2426113 3', mRNA sequence /clone=IMAGE:2426113 /clone_end=3' /gb=AI866216 /gi=5530323 /ug=Hs.413738 /len=133	AI866216	Hs.413738	
13305	0.03016	apoptosis inhibitor 5 (API5), mRNA /cds=(133,1647) /gb=NM_006595 /gi=5729729 /ug=Hs.227913 /len=3739	NM_006595	Hs.227913	NP_006586
13309	0.014175	nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA /cds=(217,3171) /gb=NM_000901 /gi=4505198 /ug=Hs.1790 /len=5749	NM_000901	Hs.1790	NP_000892
13316	0.039781	ring finger protein 19 (RNF19), mRNA /cds=(318,2834) /gb=NM_015435 /gi=19923421 /ug=Hs.48320 /len=4357	NM_015435	Hs.48320	NP_056250
13319	0.007887	cDNA FLJ33540 fis, clone BRAMY2007613. /gb=AK090859 /gi=21749098 /ug=Hs.21213 /len=2030	AK090859	Hs.21213	
13330	0.008602	bridging integrator 2 (BIN2), mRNA /cds=(39,1736) /gb=NM_016293 /gi=7706486 /ug=Hs.14770 /len=2206	NM_016293	Hs.14770	NP_057377
13335	0.004165	hypothetical protein FLJ12118 (FLJ12118), mRNA /cds=(24,1718) /gb=NM_024537 /gi=13375694 /ug=Hs.381043 /len=1843	NM_024537	Hs.381043	NP_078813

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13339	0.022547	mRNA for KIAA1133 protein, partial cds. /cds=(1,2676) /gb=AB051436 /gi=13195720 /ug=Hs.318584 /len=6542	AB051436	Hs.318584	
13388	0.014175	fos-related antigen DNA, exon 4	X98050		
13391	0.045456	chondroitin sulfate GalNAcT-2 (GALNACT-2), mRNA /cds=(336,1964) /gb=NM_018590 /gi=24429591 /ug=Hs.180758 /len=3745	NM_018590	Hs.180758	NP_061060
13425	0.02428	EST(wk79e07.x1 NCI_CGAP_Pan1 clone IMAGE:2421636 3')	AI813780		
13457	0.045456	translin (TSN), mRNA /cds=(236,922) /gb=NM_004622 /gi=20302160 /ug=Hs.75066 /len=3408	NM_004622	Hs.75066	NP_004613
13459	0.005026	N-ethylmaleimide-sensitive factor (NSF), mRNA /cds=(61,2295) /gb=NM_006178 /gi=11079227 /ug=Hs.108802 /len=3960	NM_006178	Hs.108802	NP_006169
13467	0.006047	EST(zf04d06.r1 NCI_CGAP_GCB1 clone IMAGE:712139 5')	AA280235		NP_005728
13469	0.02428	clone IMAGE:5299642, mRNA /gb=BC041913 /gi=27469540 /ug=Hs.17132 /len=2227	BC041913	Hs.17132	
13507	0.020917	ho25d05.x1 NCI_CGAP_Co14 cDNA clone IMAGE:3038409 3', mRNA sequence /clone=IMAGE:3038409 /clone_end=3' /gb=BE042545 /gi=8359683 /ug=Hs.276275 /len=448	BE042545	Hs.276275	
13520	0.005026	EST(tz32c11.x1 NCI_CGAP_Ut2 clone IMAGE:2290292 3')	AI631079		NP_079436
13523	0.02428	UI-H-DIO-auw-o-12-0-UI.s1 NCI_CGAP_DIO cDNA clone IMAGE:5875427 3', mRNA sequence /clone=IMAGE:5875427 /clone_end=3' /gb=BM997944 /gi=19722845 /ug=Hs.444026 /len=753	BM997944	Hs.444026	
13577	0.019388	DKFZP586L2024 protein (NESHBP), mRNA /cds=(364,1824) /gb=NM_015429 /gi=14149685 /ug=Hs.58419 /len=3023	NM_015429	Hs.58419	NP_056244
13599	0.03016	mRNA; cDNA DKFZp313E1012 (from clone DKFZp313E1012) /gb=AL832661 /gi=21733237 /ug=Hs.94694 /len=3233	AL832661	Hs.94694	
13601	0.002549	similar to rat myomegalin (LOC64182), mRNA /cds=(336,1268) /gb=NM_022359 /gi=21314705 /ug=Hs.333512 /len=1717	NM_022359	Hs.333512	NP_071754
13602	4.81E-04	UI-1-BC1p-asi-a-02-0-UI.s1 NCI_CGAP_PI3 cDNA clone UI-1-BC1p-asi-a-02-0-UI 3', mRNA sequence /clone=UI-1-BC1p-asi-a-02-0-UI /clone_end=3' /gb=BQ011545 /gi=19736446 /ug=Hs.361171 /len=1143	BQ011545	Hs.361171	

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13619	0.045456	FLJ30633 fis, clone CTONG2002418, weakly similar to Homo sapiens scaffold attachment factor B (SAF-B) mRNA (AK055195.1)	AK055195	Hs.331328	NP_079031
13642	0.045456	calpastatin (CAST), transcript variant 2, mRNA /cds=(155,2215) /gb=NM_173060 /gi=27765084 /ug=Hs.359682 /len=4296	NM_173060	Hs.359682	NP_775085
13670	0.009373	hypothetical protein FLJ11506 (FLJ11506), mRNA /cds=(16,963) /gb=NM_024666 /gi=20070334 /ug=Hs.77703 /len=2774	NM_024666	Hs.77703	NP_078942
13702	0.02428	mRNA for KIAA0551 protein, partial cds. /cds=(192,4349) /gb=AB011123 /gi=20521082 /ug=Hs.170204 /len=5727	AB011123	Hs.170204	
13713	0.022547	heterogeneous nuclear ribonucleoprotein H2 (H') (HNRPH2), mRNA /cds=(79,1428) /gb=NM_019597 /gi=14141155 /ug=Hs.278857 /len=2220	NM_019597	Hs.278857	NP_062543
13716	0.03016	chromosome 15 open reading frame 12 (C15orf12), nuclear gene encoding mitochondrial protein, mRNA /cds=(48,602) /gb=NM_018285 /gi=8922793 /ug=Hs.6118 /len=1115	NM_018285	Hs.6118	NP_060755
13747	0.022547	hypothetical protein MGC23401 (MGC23401), mRNA /cds=(258,1334) /gb=NM_144982 /gi=21450672 /ug=Hs.245383 /len=1510	NM_144982	Hs.245383	NP_659419
13750	0.022547	heterogeneous nuclear ribonucleoprotein D like (HNRPDL), transcript variant 1, mRNA /cds=(581,1843) /gb=NM_005463 /gi=14110410 /ug=Hs.372673 /len=3514	NM_005463	Hs.372673	NP_112740
13751	0.037168	hypothetical protein MGC17330 (MGC17330), mRNA /cds=(148,939) /gb=NM_052880 /gi=16418388 /ug=Hs.26670 /len=2427	NM_052880	Hs.26670	NP_443112
13755	0.039781	cyclin H (CCNH), mRNA /cds=(233,1204) /gb=NM_001239 /gi=17738313 /ug=Hs.514 /len=1398	NM_001239	Hs.514	NP_001230
13768	0.018499	likely ortholog of mouse hypoxia induced gene 1 (HIG1), mRNA /cds=(93,374) /gb=NM_014056 /gi=7661619 /ug=Hs.7917 /len=1362	NM_014056	Hs.7917	NP_054775
13786	0.019388	mitochondrion, complete genome	NC_001807		
13797	0.02428	603041572T1 NIH_MGC_116 cDNA clone IMAGE:5163112 3', mRNA sequence /clone=IMAGE:5163112 /clone_end=3' /gb=BI517954 /gi=15342746 /ug=Hs.398211 /len=964	BI517954	Hs.398211	

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	D scription	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13807	0.026124	solute carrier family 16 (monocarboxylic acid transporters), member 1 (SLC16A1), mRNA /cds=(194,1696) /gb=NM_003051 /gi=19923752 /ug=Hs.75231 /len=3410	NM_003051	Hs.75231	NP_003042
13826	0.032363	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12 (CLECSF12), mRNA /cds=(72,677) /gb=NM_022570 /gi=13384603 /ug=Hs.161786 /len=2354	NM_022570	Hs.161786	NP_072092
13835	0.006608	mRNA for KIAA1078 protein, partial cds. /cds=(1,4098) /gb=AB029001 /gi=20521755 /ug=Hs.23585 /len=6740	AB029001	Hs.23585	
13839	0.02428	TEA domain family member 1 (SV40 transcriptional enhancer factor) mRNA; cDNA DKFZp434N1435 (from clone DKFZp434N1435) /cds=UNKNOWN /gb=AL133574 /gi=6599153 /ug=Hs.42458 /len=4459	AL133574	Hs.42458	NP_068780
13844	0.01661	zinc finger protein 11b (KOX 2) (ZNF11B), mRNA /cds=(116,2452) /gb=NM_006955 /gi=24307874 /ug=Hs.378077 /len=5958	NM_006955	Hs.378077	NP_008886
13856	0.010202	myeloid differentiation primary response gene (88) (MYD88), mRNA /cds=(40,930) /gb=NM_002468 /gi=19923143 /ug=Hs.82116 /len=2678	NM_002468	Hs.82116	NP_002459
13927	0.029098	df22c07.w1 Morton Fetal Cochlea cDNA clone IMAGE:2484085 3', mRNA sequence /clone=IMAGE:2484085 /clone_end=3' /gb=BI492292 /gi=15331636 /ug=Hs.379172 /len=359	BI492292	Hs.379172	
13932	0.041995	EST(zr99b03.r1 NCI_CGAP_GCB1 clone IMAGE:683789 5')	AA236732		NP_690869
13935	0.01205	CD68 antigen (CD68), mRNA /cds=(16,1080) /gb=NM_001251 /gi=4557434 /ug=Hs.246381 /len=1722	NM_001251	Hs.246381	NP_001242
13950	0.048529	hypothetical protein FLJ10330 (FLJ10330), mRNA /cds=(77,1717) /gb=NM_018061 /gi=8922357 /ug=Hs.342307 /len=3239	NM_018061	Hs.342307	NP_060531
13961	0.03016	Novel	SEQ.ID.No.90		
13972	0.017954	zo15e02.s1 Stratagene colon (#937204) cDNA clone IMAGE:586970 3' similar to contains Alu repetitive element;contains element PTR5 repetitive element ;, mRNA sequence /clone=IMAGE:586970 /clone_end=3' /gb=AA130992 /gi=1692483 /ug=Hs.426360 /len=489	AA130992	Hs.426360	

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unique Accession No.	Protein Accession No.
13986	0.039781	phosphodiesterase 6D, cGMP-specific, rod, delta (PDE6D), mRNA /cds=(151,603) /gb=NM_002601 /gi=4505670 /ug=Hs.48291 /len=1131	NM_002601	Hs.48291	NP_002592
14085	0.02428	EST (np87f03.s1 NCI_CGAP_Thy1 IMAGE:1133309)	AA632677		
14092	0.026124	hypothetical protein DKFZp434K1421 (DKFZP434K1421), mRNA /cds=(29,1705) /gb=NM_032141 /gi=14149806 /ug=Hs.374609 /len=2547	NM_032141	Hs.374609	NP_115517
14094	0.028082	EST (wh67d04.x1 NCI_CGAP_Kid11 IMAGE:2385799 3')	AI766049		
14132	0.010202	EST (ie64h03.x1 Homo sapiens cDNA, 3' end/clone_end=3' /gb=BI963813 /gi=16338218 /ug=Hs.349015/len=555)	BI963813	Hs.349015	NP_116159
14175	0.013076	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994
14209	0.034698	BX109160 Soares_NhHMPu_S1 cDNA clone IMAGp998H024744, mRNA sequence /clone=IMAGp998H024744, IMAGE:1933489 /gb=BX109160 /gi=27877586 /ug=Hs.308982 /len=483	BX109160	Hs.308982	
14243	0.007223	cDNA FLJ36574 fis, clone TRACH2012376. /gb=AK093893 /gi=21752845 /ug=Hs.356595 /len=1952	AK093893	Hs.356595	
14245	0.034698	hypothetical protein FLJ32894 (FLJ32894), mRNA /cds=(50,550) /gb=NM_144667 /gi=21389550 /ug=Hs.350668 /len=1710	NM_144667	Hs.350668	NP_653268
14255	0.032363	EST wt25d05.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2508489 3' similar to contains Alu repetitive element; contains L1.t1 L1 repetitive element;	AI962961		
14288	0.013076	small acidic protein (SMAP), mRNA /cds=(137,688) /gb=NM_014267 /gi=20070245 /ug=Hs.78050 /len=1504	NM_014267	Hs.78050	NP_055082
14289	0.003316	clone DJ0798C17, complete sequence	AC004889		
14291	0.020917	calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA /cds=(69,518) /gb=NM_001743 /gi=20428653 /ug=Hs.425808 /len=1128	NM_001743	Hs.425808	NP_001734
14304	0.019388	cDNA: FLJ23111 fis, clone LNG07835. /gb=AK026764 /gi=10439690 /ug=Hs.268231 /len=2263	AK026764	Hs.268231	

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14363	0.037168	ESTs, cDNA, 3' end /clone=IMAGE:2355101 /clone_end=3' /gb=AI719659 /gi=5036915 /ug=Hs.372094 /len=528	AI719659	Hs.372094	
14375	0.034482	ESTs, cDNA, 3' end /clone=IMAGE:2402646 /clone_end=3' /gb=AI768858 /gi=5235367 /ug=Hs.157149 /len=562	AI768858	Hs.157149	NP_066012
14386	0.007887	UI-E-EJ0-aik-i-20-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-aik-i-20-0-UI 5', mRNA sequence /clone=UI-E-EJ0-aik-i-20-0-UI /clone_end=5' /gb=BM727413 /gi=19048746 /ug=Hs.112619 /len=1667	BM727413	Hs.112619	
14387	0.013076	likely ortholog of rat V-1 protein (V-1), mRNA /cds=(229,585) /gb=NM_145808 /gi=21956644 /ug=Hs.21321 /len=3770	NM_145808	Hs.21321	NP_665807
14452	0.028082	No significant match	SEQ.ID.No.35		
14453	0.048529	NO significant match, ORF+1(16~273)	SEQ.ID.No.41		
14455	0.001216	No significant match, ORF+3(135~404)	SEQ.ID.No.50		
14475	0.005512	EST, cDNA: FLJ23266 fis, clone COL06676, highly similar to HUMFRCC Homo sapiens clone s153 mRNA	AK026919		
14524	0.026124	EST (wa75f06.x1 Soares NFL T GBC S1	AI685268		
14528	0.028082	EST (EST34421 Embryo, 6 week l cDNA 5' end similar to EST containing L1 repeat)	AA330691		
14561	0.042541	mRNA; cDNA DKFZp451B1818 (from clone DKFZp451B1818) /gb=AL832623 /gi=21733198 /ug=Hs.77554 /len=6240	AL832623	Hs.77554	
14600	0.022547	hypothetical gene supported by AY007122 (LOC92719)	XM_046853		
14635	0.008602	hypothetical protein DKFZp434G1415 (DKFZP434G1415), mRNA /cds=(35,2140) /gb=NM_031292 /gi=13775209 /ug=Hs.151093 /len=3495	NM_031292	Hs.151093	NP_112582
14637	0.048529	hypothetical protein PRO1331 (PRO1331), mRNA /cds=(423,617) /gb=NM_030778 /gi=13562115 /ug=Hs.301824 /len=1634	NM_030778	Hs.301824	NP_110405
14690	0.006608	cDNA FLJ35033 fis, clone OCBBF2016590, weakly similar to CELL SURFACE ANTIGEN 114/A10 PRECURSOR. /cds=(407,934) /gb=AK092352 /gi=21750925 /ug=Hs.156113 /len=2884	AK092352	Hs.156113	
14798	0.039781	EST(cDNA clone IMAGE:4731577 5')	BG621355		NP_002700

Genes Corresponding To Differentially Expressed Genes in Figure 8 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14808	0.045456	ESTs, cDNA, 5' end /clone=IMAGE:3055219 /clone_end=5' /gb=AW402596 /gi=6921298 /ug=Hs.103296 /len=593	AW402596	Hs.103296	NP_775767
14833	0.019388	EST380251 MAGE resequences, MAGJ cDNA, mRNA sequence /gb=AW968281 /gi=8158016 /ug=Hs.319460 /len=689	AW968281	Hs.319460	
14842	0.017954	mitochondrion, complete genome	NC_001807		
14934	0.014175	No significant match (ORF: +1:1~102[102])	SEQ.ID.No.59		

TABLE 3B					
Genes Corresponding to Differentially Expressed Genes in Figure 9 - Obesity					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1	0.041454	vacuolar protein sorting 28 (yeast) (VPS28), mRNA /cds=(62,727) /gb=NM_016208 /gi=7705884 /ug=Hs.339697 /len=928	NM_016208	Hs.339697	NP_057292
214	0.02042	neuronal thread protein AD7c-NTP	NP_055301		
257	0.005038	KIAA0301 gene, partial cds	AB002299		NP_055426
288	0.002317	phosphodiesterase 8B (PDE8B), mRNA /cds=(46,2703) /gb=NM_003719 /gi=26006850 /ug=Hs.78106 /len=3567	NM_003719	Hs.78106	NP_003710
298	0.025168	KIAA0429 gene product (KIAA0429), mRNA /cds=(2374,3444) /gb=NM_014751 /gi=7662113 /ug=Hs.77694 /len=5645	NM_014751	Hs.77694	NP_055566
323	0.005852	associated molecule with the SH3 domain of STAM (AMSH), mRNA /cds=(188,1462) /gb=NM_006463 /gi=17738303 /ug=Hs.12479 /len=2107	NM_006463	Hs.12479	NP_006454
357	0.007162	deleted in pancreatic carcinoma (DPC4) gene, exon 3	AF045440		
383	0.031506	zinc finger protein 223 (ZNF223), mRNA /cds=(239,1687) /gb=NM_013361 /gi=7019588 /ug=Hs.279782 /len=2033	NM_013361	Hs.279782	NP_037493
423	0.012975	biotinidase (BTD), mRNA /cds=(36,1667) /gb=NM_000060 /gi=4557372 /ug=Hs.78885 /len=2016	NM_000060	Hs.78885	NP_000051
429	0.026411	NPD009 protein (NPD009), mRNA /cds=(1327,1677) /gb=NM_020686 /gi=24476005 /ug=Hs.283675 /len=2514	NM_020686	Hs.283675	NP_065737
434	0.012537	phosphoglycerate kinase 1 (PGK1), mRNA /cds=(70,1323) /gb=NM_000291 /gi=22095338 /ug=Hs.78771 /len=2338	NM_000291	Hs.78771	NP_000282
450	0.028189	nuclear factor NF-IL6	X52560		
453	0.012175	WD repeat domain 1 (WDR1), transcript variant 1, mRNA /cds=(203,2023) /gb=NM_017491 /gi=17105397 /ug=Hs.85100 /len=3079	NM_017491	Hs.85100	NP_059830
477	0.034563	microfibrillar-associated protein 4 (MFAP4), mRNA /cds=(26,793) /gb=NM_002404 /gi=23111004 /ug=Hs.296049 /len=1830	NM_002404	Hs.296049	NP_002395
512	0.001459	myosin IXB (MYO9B), mRNA /cds=(1,6069) /gb=NM_004145 /gi=4758749 /ug=Hs.159629 /len=6069	NM_004145	Hs.159629	NP_004136
565	0.022932	topoisomerase (DNA) III alpha (TOP3A), mRNA /cds=(230,3235) /gb=NM_004618 /gi=20143947 /ug=Hs.91175 /len=3807	NM_004618	Hs.91175	NP_004609

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
579	0.046542	Rad50-interacting protein 1 (FLJ11785), mRNA /cds=(24,2489) /gb=NM_021930 /gi=19923579 /ug=Hs.44625 /len=2855	NM_021930	Hs.44625	NP_068749
584	0.036865	isocitrate dehydrogenase 1 (NADP), soluble (IDH1), mRNA /cds=(235,1479) /gb=NM_005896 /gi=28178824 /ug=Hs.11223 /len=2339	NM_005896	Hs.11223	NP_005887
589	0.037157	AGENCOURT_6640990 NIH_MGC_68 cDNA clone IMAGE:5735856 5', mRNA sequence /clone=IMAGE:5735856 /clone_end=5' /gb=BM907553 /gi=19357932 /ug=Hs.424427 /len=645	BM907553	Hs.424427	
613	0.047341	PEF protein with a long N-terminal hydrophobic domain (peflin) (PEF), mRNA /cds=(13,867) /gb=NM_012392 /gi=6912581 /ug=Hs.241531 /len=1641	NM_012392	Hs.241531	NP_036524
615	0.041872	cDNA FLJ11904 fis, clone HEMBB1000048. /gb=AK021966 /gi=10433275 /ug=Hs.285519 /len=2134	AK021966	Hs.285519	
617	0.049654	solute carrier family 2 (facilitated glucose transporter), member 10 (SLC2A10), mRNA /cds=(251,1876) /gb=NM_030777 /gi=21361923 /ug=Hs.305971 /len=4396	NM_030777	Hs.305971	NP_110404
625	0.005892	fragile X mental retardation 1 (FMR1), mRNA /cds=(220,2118) /gb=NM_002024 /gi=4503764 /ug=Hs.89764 /len=4362	NM_002024	Hs.89764	NP_002015
627	0.017523	methionine-tRNA synthetase (MARS), mRNA /cds=(24,2726) /gb=NM_004990 /gi=14043021 /ug=Hs.279946 /len=2795	NM_004990	Hs.279946	NP_004981
634	0.020686	mitofusin 1 (MFN1), transcript variant 1, mRNA /cds=(84,2309) /gb=NM_033540 /gi=16117784 /ug=Hs.197877 /len=3275	NM_033540	Hs.197877	NP_284941
652	0.01004	cDNA FLJ38331 fis, clone FCBBF3025285, moderately similar to Mus musculus peripheral benzodiazepine receptor associated protein (Pap7) mRNA. /gb=AK095650 /gi=21754954 /ug=Hs.9052 /len=3547	AK095650	Hs.9052	
657	0.00593	FLJ30577 fis, clone BRAWH2006760 /cds=UNKNOWN /gb=AK055139 /gi=16549803 /ug=Hs.324815 /len=2353	AK055139	Hs.324815	
658	0.029283	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 /len=1705	NM_006855	Hs.250696	NP_057839

Spot	p-value	D scription	Gene Accession No.	Unigene Accession No.	Protein Accession No.
662	0.005051	insulin-like growth factor binding protein 5 (IGFBP5), mRNA /cds=(752,1570) /gb=NM_000599 /gi=10834981 /ug=Hs.380833 /len=1722	NM_000599	Hs.380833	NP_000590
668	0.035062	KIAA0391 gene product (KIAA0391), mRNA /cds=(360,2063) /gb=NM_014672 /gi=7662093 /ug=Hs.154668 /len=5677	NM_014672	Hs.154668	NP_055487
670	0.036456	cytidine deaminase (CDA), mRNA /cds=(118,558) /gb=NM_001785 /gi=11386156 /ug=Hs.72924 /len=892	NM_001785	Hs.72924	NP_001776
691	0.014281	U5 snRNP-specific protein, 200-KD (U5-200KD), mRNA /cds=(189,5624) /gb=NM_014014 /gi=24307974 /ug=Hs.246112 /len=5898	NM_014014	Hs.246112	NP_054733
693	9.54E-04	ubiquitin-conjugating enzyme E2L 3 (UBE2L3), mRNA /cds=(16,480) /gb=NM_003347 /gi=4507788 /ug=Hs.108104 /len=2845	NM_003347	Hs.108104	NP_003338
697	0.044049	interferon, alpha-inducible protein (clone IFI-6-16) (G1P3), transcript variant 3, mRNA /cds=(108,524) /gb=NM_022873 /gi=13259549 /ug=Hs.265827 /len=841	NM_022873	Hs.265827	NP_075011
721	9.54E-04	mitochondrion, complete genome	NC_001807		
726	1.64E-04	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747	NM_012479	Hs.25001	NP_036611
772	0.001525	acid sphingomyelinase (ASM) gene, exons a, and alternative a (3' end), b and c (5' end).	M59917		
787	0.008356	cargo selection protein (mannose 6 phosphate receptor binding protein) (TIP47), mRNA /cds=(67,1371) /gb=NM_005817 /gi=20127485 /ug=Hs.140452 /len=2239	NM_005817	Hs.140452	NP_005808
793	0.012175	glyoxalase I (GLO1), mRNA /cds=(88,642) /gb=NM_006708 /gi=5729841 /ug=Hs.75207 /len=1993	NM_006708	Hs.75207	NP_006699
794	0.004048	zn87g06.x5 Stratagene lung carcinoma 937218 cDNA clone IMAGE:565210 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;, mRNA sequence /clone=IMAGE:565210 /clone_end=3' /gb=AI732466 /gi=5053579 /ug=Hs.193133 /len=526	AI732466	Hs.193133	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
807	0.017281	KIAA0102 gene product (KIAA0102), mRNA /cds=(308,679) /gb=NM_014752 /gi=7661907 /ug=Hs.77665 /len=1370	NM_014752	Hs.77665	NP_055567
808	0.005051	PIX1 mRNA (ORF)	AF037219		NP_570854
809	0.003193	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) (MCCC1), mRNA /cds=(133,2310) /gb=NM_020166 /gi=13518227 /ug=Hs.47649 /len=2528	NM_020166	Hs.47649	NP_064551
831	0.039115	Microfibril-associated glycoprotein-2 (MAGP2), mRNA /cds=(214,735) /gb=NM_003480 /gi=4505088 /ug=Hs.300946 /len=1119	NM_003480	Hs.300946	NP_003471
837	0.007261	serine/arginine repetitive matrix 2 (SRRM2), mRNA /cds=(226,8484) /gb=NM_016333 /gi=19923465 /ug=Hs.197114 /len=9027	NM_016333	Hs.197114	NP_057417
847	0.037157	peroxisomal biogenesis factor 3 (PEX3), mRNA /cds=(64,1185) /gb=NM_003630 /gi=4505726 /ug=Hs.7277 /len=1979	NM_003630	Hs.7277	NP_003621
851	6.22E-04	of89c05.s1 NCI_CGAP_Li5 cDNA clone IMAGE:1437512 3' similar to contains Alu repetitive element, mRNA sequence /clone=IMAGE:1437512 /clone_end=3' /gb=AA894384 /gi=3030785 /ug=Hs.432123 /len=296	AA894384	Hs.432123	
865	0.001133	mitochondrion, complete genome	NC_001807		
877	0.006234	ring finger protein 11 (RNF11), mRNA /cds=(128,592) /gb=NM_014372 /gi=7657519 /ug=Hs.96334 /len=2529	NM_014372	Hs.96334	NP_055187
909	0.026411	integral membrane protein Tmp21-l (p23)	AJ004913		NP_006818
918	0.001283	AGENCOURT_6456859 NIH_MGC_92 cDNA clone IMAGE:5576908 5', mRNA sequence /clone=IMAGE:5576908 /clone_end=5' /gb=BM466169 /gi=18515211 /ug=Hs.439148 /len=1150	BM466169	Hs.439148	
921	0.012975	mitochondrion, complete genome	NC_001807		
923	0.013819	eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa (EIF3S3), mRNA /cds=(6,1064) /gb=NM_003756 /gi=4503514 /ug=Hs.58189 /len=1280	NM_003756	Hs.58189	NP_003747
930	0.008208	FK506 binding protein 9, 63 kDa (FKBP9), mRNA /cds=(457,885) /gb=NM_007270 /gi=24307926 /ug=Hs.302749 /len=2517	NM_007270	Hs.302749	NP_009201
931	0.041454	signal recognition particle 54kDa (SRP54), mRNA /cds=(225,1739) /gb=NM_003136 /gi=20149548 /ug=Hs.49346 /len=2164	NM_003136	Hs.49346	NP_003127

Spot	p-value	Description	Gen Accession No.	Unigene Accession No.	Protein Accession No.
943	0.004687	XIST, coding sequence "a" mRNA (locus DXS399E). /gb=X56199 /gi=37987 /ug=Hs.352403 /len=1614	X56199	Hs.352403	
954	0.029809	cell cycle progression 8 protein (CPR8), mRNA /cds=(13,1140) /gb=NM_004748 /gi=4758047 /ug=Hs.82506 /len=1856	NM_004748	Hs.82506	NP_004739
980	0.033283	cleavage and polyadenylation specific factor 6, 68kDa (CPSF6), mRNA /cds=(35,1690) /gb=NM_007007 /gi=5901927 /ug=Hs.64542 /len=3426	NM_007007	Hs.64542	NP_008938
998	0.017682	down-regulator of transcription 1, TBP-binding (negative cofactor 2) (DR1), mRNA /cds=(548,1078) /gb=NM_001938 /gi=4503380 /ug=Hs.16697 /len=1375	NM_001938	Hs.16697	NP_001929
1001	0.031506	RAD23 B (S. cerevisiae) (RAD23B), mRNA /cds=(352,1581) /gb=NM_002874 /gi=19924138 /ug=Hs.404283 /len=2943	NM_002874	Hs.404283	NP_002865
1008	0.039257	Alg5, S. cerevisiae, of (ALG5), mRNA /cds=(28,1002) /gb=NM_013338 /gi=9665250 /ug=Hs.227933 /len=1125	NM_013338	Hs.227933	NP_037470
1015	0.013819	actinin, alpha 1 (ACTN1), mRNA /cds=(184,2862) /gb=NM_001102 /gi=12025669 /ug=Hs.119000 /len=3398	NM_001102	Hs.119000	NP_001093
1021	0.015649	tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), mRNA /cds=(67,2439) /gb=NM_006290 /gi=26051241 /ug=Hs.211600 /len=4446	NM_006290	Hs.211600	NP_006281
1023	0.022422	v-fos FBJ murine osteosarcoma viral oncogene (FOS), mRNA /cds=(156,1298) /gb=NM_005252 /gi=6552332 /ug=Hs.25647 /len=2084	NM_005252	Hs.25647	NP_005243
1026	0.023762	methionine adenosyltransferase II, beta (MAT2B), mRNA /cds=(73,1077) /gb=NM_013283 /gi=20127525 /ug=Hs.54642 /len=2054	NM_013283	Hs.54642	NP_037415
1028	0.025168	ATP synthase, H transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=NM_006886 /gi=21327678 /ug=Hs.177530 /len=417	NM_006886	Hs.177530	NP_008817
1036	0.031506	mRNA for KIAA1518 protein, partial cds. /cds=(482,3112) /gb=AB040951 /gi=7959302 /ug=Hs.284208 /len=5370	AB040951	Hs.284208	NP_056308
1051	0.029809	HSPC133 protein (HSPC133), mRNA /cds=(83,481) /gb=NM_014168 /gi=7661791 /ug=Hs.273063 /len=963	NM_014168	Hs.273063	NP_054887

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1080	0.026411	Similar to RIKEN cDNA 4833424O15 gene, clone IMAGE:4793707, mRNA /gb=BC040174 /gi=25777829 /ug=Hs.312481 /len=3745	BC040174	Hs.312481	
1120	0.046149	clone 25032 mRNA sequence /cds=UNKNOWN /gb=AF131764 /gi=4406586 /ug=Hs.13399 /len=1798	AF131764	Hs.13399	NP_071919
1168	0.002566	thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556	NM_021109	Hs.75968	NP_066932
1170	0.017682	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_079425	Hs.77385	NP_524149
1174	0.025168	eukaryotic translation initiation factor 3, subunit 6 interacting protein (EIF3S6IP), mRNA /cds=(34,1728) /gb=NM_016091 /gi=7705432 /ug=Hs.119503 /len=1901	NM_016091	Hs.119503	NP_057175
1189	0.00181	mRNA; cDNA DKFZp451A142 (from clone DKFZp451A142) /cds=(39,1898) /gb=AL834245 /gi=21739785 /ug=Hs.124918 /len=4902	AL834245	Hs.124918	
1193	0.031405	CGI-100 protein (CGI-100), mRNA /cds=(113,802) /gb=NM_016040 /gi=19923441 /ug=Hs.348996 /len=3635	NM_016040	Hs.348996	NP_057124
1194	0.013385	proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA /cds=(86,811) /gb=NM_002790 /gi=23110941 /ug=Hs.76913 /len=1023	NM_002790	Hs.76913	NP_002781
1236	0.037084	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) (MMP9), mRNA /cds=(20,2143) /gb=NM_004994 /gi=4826835 /ug=Hs.151738 /len=2334	NM_004994	Hs.151738	NP_004985
1267	0.008955	hypothetical protein DKFZp586K0717 (DKFZP586K0717), mRNA /cds=(168,1730) /gb=NM_030917 /gi=13569873 /ug=Hs.334812 /len=1914	NM_030917	Hs.334812	NP_112179
1301	0.003233	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
1305	0.037084	cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA /cds=(90,281) /gb=NM_001867 /gi=18105039 /ug=Hs.430075 /len=448	NM_001867	Hs.430075	NP_001858

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1306	0.023762	poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA /cds=(503,2404) /gb=NM_002568 /gi=4505574 /ug=Hs.172182 /len=2848	NM_002568	Hs.172182	NP_002559
1343	0.033283	hypothetical protein FLJ12438 (FLJ12438), mRNA /cds=(174,1340) /gb=NM_021933 /gi=11345471 /ug=Hs.8595 /len=1575	NM_021933	Hs.8595	NP_068752
1349	0.009309	mRNA; cDNA DKFZp313D2314 (from clone DKFZp313D2314) /gb=AL832057 /gi=21732598 /ug=Hs.3685 /len=3141	AL832057	Hs.3685	
1386	0.034454	AGENCOURT_6424254 NIH_MGC_67 cDNA clone IMAGE:5491531 5', mRNA sequence /clone=IMAGE:5491531 /clone_end=5' /gb=BM479954 /gi=18528996 /ug=Hs.381243 /len=1112	BM479954	Hs.381243	
1418	0.013819	voltage-dependent anion channel 2 (VDAC2), mRNA /cds=(63,947) /gb=NM_003375 /gi=4507880 /ug=Hs.78902 /len=1404	NM_003375	Hs.78902	NP_003366
1419	0.017682	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) (CD74), mRNA /cds=(8,706) /gb=NM_004355 /gi=10835070 /ug=Hs.84298 /len=1304	NM_004355	Hs.84298	NP_004346
1431	0.011417	inhibitor of growth family, member 1 (ING1), mRNA /cds=(433,1701) /gb=NM_005537 /gi=19923770 /ug=Hs.46700 /len=2886	NM_005537	Hs.46700	NP_005528
1450	0.039115	EST384321 MAGE resequences, MAGL cDNA, mRNA sequence /gb=AW972232 /gi=8162078 /ug=Hs.152375 /len=617	AW972232	Hs.152375	
1455	0.013385	CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA /cds=(260,2668) /gb=NM_001253 /gi=16357499 /ug=Hs.155174 /len=3012	NM_001253	Hs.155174	NP_001244
1467	0.037084	SON DNA binding protein (SON), transcript variant e, mRNA /cds=(50,6376) /gb=NM_058183 /gi=21040317 /ug=Hs.92909 /len=8482	NM_058183	Hs.92909	NP_620305
1469	0.016639	potassium channel modulatory factor (PCMF), mRNA /cds=(54,1199) /gb=NM_020122 /gi=10047127 /ug=Hs.5392 /len=1595	NM_020122	Hs.5392	NP_064507
1497	0.005439	hypothetical protein MGC45474 (MGC45474), mRNA /cds=(218,2035) /gb=NM_152369 /gi=22748794 /ug=Hs.234101 /len=2384	NM_152369	Hs.234101	
1500	0.031405	KIAA0824 (=PCF11p homolog)	AB020631		NP_056969

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1535	0.004048	mRNA for KIAA0752 protein, partial cds. /cds=(1,1006) /gb=AB018295 /gi=3882224 /ug=Hs.126779 /len=4332	AB018295	Hs.126779	NP_775934
1539	0.00295	LENG5 protein (LENG5), mRNA /cds=(113,1285) /gb=NM_024075 /gi=13129061 /ug=Hs.15580 /len=1364	NM_024075	Hs.15580	NP_076980
1574	0.019933	similar to triple functional domain (PTPRF interacting) (LOC115557), mRNA /cds=(331,1755) /gb=NM_133483 /gi=19311007 /ug=Hs.61581 /len=2166	NM_133483	Hs.61581	NP_597840
1577	0.045762	POM121 membrane glycoprotein (rat) (POM121), mRNA /cds=(978,3932) /gb=NM_172020 /gi=26051277 /ug=Hs.295112 /len=6014	NM_172020	Hs.295112	NP_742017
1651	0.035141	zinc finger protein 384 (ZNF384), mRNA /cds=(499,2229) /gb=NM_133476 /gi=20143968 /ug=Hs.103315 /len=3291	NM_133476	Hs.103315	NP_597733
1665	0.026411	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
1673	0.043451	endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 (HERPUD1), mRNA /cds=(96,1271) /gb=NM_014685 /gi=7661869 /ug=Hs.146393 /len=1884	NM_014685	Hs.146393	NP_055500
1709	0.048172	KIAA0399	AB007859		NP_055928
1724	8.74E-04	zinc finger RNA binding protein (ZFR), mRNA /cds=(44,1300) /gb=NM_016107 /gi=7706372 /ug=Hs.173518 /len=2734	NM_016107	Hs.173518	NP_057191
1751	0.039257	insulin induced protein 2 (LOC51141), mRNA /cds=(141,857) /gb=NM_016133 /gi=23821030 /ug=Hs.7089 /len=1358	NM_016133	Hs.7089	NP_057217
1756	0.013819	uronyl-2-sulfotransferase (UST), mRNA /cds=(104,1324) /gb=NM_005715 /gi=5032218 /ug=Hs.134015 /len=4196	NM_005715	Hs.134015	NP_005706
1830	0.033283	calmodulin-I (CALM1) mRNA, 3'UTR, partial sequence. /gb=U16850 /gi=576644 /ug=Hs.374441 /len=2383	U16850	Hs.374441	
1927	0.036435	EST (tg16b07.x1 NCI_CGAP_CLL1 clone IMAGE:2108917 3' TR:Q14526 Q14526 HIC-1 GENE FRAGMENT)	AI391567		NP_006488
1974	0.045762	CDC20 cell division cycle 20 (S. cerevisiae) (CDC20), mRNA /cds=(111,1610) /gb=NM_001255 /gi=4557436 /ug=Hs.82906 /len=1686	NM_001255	Hs.82906	NP_001246

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Prot in Accession No.
1988	0.029809	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein) (ST13), mRNA /cds=(144,1253) /gb=NM_003932 /gi=21237722 /ug=Hs.119222 /len=3214	NM_003932	Hs.119222	NP_003923
2033	0.012175	calmodulin 1 (phosphorylase kinase, delta) (CALM1), mRNA /cds=(200,649) /gb=NM_006888 /gi=5901911 /ug=Hs.282410 /len=1526	NM_006888	Hs.282410	NP_008819
2036	0.041237	ATPase, H transporting, lysosomal 56/58kDa, V1 subunit B, isoform 2 (ATP6V1B2), mRNA /cds=(208,1743) /gb=NM_001693 /gi=19913427 /ug=Hs.1697 /len=3054	NM_001693	Hs.1697	NP_001684
2041	0.048653	ribosomal protein L32 (RPL32), mRNA /cds=(51,458) /gb=NM_000994 /gi=15812220 /ug=Hs.169793 /len=521	NM_000994	Hs.169793	NP_000985
2073	0.002372	transcription factor B1, mitochondrial (TFB1M), mRNA /cds=(73,1113) /gb=NM_016020 /gi=7705784 /ug=Hs.279908 /len=1290	NM_016020	Hs.279908	NP_057104
2074	0.039115	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) (CLU), mRNA /cds=(48,1397) /gb=NM_001831 /gi=4502904 /ug=Hs.75106 /len=1676	NM_001831	Hs.75106	NP_001822
2077	0.019933	musculus exoribonuclease 1 (Xrn1)	NM_011916		NP_036046
2105	0.041237	potassium channel, subfamily K, member 1 (KCNK1), mRNA /cds=(183,1193) /gb=NM_002245 /gi=15451900 /ug=Hs.79351 /len=1901	NM_002245	Hs.79351	NP_002236
2175	0.025168	clone IMAGE:4799018, mRNA /gb=BC045722 /gi=28277129 /ug=Hs.153527 /len=2587	BC045722	Hs.153527	
2194	0.011417	monocytic leukemia zinc finger protein-related factor (MORF), mRNA /cds=(316,6537) /gb=NM_012330 /gi=6912511 /ug=Hs.27590 /len=6537	NM_012330	Hs.27590	NP_036462
2211	0.017682	L-isoaspartyl/D-aspartyl O-methyltransferase (PCMT1) gene, exon 1,	U49740		
2230	0.041237	PMS1 postmeiotic segregation increased 1 (S. cerevisiae) (PMS1), mRNA /cds=(81,2879) /gb=NM_000534 /gi=11496979 /ug=Hs.111749 /len=3121	NM_000534	Hs.111749	NP_000525
2231	0.026643	TTN gene for titin	AJ277892		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2242	0.031506	uncharacterized hypothalamus protein HT010 (HT010), mRNA /cds=(227,1420) /gb=NM_018471 /gi=8923807 /ug=Hs.6375 /len=2140	NM_018471	Hs.6375	NP_060941
2273	0.033283	Pirin (PIR), mRNA /cds=(231,1103) /gb=NM_003662 /gi=4505822 /ug=Hs.424966 /len=1318	NM_003662	Hs.424966	NP_003653
2303	0.035141	cDNA FLJ13446 fis, clone PLACE1002968. /gb=AK023508 /gi=10435460 /ug=Hs.201925 /len=1712	AK023508	Hs.201925	
2307	0.002773	matrilin 3 (MATN3) precursor, mRNA /cds=(64,1524) /gb=NM_002381 /gi=13518040 /ug=Hs.278461 /len=2599	NM_002381	Hs.278461	NP_002372
2309	0.025168	GTPase-activating protein GAPIII	U20238		NP_033051
2317	0.006234	mRNA for KIAA0570 protein, partial cds. /cds=(480,10718) /gb=AB011142 /gi=20521084 /ug=Hs.180948 /len=11269	AB011142	Hs.180948	
2318	0.045762	mRNA for KIAA0611 protein, partial cds. /cds=(1,2740) /gb=AB014511 /gi=3327035 /ug=Hs.406434 /len=7176	AB014511	Hs.406434	
2480	0.025168	topoisomerase (DNA) I (TOP1), mRNA /cds=(247,2544) /gb=NM_003286 /gi=19913404 /ug=Hs.317 /len=3734	NM_003286	Hs.317	NP_003277
2506	0.022422	bHLH-PAS transcription factor MOP9 (MOP9) mRNA, long form, complete cds, alternatively spliced /cds=(58,1815) /gb=AF231338 /gi=7963663 /ug=Hs.222024 /len=2008	AF231338	Hs.222024	NP_064568
2542	0.039115	leucyl-tRNA synthetase (LARS), mRNA /cds=(73,3603) /gb=NM_020117 /gi=24496788 /ug=Hs.6762 /len=4248	NM_020117	Hs.6762	NP_064502
2557	0.03939	leucine-rich PPR-motif containing (LRPPRC), mRNA /cds=(46,3867) /gb=NM_133259 /gi=18959201 /ug=Hs.182490 /len=4782	NM_133259	Hs.182490	NP_573566
2625	0.033283	hypothetical protein (KIAA0714)	AB018257		
2652	0.013819	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 2b, mRNA /cds=(229,2481) /gb=NM_007289 /gi=6042203 /ug=Hs.1298 /len=5725	NM_007289	Hs.1298	NP_009220
2678	0.010023	protein-L-isoaspartate (D-aspartate) O-methyltransferase (PCMT1), mRNA /cds=(74,757) /gb=NM_005389 /gi=4885538 /ug=Hs.79137 /len=1599	NM_005389	Hs.79137	NP_005380

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2687	0.019933	v-fos FBJ murine osteosarcoma viral oncogene (FOS), mRNA /cds=(156,1298) /gb=NM_005252 /gi=6552332 /ug=Hs.25647 /len=2084	NM_005252	Hs.25647	NP_005243
2713	0.033283	caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 CAV1	AJ133269		
2741	0.010023	golgi SNAP receptor complex member 1 (GOSR1), mRNA /cds=(13,765) /gb=NM_004871 /gi=4758455 /ug=Hs.8868 /len=999	NM_004871	Hs.8868	NP_004862
2743	0.039115	clone MGC:9947 IMAGE:3876105, mRNA, complete cds /cds=(51,2216) /gb=BC013590 /gi=15488925 /ug=Hs.2437 /len=2651	BC013590	Hs.2437	
2745	0.035141	calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	AF223391		
2779	0.009383	nuclear factor (erythroid-derived 2)-like 2 (NFE2L2), mRNA /cds=(114,1931) /gb=NM_006164 /gi=20149575 /ug=Hs.155396 /len=2439	NM_006164	Hs.155396	NP_006155
2782	0.005811	high mobility group 2 protein (HMG-2)	M83665		
2797	0.028189	zinc finger homeobox 1b (ZFHX1B), mRNA /cds=(445,4089) /gb=NM_014795 /gi=7662183 /ug=Hs.34871 /len=5523	NM_014795	Hs.34871	NP_055610
2815	0.006684	proteasome (prosome, macropain) subunit, alpha type, 6 (PSMA6), mRNA /cds=(110,850) /gb=NM_002791 /gi=23110943 /ug=Hs.410276 /len=1035	NM_002791	Hs.410276	NP_002782
2843	0.002372	UI-E-EJ0-ahj-n-19-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahj-n-19-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahj-n-19-0-UI /clone_end=5' /gb=BM701108 /gi=19014366 /ug=Hs.401941 /len=1923	BM701108	Hs.401941	
2848	0.006234	BJ-HCC-24 tumor antigen mRNA, complete cds /cds=(2,1240) /gb=AY121805 /gi=22002585 /ug=Hs.433489 /len=1488	AY121805	Hs.433489	
2849	0.008208	chromosome 14 open reading frame 2 (C14orf2), mRNA /cds=(61,237) /gb=NM_004894 /gi=4758939 /ug=Hs.109052 /len=627	NM_004894	Hs.109052	NP_004885
2850	0.009383	helicase II (RAD54L) mRNA, complete cds. /cds=(54,4979) /gb=U09820 /gi=606832 /ug=Hs.96264 /len=6115	U09820	Hs.96264	NP_612115
2870	0.029809	threonyl-tRNA synthetase (TARS), mRNA /cds=(135,2270) /gb=NM_152295 /gi=25054078 /ug=Hs.84131 /len=2662	NM_152295	Hs.84131	NP_689508

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2875	0.043451	deubiquitinating enzyme (UNPH4)= AF153604 ubiquitin-specific protease homolog (UPH)	AF106069		NP_006304
2884	0.035141	mitochondrial ribosomal protein S30 (MRPS30), mRNA /cds=(39,1358) /gb=NM_016640 /gi=16950598 /ug=Hs.28555 /len=1482	NM_016640	Hs.28555	NP_057724
2910	0.026643	Sm protein F (LSM6), mRNA /cds=(82,324) /gb=NM_007080 /gi=5901997 /ug=Hs.42438 /len=596	NM_007080	Hs.42438	NP_009011
2913	9.20E-05	mortality factor 4 like 1 (MORF4L1), mRNA /cds=(132,1103) /gb=NM_006791 /gi=5803101 /ug=Hs.6353 /len=1766	NM_006791	Hs.6353	NP_006782
2928	0.022422	ligase IV, DNA, ATP-dependent (LIG4), mRNA /cds=(274,3009) /gb=NM_002312 /gi=23199992 /ug=Hs.166091 /len=3325	NM_002312	Hs.166091	NP_002303
2947	0.011417	hemoglobin, alpha 2 (HBA2), mRNA /cds=(38,466) /gb=NM_000517 /gi=14043068 /ug=Hs.347939 /len=575	NM_000517	Hs.347939	NP_000508
2967	0.016639	matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) (MMP2), mRNA /cds=(290,2272) /gb=NM_004530 /gi=11342665 /ug=Hs.111301 /len=3069	NM_004530	Hs.111301	NP_004521
2990	0.033283	cDNA FLJ31057 fis, clone HSYRA2000787. /gb=AK055619 /gi=16550395 /ug=Hs.296261 /len=2168	AK055619	Hs.296261	
3011	0.035141	mitochondrion, complete genome	NC_001807		
3029	0.022422	Yip1p-interacting factor (YIF1P), mRNA /cds=(116,997) /gb=NM_020470 /gi=9994168 /ug=Hs.406422 /len=1078	NM_020470	Hs.406422	NP_065203
3034	0.043451	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SERPINB6), mRNA /cds=(75,1205) /gb=NM_004568 /gi=28077084 /ug=Hs.41072 /len=1361	NM_004568	Hs.41072	NP_004559
3038	0.043451	golgi phosphoprotein 3 (coat-protein) (GOLPH3), mRNA /cds=(241,1137) /gb=NM_022130 /gi=20149665 /ug=Hs.18271 /len=2655	NM_022130	Hs.18271	NP_071413
3062	0.006234	myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), mRNA /cds=(115,630) /gb=NM_006471 /gi=5453739 /ug=Hs.180224 /len=944	NM_006471	Hs.180224	NP_006462
3065	0.041237	KIAA0433 protein (KIAA0433), mRNA /cds=(510,4241) /gb=NM_015216 /gi=7662117 /ug=Hs.26179 /len=5814	NM_015216	Hs.26179	NP_056031

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3070	0.041237	signal sequence receptor, beta (translocon-associated protein beta) (SSR2), mRNA /cds=(51,602) /gb=NM_003145 /gi=6552341 /ug=Hs.74564 /len=1093	NM_003145	Hs.74564	NP_003136
3071	0.006234	endothelin receptor type A (EDNRA), mRNA /cds=(485,1768) /gb=NM_001957 /gi=4503464 /ug=Hs.76252 /len=4105	NM_001957	Hs.76252	NP_001948
3072	0.017682	trichorhinophalangeal syndrome I (TRPS1), mRNA /cds=(639,4484) /gb=NM_014112 /gi=7657658 /ug=Hs.26102 /len=10011	NM_014112	Hs.26102	NP_054831
3073	0.003487	KIAA0174 gene product (KIAA0174), mRNA /cds=(64,1158) /gb=NM_014761 /gi=7661971 /ug=Hs.75824 /len=2348	NM_014761	Hs.75824	NP_055576
3076	0.033283	hypothetical protein FLJ20707 (FLJ20707), mRNA /cds=(83,2173) /gb=NM_032560 /gi=19923643 /ug=Hs.334657 /len=2794	NM_032560	Hs.334657	NP_115949
3108	0.011417	glycogen synthase 1 (muscle) (GYS1), mRNA /cds=(161,2374) /gb=NM_002103 /gi=4504232 /ug=Hs.772 /len=3531	NM_002103	Hs.772	NP_002094
3113	0.029809	phosphodiesterase 4D interacting protein (myomegalin) (PDE4DIP), mRNA /cds=(658,4056) /gb=NM_014644 /gi=11036643 /ug=Hs.265848 /len=5676	NM_014644	Hs.265848	NP_055459
3136	0.015649	splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(219,542) /gb=NM_006925 /gi=5902077 /ug=Hs.166975 /len=1865	NM_006925	Hs.166975	NP_008856
3137	0.025168	yp24c06.s1 Soares breast 3NbHBst cDNA clone IMAGE:188362 3' similar to gb:M10942_cds1 metallothionein-le gene mRNA sequence /clone=IMAGE:188362 /clone_end=3' /gb=H43642 /gi=919694 /ug=Hs.418241 /len=452	H43642	Hs.418241	
3138	0.001342	NCAG1 (NCAG1), mRNA /cds=(1477,5145) /gb=NM_032160 /gi=23943786 /ug=Hs.124673 /len=9528	NM_032160	Hs.124673	NP_115536
3139	0.045762	mRNA for KIAA0530 protein, partial cds. /cds=(1,4693) /gb=AB011102 /gi=3043583 /ug=Hs.173081 /len=6578	AB011102	Hs.173081	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3140	0.037084	DKFZp451H2115_r1 451 (synonym: hlcc1) spinal cord cDNA clone DKFZp451H2115 5', mRNA sequence /clone=DKFZp451H2115 /clone_end=5' /gb=AL589315 /gi=13243087 /ug=Hs.332004 /len=517	AL589315	Hs.332004	
3144	0.00104	solute carrier family 20 (phosphate transporter), member 1 (SLC20A1), mRNA /cds=(371,2410) /gb=NM_005415 /gi=7382462 /ug=Hs.78452 /len=3220	NM_005415	Hs.78452	NP_005406
3165	0.031506	SOCS box-containing WD protein SWiP-1 (WSB1), transcript variant 3, mRNA /cds=(317,1051) /gb=NM_134264 /gi=20143909 /ug=Hs.187991 /len=4243	NM_134264	Hs.187991	NP_599027
3166	0.037084	hypothetical protein FLJ13855 (FLJ13855), mRNA /cds=(328,1068) /gb=NM_023079 /gi=20149671 /ug=Hs.168232 /len=3053	NM_023079	Hs.168232	NP_075567
3172	0.006684	myocyte-specific enhancer factor 2A (MEF2A) gene, last coding exon, and complete cds	U49020		
3174	1.92E-04	lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA /cds=(69,476) /gb=NM_002305 /gi=6006015 /ug=Hs.382367 /len=526	NM_002305	Hs.382367	NP_002296
3175	0.018779	spermidine/spermine N1-acetyltransferase (SAT), mRNA /cds=(166,681) /gb=NM_002970 /gi=4506788 /ug=Hs.28491 /len=1060	NM_002970	Hs.28491	NP_002961
3180	0.045762	ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794 /ug=Hs.418650 /len=801	NM_002032	Hs.418650	NP_002023
3191	0.045762	hypothetical protein MGC14353 (MGC14353), mRNA /cds=(77,448) /gb=NM_032731 /gi=21362103 /ug=Hs.74346 /len=728	NM_032731	Hs.74346	NP_116120
3219	4.63E-04	actin, alpha, cardiac muscle (ACTC), mRNA /cds=(1,1134) /gb=NM_005159 /gi=10938011 /ug=Hs.118127 /len=1294	NM_005159	Hs.118127	NP_005150
3233	0.002995	uncharacterized hematopoietic stem/progenitor cells protein MDS027 (MDS027), mRNA /cds=(21,248) /gb=NM_018462 /gi=27544938 /ug=Hs.421654 /len=888	NM_018462	Hs.421654	NP_060932
3244	0.024901	hypothetical protein FLJ13352 (FLJ13352), mRNA /cds=(97,1053) /gb=NM_024592 /gi=13375784 /ug=Hs.22972 /len=2271	NM_024592	Hs.22972	NP_078868

Spot	p-value	Description	Gen Accession No.	Unigene Accession No.	Protein Accession No.
3254	0.035141	splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(156,821) /gb=NM_003016 /gi=4506898 /ug=Hs.73965 /len=1879	NM_003016	Hs.73965	NP_003007
3280	0.010023	RETROVIRUS-RELATED POLYPROTEIN	P11369		
3288	0.005811	cyclin G2 (CCNG2), mRNA /cds=(136,1170) /gb=NM_004354 /gi=4757935 /ug=Hs.79069 /len=2044	NM_004354	Hs.79069	NP_004345
3294	0.035141	NCK adaptor protein 1 (NCK1), mRNA /cds=(117,1250) /gb=NM_006153 /gi=20070226 /ug=Hs.54589 /len=1947	NM_006153	Hs.54589	NP_006144
3316	0.003487	glutathione S-transferase M3 (brain) (GSTM3), mRNA /cds=(311,988) /gb=NM_000849 /gi=23065551 /ug=Hs.2006 /len=1572	NM_000849	Hs.2006	NP_000840
3318	0.019933	endothelial protein C receptor	AB026584		
3327	0.048172	goliath protein (GP), mRNA /cds=(428,1258) /gb=NM_018434 /gi=20127393 /ug=Hs.155718 /len=1445	NM_018434	Hs.155718	NP_060904
3328	0.029809	retinoblastoma-like 2 (p130) (RBL2), mRNA /cds=(70,3489) /gb=NM_005611 /gi=21361291 /ug=Hs.79362 /len=4853	NM_005611	Hs.79362	NP_005602
3354	0.005038	ribosomal protein L23 (RPL23), mRNA /cds=(27,449) /gb=NM_000978 /gi=14591907 /ug=Hs.234518 /len=493	NM_000978	Hs.234518	NP_000969
3390	0.041237	phosphoribosyl pyrophosphate synthetase associated protein 2 (PRPSAP2), mRNA /cds=(212,1321) /gb=NM_002767 /gi=22538484 /ug=Hs.13339 /len=1890	NM_002767	Hs.13339	NP_002758
3405	0.022422	lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA /cds=(69,476) /gb=NM_002305 /gi=6006015 /ug=Hs.382367 /len=526	NM_002305	Hs.382367	NP_002296
3428	0.026643	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing) (ERCC3), mRNA /cds=(96,2444) /gb=NM_000122 /gi=4557562 /ug=Hs.77929 /len=2751	NM_000122	Hs.77929	NP_000113
3440	0.00767	TERF1 (TRF1)-interacting nuclear factor 2 (TINF2), mRNA /cds=(263,1327) /gb=NM_012461 /gi=6912715 /ug=Hs.7797 /len=2095	NM_012461	Hs.7797	NP_036593
3461	0.025168	ribosomal protein S3 (RPS3), mRNA /cds=(19,750) /gb=NM_001005 /gi=15718686 /ug=Hs.414990 /len=843	NM_001005	Hs.414990	NP_000996

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3512	0.043451	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
3520	0.016639	mRNA; cDNA DKFZp586F2423 (from clone DKFZp586F2423) /gb=AL080209 /gi=5262698 /ug=Hs.13659 /len=4254	AL080209	Hs.13659	
3538	0.035141	insulin-like growth factor binding protein 6 (IGFBP6), mRNA /cds=(54,776) /gb=NM_002178 /gi=11321592 /ug=Hs.274313 /len=952	NM_002178	Hs.274313	NP_002169
3539	0.037084	ubiquitin C (UBC), mRNA /cds=(136,2193) /gb=NM_021009 /gi=20149305 /ug=Hs.183704 /len=2309	NM_021009	Hs.183704	NP_066289
3548	0.011417	eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA /cds=(23,1360) /gb=NM_001568 /gi=4503520 /ug=Hs.106673 /len=1510	NM_001568	Hs.106673	NP_001559
3567	0.045762	FUS/TLS protein gene, alternatively spliced products, exons 1 through 15 and complete cds	AF071213		
3599	0.031506	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 /len=1705	NM_006855	Hs.250696	NP_057839
3606	0.035141	nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs) (NOLA3), mRNA /cds=(98,292) /gb=NM_018648 /gi=15011920 /ug=Hs.14317 /len=556	NM_018648	Hs.14317	NP_061118
3607	0.028189	mitochondrion, complete genome	NC_001807		
3609	0.005038	mortality factor 4 like 1 (MORF4L1), mRNA /cds=(132,1103) /gb=NM_006791 /gi=5803101 /ug=Hs.6353 /len=1766	NM_006791	Hs.6353	NP_006782
3619	0.043451	cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419 /len=802	NM_001861	Hs.433419	NP_001852
3641	1.56E-04	hypothetical protein CL25084 (CL25084), mRNA /cds=(132,1583) /gb=NM_015701 /gi=20070263 /ug=Hs.7100 /len=2412	NM_015701	Hs.7100	NP_056516
3642	0.001721	chromosome 1 open reading frame 22 (C1orf22), mRNA /cds=(54,2723) /gb=NM_025191 /gi=19923618 /ug=Hs.279951 /len=6298	NM_025191	Hs.279951	NP_079467

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3643	0.048172	chitinase 3-like 2 (CHI3L2), mRNA /cds=(36,1193) /gb=NM_004000 /gi=11993934 /ug=Hs.154138 /len=1418	NM_004000	Hs.154138	NP_003991
3733	0.048172	MAGEF1 protein (MAGEF1), mRNA /cds=(177,1103) /gb=NM_022149 /gi=11545891 /ug=Hs.306123 /len=1615	NM_022149	Hs.306123	NP_071432
3751	0.033283	S100 calcium binding protein A11 (calgizzarin) (S100A11), mRNA /cds=(121,438) /gb=NM_005620 /gi=5032056 /ug=Hs.417004 /len=595	NM_005620	Hs.417004	NP_005611
3763	0.01471	UI-E-EO1-aja-c-22-0-UI.s1 UI-E-EO1 cDNA clone UI-E-EO1-aja-c-22-0-UI 3', mRNA sequence /clone=UI-E-EO1-aja-c-22-0-UI /clone_end=3' /gb=BM680199 /gi=18990095 /ug=Hs.355581 /len=1071	BM680199	Hs.355581	
3787	0.008208	secretory leukocyte protease inhibitor (antileukoproteinase) (SLPI), mRNA /cds=(23,421) /gb=NM_003064 /gi=15834622 /ug=Hs.251754 /len=598	NM_003064	Hs.251754	NP_003055
3805	0.012975	hypothetical protein FLJ10350 (FLJ10350), mRNA /cds=(676,2340) /gb=NM_018067 /gi=21361780 /ug=Hs.177596 /len=2811	NM_018067	Hs.177596	NP_060537
3828	0.035141	osteoblast specific factor 2 (fasciclin I-like) (OSF-2), mRNA /cds=(12,2522) /gb=NM_006475 /gi=5453833 /ug=Hs.136348 /len=3213	NM_006475	Hs.136348	NP_006466
3830	0.018779	eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=NM_001959 /gi=16519564 /ug=Hs.421608 /len=961	NM_001959	Hs.421608	NP_066944
3835	0.018779	NEL-like 2 (chicken) (NELL2), mRNA /cds=(97,2547) /gb=NM_006159 /gi=5453765 /ug=Hs.79389 /len=3198	NM_006159	Hs.79389	NP_006150
3840	0.019933	sorcini (SRI), mRNA /cds=(13,609) /gb=NM_003130 /gi=4507206 /ug=Hs.422340 /len=952	NM_003130	Hs.422340	NP_003121
3856	0.002566	translocase of inner mitochondrial membrane 10 (yeast) homolog (TIMM10)	NM_012456		NP_036588
3861	0.011417	basigin (BSG), mRNA /cds=(58,867) /gb=NM_001728 /gi=4502458 /ug=Hs.74631 /len=1638	NM_001728	Hs.74631	NP_001719
3872	0.028189	6-phosphogluconolactonase (PGLS), mRNA /cds=(18,794) /gb=NM_012088 /gi=6912585 /ug=Hs.100071 /len=1010	NM_012088	Hs.100071	NP_036220

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3888	0.041237	SAC2 suppressor of actin mutations 2-like (yeast) (SACM2L), transcript variant 1, mRNA /cds=(245,2416) /gb=NM_080564 /gi=18379336 /ug=Hs.169407 /len=2985	NM_080564	Hs.169407	NP_542131
3917	0.048172	ribosomal protein L30 (RPL30), mRNA /cds=(71,418) /gb=NM_000989 /gi=15812218 /ug=Hs.334807 /len=524	NM_000989	Hs.334807	NP_000980
3924	0.010701	ubiquitin specific protease 10 (USP10), mRNA /cds=(114,2510) /gb=NM_005153 /gi=24307888 /ug=Hs.78829 /len=3009	NM_005153	Hs.78829	NP_005144
3936	0.043451	hypothetical protein AF311304 (AF311304), mRNA /cds=(21,185) /gb=NM_031214 /gi=13654285 /ug=Hs.300624 /len=1138	NM_031214	Hs.300624	NP_112491
3942	0.010979	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) (SPTAN1), mRNA /cds=(103,7521) /gb=NM_003127 /gi=4507190 /ug=Hs.77196 /len=7787	NM_003127	Hs.77196	NP_003118
3954	0.002192	esophageal cancer related gene 4 protein (ECRG4), mRNA /cds=(109,555) /gb=NM_032411 /gi=14165275 /ug=Hs.43125 /len=772	NM_032411	Hs.43125	NP_115787
3970	0.043451	HSPC182 protein (HSPC182), mRNA /cds=(66,650) /gb=NM_014188 /gi=7661831 /ug=Hs.30026 /len=1059	NM_014188	Hs.30026	NP_054907
3976	0.01471	SFRS protein kinase 2 (SRPK2), mRNA /cds=(188,2248) /gb=NM_003138 /gi=4507220 /ug=Hs.78353 /len=3745	NM_003138	Hs.78353	NP_003129
3990	0.041237	hypothetical protein HSPC155 (HSPC155), mRNA /cds=(241,744) /gb=NM_016406 /gi=7705480 /ug=Hs.177507 /len=1137	NM_016406	Hs.177507	NP_057490
4000	0.028189	KIAA1156	AB032982		NP_055665
4004	0.001585	bromodomain containing 2 (BRD2), mRNA /cds=(1702,4107) /gb=NM_005104 /gi=12408641 /ug=Hs.75243 /len=4693	NM_005104	Hs.75243	NP_005095
4022	0.043451	MDS024 protein (MDS024), mRNA /cds=(65,838) /gb=NM_021820 /gi=11141892 /ug=Hs.425659 /len=2103	NM_021820	Hs.425659	NP_068592
4037	5.57E-04	coagulation factor VIII	AF062515		
4038	0.006234	multiple PDZ domain protein (MPDZ), mRNA /cds=(47,6175) /gb=NM_003829 /gi=4505230 /ug=Hs.169378 /len=6582	NM_003829	Hs.169378	NP_003820

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4046	2.04E-05	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa (POLR2C), transcript variant gamma, mRNA /cds=(58,885) /gb=NM_032940 /gi=14702170 /ug=Hs.79402 /len=1782	NM_032940	Hs.79402	NP_116558
4092	0.028189	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) (NDUFS3), mRNA /cds=(13,807) /gb=NM_004551 /gi=4758787 /ug=Hs.429506 /len=899	NM_004551	Hs.429506	NP_004542
4093	0.01471	coated vesicle membrane protein (RNP24), mRNA /cds=(24,629) /gb=NM_006815 /gi=21314646 /ug=Hs.75914 /len=2060	NM_006815	Hs.75914	NP_006806
4103	0.001459	protein kinase C, nu (PRKCN), mRNA /cds=(556,3228) /gb=NM_005813 /gi=6563384 /ug=Hs.143460 /len=5792	NM_005813	Hs.143460	NP_005804
4118	0.043451	HSPC154 protein (HSPC154), mRNA /cds=(200,946) /gb=NM_014177 /gi=7661809 /ug=Hs.7922 /len=1343	NM_014177	Hs.7922	NP_054896
4121	0.025168	natural killer cell enhancing factor (NKEFA)	L19184		NP_002565
4131	0.039115	thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556	NM_021109	Hs.75968	NP_066932
4133	0.00767	vimentin (VIM), mRNA /cds=(123,1523) /gb=NM_003380 /gi=4507894 /ug=Hs.297753 /len=1851	NM_003380	Hs.297753	NP_000995
4152	0.035141	CG9469 gene product	AAF57414		
4159	0.048172	suppressor of Ty 3 (S. cerevisiae) (SUPT3H), mRNA /cds=(72,1025) /gb=NM_003599 /gi=4507308 /ug=Hs.304173 /len=1165	NM_003599	Hs.304173	NP_003590
4189	9.54E-04	fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4), transcript variant 2, mRNA /cds=(507,2642) /gb=NM_022977 /gi=12669908 /ug=Hs.81452 /len=5356	NM_022977	Hs.81452	NP_075266
4194	0.009383	peptidase D (PEPD), mRNA /cds=(17,1498) /gb=NM_000285 /gi=4557834 /ug=Hs.73947 /len=1888	NM_000285	Hs.73947	NP_000276
4200	0.012175	PTD013 protein (PTD013), mRNA /cds=(87,812) /gb=NM_015952 /gi=7706269 /ug=Hs.22679 /len=982	NM_015952	Hs.22679	NP_057036
4206	0.048172	ring finger protein 4 (RNF4), mRNA /cds=(271,843) /gb=NM_002938 /gi=4506560 /ug=Hs.66394 /len=2918	NM_002938	Hs.66394	NP_002929

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4213	0.035141	collagen, type V, alpha 2 (COL5A2), mRNA /cds=(158,4648) /gb=NM_000393 /gi=16554580 /ug=Hs.82985 /len=6217	NM_000393	Hs.82985	NP_000384
4223	1.27E-04	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 (SLC25A20), mitochondrial protein encoded by nuclear gene, mRNA /cds=(37,942) /gb=NM_000387 /gi=6006040 /ug=Hs.13845 /len=1219	NM_000387	Hs.13845	NP_000378
4267	0.029809	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein (ID1), mRNA /cds=(36,500) /gb=NM_002165 /gi=4504568 /ug=Hs.75424 /len=926	NM_002165	Hs.75424	NP_851998
4294	0.029809	hypothetical protein FLJ20729 (FLJ20729), mRNA /cds=(135,1547) /gb=NM_017953 /gi=20149642 /ug=Hs.5111 /len=2821	NM_017953	Hs.5111	NP_060423
4317	0.039115	accessory protein BAP31 (DXS1357E), mRNA /cds=(137,877) /gb=NM_005745 /gi=10047078 /ug=Hs.291904 /len=1314	NM_005745	Hs.291904	NP_005736
4339	0.043451	lamin B receptor (LBR), mRNA /cds=(76,1923) /gb=NM_002296 /gi=4504960 /ug=Hs.152931 /len=3714	NM_002296	Hs.152931	NP_002287
4364	0.039115	oxysterol binding protein-like 8 (OSBPL8), mRNA /cds=(481,3150) /gb=NM_020841 /gi=22035617 /ug=Hs.109694 /len=7239	NM_020841	Hs.109694	NP_065892
4369	0.035141	ribosomal protein L36 (RPL36), transcript variant 2, mRNA /cds=(153,470) /gb=NM_015414 /gi=16117793 /ug=Hs.433411 /len=545	NM_015414	Hs.433411	NP_378669
4390	0.013819	ataxia telangiectasia and Rad3 related (ATR), mRNA /cds=(106,8040) /gb=NM_001184 /gi=20143978 /ug=Hs.77613 /len=8265	NM_001184	Hs.77613	NP_001175
4407	0.045762	15 kDa selenoprotein (SEP15), mRNA /cds=(5,493) /gb=NM_004261 /gi=20127464 /ug=Hs.90606 /len=1519	NM_004261	Hs.90606	NP_004252
4419	0.029809	KIAA0742	AB018285		NP_060903
4425	0.005038	gene amplified in squamous cell carcinoma 1 (GASC1), mRNA /cds=(151,3321) /gb=NM_015061 /gi=24307986 /ug=Hs.149918 /len=4239	NM_015061	Hs.149918	NP_055876
4435	0.010701	clone IMAGE:3633225, mRNA /gb=BC012758 /gi=15706478 /ug=Hs.356377 /len=1914	BC012758	Hs.356377	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4440	0.031506	alcohol dehydrogenase 5 (class III), chi polypeptide (ADH5), mRNA /cds=(163,1287) /gb=NM_000671 /gi=11496890 /ug=Hs.78989 /len=2496	NM_000671	Hs.78989	NP_000662
4462	0.016639	collagen, type I, alpha 2 (COL1A2), mRNA /cds=(138,4238) /gb=NM_000089 /gi=21536289 /ug=Hs.179573 /len=5084	NM_000089	Hs.179573	NP_000080
4509	0.019933	likely ortholog of mouse deleted in polyposis 1 (DP1), mRNA /cds=(38,595) /gb=NM_005669 /gi=24307896 /ug=Hs.178112 /len=3000	NM_005669	Hs.178112	NP_005660
4513	0.029809	hepatitis B virus x interacting protein (HBXIP), mRNA /cds=(56,331) /gb=NM_006402 /gi=5454169 /ug=Hs.433355 /len=605	NM_006402	Hs.433355	NP_006393
4515	0.045762	cell recognition molecule CASPR3 (CASPR3), transcript variant 1, mRNA /cds=(408,3872) /gb=NM_033655 /gi=16306508 /ug=Hs.212839 /len=5017	NM_033655	Hs.212839	NP_387504
4530	0.00767	I factor (complement) (IF), mRNA /cds=(15,1766) /gb=NM_000204 /gi=4504578 /ug=Hs.36602 /len=1963	NM_000204	Hs.36602	NP_000195
4531	0.048172	erythrocyte membrane protein band 4.1-like 2 (EPB41L2), mRNA /cds=(45,3062) /gb=NM_001431 /gi=4503578 /ug=Hs.7857 /len=4336	NM_001431	Hs.7857	NP_001422
4536	0.035141	splicing factor, arginine/serine-rich 2, interacting protein (SF2AS1), mRNA /cds=(1211,4657) /gb=NM_004719 /gi=4759171 /ug=Hs.51957 /len=5307	NM_004719	Hs.51957	NP_004710
4540	0.007162	decay accelerating factor for complement (CD55, Cromer blood group system) (DAF), mRNA /cds=(66,1211) /gb=NM_000574 /gi=10835142 /ug=Hs.1369 /len=2102	NM_000574	Hs.1369	NP_000565
4556	0.045762	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL), mRNA /cds=(52,2595) /gb=NM_002863 /gi=4506352 /ug=Hs.771 /len=2643	NM_002863	Hs.771	NP_002854
4584	0.008779	Rho-associated, coiled-coil containing protein kinase 1 (ROCK1), mRNA /cds=(1,4065) /gb=NM_005406 /gi=4885582 /ug=Hs.17820 /len=4065	NM_005406	Hs.17820	NP_005397
4654	0.041237	RNA helicase-related protein (RNAHP), mRNA /cds=(18,2147) /gb=NM_007372 /gi=11321631 /ug=Hs.8765 /len=3347	NM_007372	Hs.8765	NP_031398

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4672	0.017682	coronin, actin binding protein, 1C (CORO1C), mRNA /cds=(97,1521) /gb=NM_014325 /gi=27477119 /ug=Hs.17377 /len=3828	NM_014325	Hs.17377	NP_055140
4678	0.002372	hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA /cds=(49,2259) /gb=NM_000414 /gi=4504504 /ug=Hs.75441 /len=2593	NM_000414	Hs.75441	NP_000405
4693	0.002192	H3 histone, family 3B (H3.3B) (H3F3B), mRNA /cds=(118,528) /gb=NM_005324 /gi=21264598 /ug=Hs.180877 /len=1662	NM_005324	Hs.180877	NP_005315
4694	0.001459	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) (HIF1A), mRNA /cds=(265,2745) /gb=NM_001530 /gi=4504384 /ug=Hs.197540 /len=3933	NM_001530	Hs.197540	NP_851397
4703	0.013819	leukotriene A4 hydrolase (LTA4H), mRNA /cds=(69,1904) /gb=NM_000895 /gi=4505028 /ug=Hs.81118 /len=2060	NM_000895	Hs.81118	NP_000886
4720	0.026643	heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA /cds=(91,1992) /gb=NM_005826 /gi=14141188 /ug=Hs.15265 /len=2663	NM_005826	Hs.15265	NP_005817
4724	0.035141	Niemann-Pick disease, type C1 (NPC1), mRNA /cds=(124,3960) /gb=NM_000271 /gi=4557802 /ug=Hs.76918 /len=4673	NM_000271	Hs.76918	NP_000262
4736	0.003758	E74-like factor 1 (ets domain transcription factor) (ELF1), mRNA /cds=(256,2115) /gb=NM_172373 /gi=27363483 /ug=Hs.154365 /len=3526	NM_172373	Hs.154365	NP_758961
4741	0.033283	hypothetical protein MGC21981 (MGC21981), mRNA /cds=(66,764) /gb=NM_153267 /gi=23397567 /ug=Hs.131987 /len=1727	NM_153267	Hs.131987	NP_694999
4758	0.026643	inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA /cds=(86,1366) /gb=NM_002192 /gi=4504698 /ug=Hs.727 /len=1840	NM_002192	Hs.727	NP_002183
4769	0.018779	mitochondrial ribosomal protein L37 (MRPL37), nuclear gene encoding mitochondrial protein, mRNA /cds=(78,1349) /gb=NM_016491 /gi=22547133 /ug=Hs.4209 /len=1511	NM_016491	Hs.4209	NP_057575
4774	0.019933	ribosomal protein S19 (RPS19), mRNA /cds=(70,507) /gb=NM_001022 /gi=14591914 /ug=Hs.298262 /len=569	NM_001022	Hs.298262	NP_001013
4778	0.026643	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994

Spot	p-value	Description	Gen Accession No.	Unigene Accession No.	Protein Accession No.
4782	0.01471	CDC-like kinase1 (CLK1), mRNA /cds=(156,1610) /gb=NM_004071 /gi=4758007 /ug=Hs.2083 /len=1834	NM_004071	Hs.2083	NP_004062
4794	0.012975	mitochondrion, complete genome	NC_001807		
4798	0.022422	Rho-associated, coiled-coil containing protein kinase 2 (ROCK2), mRNA /cds=(455,4621) /gb=NM_004850 /gi=6633807 /ug=Hs.58617 /len=6409	NM_004850	Hs.58617	NP_004841
4805	0.001234	high-mobility group box 1 (HMGB1), mRNA /cds=(77,724) /gb=NM_002128 /gi=20149538 /ug=Hs.6727 /len=1207	NM_002128	Hs.6727	NP_002119
4810	0.041237	mRNA; cDNA DKFZp727I051 (from clone DKFZp727I051); partial cds /cds=(1,2099) /gb=AL117478 /gi=5911952 /ug=Hs.239370 /len=2480	AL117478	Hs.239370	NP_056412
4814	0.012975	ribosomal protein L10a (RPL10A), mRNA /cds=(16,669) /gb=NM_007104 /gi=15431287 /ug=Hs.425293 /len=700	NM_007104	Hs.425293	NP_009035
4819	0.015649	ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500	NM_000991	Hs.356371	NP_000982
4821	0.01471	eukaryotic translation termination factor 1 (ETF1), mRNA /cds=(136,1449) /gb=NM_004730 /gi=4759033 /ug=Hs.77324 /len=3653	NM_004730	Hs.77324	NP_004721
4823	0.035141	SH3-domain GRB2-like endophilin B2 (SH3GLB2), mRNA /cds=(147,1334) /gb=NM_020145 /gi=24431995 /ug=Hs.30002 /len=2039	NM_020145	Hs.30002	NP_064530
4837	0.041237	UI-H-BW1-amj-g-07-0-UI.s1 NCI_CGAP_Sub7 cDNA clone IMAGE:3070261 3', mRNA sequence /clone=IMAGE:3070261 /clone_end=3' /gb=BF513214 /gi=11598393 /ug=Hs.445888 /len=620	BF513214	Hs.445888	
4848	0.005811	aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 2, mRNA /cds=(61,7308) /gb=NM_013227 /gi=6995993 /ug=Hs.2159 /len=7434	NM_013227	Hs.2159	NP_037359
4863	0.025168	FLJ14819 fis, clone OVARC1000241, moderately similar to HYPOXIA- INDUCIBLE FACTOR 1 ALPHA	AK027725		NP_690009
4874	0.016639	ankyrin repeat domain 10 (ANKRD10), mRNA /cds=(136,1398) /gb=NM_017664 /gi=8923103 /ug=Hs.172572 /len=2509	NM_017664	Hs.172572	NP_060134

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4877	0.023762	chromosome 20 open reading frame 31 (C20orf31), mRNA /cds=(83,1819) /gb=NM_018217 /gi=8922666 /ug=Hs.93871 /len=1885	NM_018217	Hs.93871	NP_060687
4878	0.009383	ribosomal protein L35a (RPL35A), mRNA /cds=(74,406) /gb=NM_000996 /gi=16117790 /ug=Hs.288544 /len=511	NM_000996	Hs.288544	NP_000987
4880	0.035141	cDNA FLJ12776 fis, clone NT2RP2001678. /gb=AK022838 /gi=10434465 /ug=Hs.372558 /len=2629	AK022838	Hs.372558	
4884	0.006293	geranylgeranyl diphosphate synthase 1 (GGPS1), mRNA /cds=(233,1135) /gb=NM_004837 /gi=21359876 /ug=Hs.55498 /len=1489	NM_004837	Hs.55498	NP_004828
4886	0.026643	proteasome (prosome, macropain) subunit, beta type, 4 (PSMB4), mRNA /cds=(24,818) /gb=NM_002796 /gi=22538466 /ug=Hs.89545 /len=925	NM_002796	Hs.89545	NP_002787
4912	0.037157	ATP synthase, H transporting, mitochondrial F0 complex, subunit g (ATP5L), mRNA /cds=(60,371) /gb=NM_006476 /gi=21359881 /ug=Hs.107476 /len=580	NM_006476	Hs.107476	NP_006467
4915	0.004357	hypothetical protein FLJ13149 (FLJ13149), mRNA /cds=(291,2585) /gb=NM_021826 /gi=11141902 /ug=Hs.112188 /len=2836	NM_021826	Hs.112188	NP_068598
4916	0.015649	collagen, type X, alpha 1 (Schmid metaphyseal chondrodysplasia) (COL10A1), mRNA /cds=(97,2139) /gb=NM_000493 /gi=18105031 /ug=Hs.179729 /len=3285	NM_000493	Hs.179729	NP_000484
4919	0.001459	KIAA0436 mRNA, partial cds. /cds=(1,2070) /gb=AB007896 /gi=2662152 /ug=Hs.110 /len=4661	AB007896	Hs.110	
4921	0.025168	cDNA FLJ10423 fis, clone NT2RP1000259. /gb=AK001285 /gi=7022444 /ug=Hs.106909 /len=1837	AK001285	Hs.106909	
4925	0.012175	tm68a09.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2163256 3', mRNA sequence /clone=IMAGE:2163256 /clone_end=3' /gb=AI498805 /gi=4390787 /ug=Hs.436349 /len=460	AI498805	Hs.436349	
4926	0.00767	nuclear receptor coactivator 1 (NCOA1), transcript variant 2, mRNA /cds=(202,4401) /gb=NM_147223 /gi=22538456 /ug=Hs.74002 /len=4721	NM_147223	Hs.74002	NP_671766

Spot	p-value	Description	Gene Accession No.	Unigene Acc ssion No.	Protein Accession No.
4942	0.018779	AF034176 mRNA (Tripodis and Ragoussis) cDNA clone ntcon5 contig /gb=AF034176 /gi=2707738 /ug=Hs.188882 /len=7232	AF034176	Hs.188882	
4944	0.005412	hypothetical protein FLJ20452 (FLJ20452), mRNA /cds=(15,614) /gb=NM_017828 /gi=21361660 /ug=Hs.351327 /len=1948	NM_017828	Hs.351327	NP_060298
4945	0.012975	eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa (EIF3S5), mRNA /cds=(7,1080) /gb=NM_003754 /gi=4503518 /ug=Hs.7811 /len=1231	NM_003754	Hs.7811	NP_003745
4946	0.001661	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_079425	Hs.77385	NP_524149
4950	0.045762	mRNA for KIAA1865 protein, partial cds. /cds=(622,2793) /gb=AB058768 /gi=14017946 /ug=Hs.179260 /len=3641	AB058768	Hs.179260	
4956	0.018779	hypothetical protein FLJ20671 (FLJ20671), mRNA /cds=(43,465) /gb=NM_017924 /gi=19923511 /ug=Hs.180201 /len=2855	NM_017924	Hs.180201	NP_060394
4957	0.012975	TcD37 (HTCD37), mRNA /cds=(137,1498) /gb=NM_021222 /gi=24308262 /ug=Hs.78524 /len=2995	NM_021222	Hs.78524	NP_067045
4958	0.016639	cDNA FLJ10235 fis, clone HEMBB1000339. /gb=AK001097 /gi=7022149 /ug=Hs.406774 /len=2530	AK001097	Hs.406774	
4962	0.027396	mRNA for KIAA1320 protein, partial cds. /cds=(2051,3754) /gb=AB037741 /gi=7243020 /ug=Hs.117414 /len=5321	AB037741	Hs.117414	
4970	0.022422	decorin (DCN), transcript variant A1, mRNA /cds=(200,1279) /gb=NM_001920 /gi=19743844 /ug=Hs.433989 /len=1751	NM_001920	Hs.433989	NP_598014
4972	0.048172	HSPC092	AF161355		NP_055238
4983	0.035151	F-box and leucine-rich repeat protein 3A (FBXL3A), mRNA /cds=(298,1584) /gb=NM_012158 /gi=16306583 /ug=Hs.7540 /len=3489	NM_012158	Hs.7540	NP_036290
4986	0.003487	adrenomedullin (ADM), mRNA /cds=(157,714) /gb=NM_001124 /gi=4501944 /ug=Hs.394 /len=1449	NM_001124	Hs.394	NP_001115
4988	0.010701	translocase of outer mitochondrial membrane 70 A (yeast) (TOMM70A), mRNA /cds=(92,1918) /gb=NM_014820 /gi=7662672 /ug=Hs.21198 /len=4017	NM_014820	Hs.21198	NP_055635

Spot	p-value	Description	Gene Accession No.	Unig ne Accession No.	Protein Accession No.
4989	0.045762	chloride intracellular channel 5 (CLIC5), mRNA /cds=(298,1053) /gb=NM_016929 /gi=8393146 /ug=Hs.283021 /len=2380	NM_016929	Hs.283021	NP_058625
4992	0.005412	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) (TFPI), mRNA /cds=(1,915) /gb=NM_006287 /gi=6715569 /ug=Hs.170279 /len=915	NM_006287	Hs.170279	NP_006278
4994	0.007162	Nedd4 binding protein 2 (N4BP2), mRNA /cds=(339,5600) /gb=NM_018177 /gi=20357506 /ug=Hs.18685 /len=6760	NM_018177	Hs.18685	NP_060647
5005	0.029809	ankyrin repeat and SOCS box-containing 1 (ASB1), mRNA /cds=(87,1094) /gb=NM_016114 /gi=22208961 /ug=Hs.153489 /len=6798	NM_016114	Hs.153489	NP_057198
5011	0.001721	ALL1 fused gene from 5q31 (AF5Q31), mRNA /cds=(338,3829) /gb=NM_014423 /gi=7656878 /ug=Hs.231967 /len=4235	NM_014423	Hs.231967	NP_055238
5016	0.025168	ribosomal protein L17 (RPL17), mRNA /cds=(287,841) /gb=NM_000985 /gi=14591906 /ug=Hs.82202 /len=898	NM_000985	Hs.82202	NP_000976
5060	5.57E-04	HIF-1 responsive RTP801 (RTP801), mRNA /cds=(198,896) /gb=NM_019058 /gi=9506686 /ug=Hs.111244 /len=1760	NM_019058	Hs.111244	NP_061931
5061	0.016639	wc09c01.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:2314656 3' similar to gb:J05016 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR mRNA sequence /clone=IMAGE:2314656 /clone_end=3' /gb=AI674177 /gi=4874657 /ug=Hs.200089 /len=526	AI674177	Hs.200089	
5069	0.009383	hsp70-interacting protein (HSPBP1), mRNA /cds=(312,1400) /gb=NM_012267 /gi=21361406 /ug=Hs.53066 /len=1795	NM_012267	Hs.53066	NP_036399
5090	0.033283	U3 small nuclear RNA gene	M14061		
5094	0.006234	sterol regulatory element binding transcription factor 2 (SREBF2), mRNA /cds=(170,3595) /gb=NM_004599 /gi=27477112 /ug=Hs.108689 /len=4325	NM_004599	Hs.108689	NP_004590
5102	2.35E-04	cofilin 1 (non-muscle) (CFL1), mRNA /cds=(52,552) /gb=NM_005507 /gi=5031634 /ug=Hs.180370 /len=1059	NM_005507	Hs.180370	NP_005498

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5105	0.017682	hypothetical protein FLJ20312 (FLJ20312), mRNA /cds=(384,803) /gb=NM_017761 /gi=20127576 /ug=Hs.7862 /len=2382	NM_017761	Hs.7862	NP_060231
5108	0.005412	calponin 2 (CNN2), mRNA /cds=(28,957) /gb=NM_004368 /gi=4758017 /ug=Hs.169718 /len=2122	NM_004368	Hs.169718	NP_004359
5111	0.00767	chromosome 14 open reading frame 94 (C14orf94), mRNA /cds=(211,1302) /gb=NM_017815 /gi=8923395 /ug=Hs.8886 /len=1618	NM_017815	Hs.8886	NP_060285
5155	0.043451	phosphoglycerate kinase 1 (PGK1), mRNA /cds=(70,1323) /gb=NM_000291 /gi=22095338 /ug=Hs.78771 /len=2338	NM_000291	Hs.78771	NP_000282
5156	0.006684	myosin regulatory light chain (MLC-B), mRNA /cds=(117,635) /gb=NM_033546 /gi=15809015 /ug=Hs.233936 /len=967	NM_033546	Hs.233936	NP_291024
5161	0.018779	basic transcription factor 3 (BTF3), mRNA /cds=(240,728) /gb=NM_001207 /gi=20070129 /ug=Hs.101025 /len=952	NM_001207	Hs.101025	NP_001198
5187	0.012175	zinc finger protein 281 (ZNF281), mRNA /cds=(24,2711) /gb=NM_012482 /gi=6912751 /ug=Hs.59757 /len=3029	NM_012482	Hs.59757	NP_036614
5192	0.043451	mRNA for KIAA0232 protein, partial cds. /cds=(435,4643) /gb=D86985 /gi=20521849 /ug=Hs.79276 /len=7840	D86985	Hs.79276	
5195	0.003233	angiopoietin-like 4 (ANGPTL4), transcript variant 1, mRNA /cds=(196,1416) /gb=NM_139314 /gi=21536397 /ug=Hs.9613 /len=1967	NM_139314	Hs.9613	NP_647475
5204	0.039115	stathmin-like 3 (STMN3), mRNA /cds=(83,625) /gb=NM_015894 /gi=14670374 /ug=Hs.285753 /len=2255	NM_015894	Hs.285753	NP_056978
5205	0.043451	mRNA for KIAA1458 protein, partial cds. /cds=(22,1860) /gb=AB040891 /gi=7959176 /ug=Hs.27263 /len=5843	AB040891	Hs.27263	
5206	0.017682	CAAX box 1 (CXX1), mRNA /cds=(335,964) /gb=NM_003928 /gi=4503180 /ug=Hs.250708 /len=1209	NM_003928	Hs.250708	NP_003919
5234	0.031506	deiodinase, iodothyronine, type II (DIO2), transcript variant 1, mRNA /cds=(707,1528) /gb=NM_013989 /gi=7549802 /ug=Hs.154424 /len=6735	NM_013989	Hs.154424	NP_054644
5235	0.012975	major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA /cds=(63,863) /gb=NM_002124 /gi=4504410 /ug=Hs.375570 /len=1182	NM_002124	Hs.375570	NP_002115
5249	0.026643	Escherichia coli K-12 MG1655 section 343 of 400 of the complete genome	AE000453		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5250	0.010023	SFRS protein kinase 1 (SRPK1), mRNA /cds=(10,1974) /gb=NM_003137 /gi=15834623 /ug=Hs.75761 /len=4244	NM_003137	Hs.75761	NP_003128
5261	0.031506	replication factor C (activator 1) 4, 37kDa (RFC4), mRNA /cds=(284,1375) /gb=NM_002916 /gi=4506490 /ug=Hs.35120 /len=1446	NM_002916	Hs.35120	NP_002907
5264	0.005412	small GTP-binding protein RAB1A	AF226873		NP_033022
5283	0.037084	transforming, acidic coiled-coil containing protein 2 (TACC2), mRNA /cds=(87,3167) /gb=NM_006997 /gi=11119413 /ug=Hs.272023 /len=3686	NM_006997	Hs.272023	NP_008928
5287	0.01471	hypothetical protein FLJ30945 fis, clone FEBRA2007613	AK055507		NP_071911
5330	0.001234	discs, large 7 (Drosophila) (DLG7), mRNA /cds=(218,2758) /gb=NM_014750 /gi=21361644 /ug=Hs.77695 /len=2979	NM_014750	Hs.77695	NP_055565
5332	0.041237	clone IMAGE:5262128, mRNA, partial cds /cds=(1,1409) /gb=BC035036 /gi=23271542 /ug=Hs.356247 /len=4728	BC035036	Hs.356247	
5386	0.037084	ATPase, H transporting, lysosomal 9kDa, V0 subunit e (ATP6V0E), mRNA /cds=(76,321) /gb=NM_003945 /gi=19913435 /ug=Hs.415629 /len=849	NM_003945	Hs.415629	NP_003936
5391	0.005412	palmdelphin (PALMD), mRNA /cds=(286,1941) /gb=NM_017734 /gi=16306484 /ug=Hs.14606 /len=2581	NM_017734	Hs.14606	NP_060204
5411	0.045762	DKFZp566J2446 (from clone DKFZp566J2446)	AL050082		NP_008944
5412	0.026643	SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA /cds=(373,1902) /gb=NM_000346 /gi=4557852 /ug=Hs.2316 /len=3936	NM_000346	Hs.2316	NP_000337
5419	0.045321	ATP synthase, H transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1 (ATP5G1), mRNA /cds=(120,530) /gb=NM_005175 /gi=4885080 /ug=Hs.80986 /len=631	NM_005175	Hs.80986	NP_005166
5420	0.001459	matrilin 3 (MATN3) precursor, mRNA /cds=(64,1524) /gb=NM_002381 /gi=13518040 /ug=Hs.278461 /len=2599	NM_002381	Hs.278461	NP_002372
5432	0.025168	zinc finger protein 202 (ZNF202), mRNA /cds=(11,1957) /gb=NM_003455 /gi=10835040 /ug=Hs.9443 /len=4053	NM_003455	Hs.9443	NP_003446
5433	0.017682	actin related protein 2/3 complex, subunit 5, 16kDa (ARPC5), mRNA /cds=(192,647) /gb=NM_005717 /gi=23238212 /ug=Hs.82425 /len=2000	NM_005717	Hs.82425	NP_005708

Spot	p-valu	Description	Gene Accession No.	Unigen Accession No.	Protein Accession No.
5438	0.010023	mitochondrion, complete genome	NC_001807		
5445	0.005051	hypothetical protein FLJ20312 (FLJ20312), mRNA /cds=(384,803) /gb=NM_017761 /gi=20127576 /ug=Hs.7862 /len=2382	NM_017761	Hs.7862	NP_060231
5448	0.037084	eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA /cds=(16,1239) /gb=NM_001967 /gi=9945313 /ug=Hs.173912 /len=1864	NM_001967	Hs.173912	NP_001958
5449	0.004357	mRNA; cDNA DKFZp667D2123 (from clone DKFZp667D2123) /gb=AL832786 /gi=21733368 /ug=Hs.283643 /len=3000	AL832786	Hs.283643	
5451	0.035141	tumor protein, translationally-controlled 1 (TPT1), mRNA /cds=(95,613) /gb=NM_003295 /gi=4507668 /ug=Hs.401448 /len=830	NM_003295	Hs.401448	NP_003286
5476	0.004687	meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA /cds=(315,2729) /gb=NM_005930 /gi=5174560 /ug=Hs.117242 /len=3676	NM_005930	Hs.117242	NP_005921
5477	0.002372	lectin, galactoside-binding, soluble, 3 (galectin 3) (LGALS3), mRNA /cds=(19,771) /gb=NM_002306 /gi=4504982 /ug=Hs.621 /len=914	NM_002306	Hs.621	NP_002297
5482	0.023762	proliferating cell nuclear antigen (PCNA), mRNA /cds=(119,904) /gb=NM_002592 /gi=4505640 /ug=Hs.78996 /len=1231	NM_002592	Hs.78996	NP_002583
5497	0.033283	zinc finger, DHHC domain containing 4 (ZDHHC4), mRNA /cds=(222,1256) /gb=NM_018106 /gi=21361700 /ug=Hs.5268 /len=1704	NM_018106	Hs.5268	NP_060576
5498	0.045762	polymerase (RNA) II (DNA directed) polypeptide G (POLR2G), mRNA /cds=(107,625) /gb=NM_002696 /gi=4505946 /ug=Hs.14839 /len=828	NM_002696	Hs.14839	NP_002687
5499	0.041237	adaptor-related protein complex 2, sigma 1 subunit (AP2S1), transcript variant AP17, mRNA /cds=(71,499) /gb=NM_004069 /gi=11038644 /ug=Hs.119591 /len=781	NM_004069	Hs.119591	NP_067586
5509	0.019933	brain protein 44-like (BRP44L), mRNA /cds=(123,452) /gb=NM_016098 /gi=7706368 /ug=Hs.108725 /len=988	NM_016098	Hs.108725	NP_057182
5511	0.010023	cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419 /len=802	NM_001861	Hs.433419	NP_001852

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5514	0.00767	ribosomal protein L4 (RPL4), mRNA /cds=(57,1340) /gb=NM_000968 /gi=16579884 /ug=Hs.286 /len=1449	NM_000968	Hs.286	NP_000959
5517	0.026643	Hypothetical protein (cDNA FLJ20702 fis, clone KAIA2174)	AK000709		
5550	0.033283	fusion, derived from t(12;16) malignant liposarcoma (FUS), mRNA /cds=(79,1659) /gb=NM_004960 /gi=4826733 /ug=Hs.99969 /len=1824	NM_004960	Hs.99969	NP_004951
5551	0.037084	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit (HADHA), mRNA /cds=(35,2326) /gb=NM_000182 /gi=20127407 /ug=Hs.75860 /len=2972	NM_000182	Hs.75860	NP_000173
5584	0.019933	regulator of nonsense transcripts 1. (RENT1), mRNA /cds=(232,3588) /gb=NM_002911 /gi=18375672 /ug=Hs.12719 /len=5300	NM_002911	Hs.12719	NP_002902
5590	0.026643	eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), mRNA /cds=(15,752) /gb=NM_004846 /gi=4757701 /ug=Hs.19122 /len=974	NM_004846	Hs.19122	NP_004837
5640	0.012175	nonhistone protein HMG1	M21683		
5644	0.029809	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700	NM_002211	Hs.287797	NP_596867
5671	0.006684	EPC-1 (=M76979 PEDF;U29953;M90493)	U57446		
5672	0.004357	clone IMAGE:5265581, mRNA /gb=BC035165 /gi=23272508 /ug=Hs.400548 /len=2237	BC035165	Hs.400548	
5752	0.013819	F-box and leucine-rich repeat protein 7 (FBXL7), mRNA /cds=(482,1957) /gb=NM_012304 /gi=21071079 /ug=Hs.76798 /len=4562	NM_012304	Hs.76798	NP_036436
5770	0.023762	APG12 autophagy 12-like (S. cerevisiae), DKFZp761A0411 (from clone DKFZp761A0411) mRNA; cDNA /cds=UNKNOWN /gb=AL161968 /gi=7328057 /ug=Hs.264482 /len=3285	AL161968	Hs.264482	NP_004698
5789	0.015649	ribosomal protein L31 (RPL31), mRNA /cds=(28,405) /gb=NM_000993 /gi=15812219 /ug=Hs.184014 /len=442	NM_000993	Hs.184014	NP_000984

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5814	0.015649	ribosomal protein L36a-like (RPL36AL), mRNA /cds=(95,415) /gb=NM_001001 /gi=16306559 /ug=Hs.419465 /len=537	NM_001001	Hs.419465	NP_000992
5821	0.028189	ribosomal protein L11 (RPL11), mRNA /cds=(21,557) /gb=NM_000975 /gi=15431289 /ug=Hs.388664 /len=609	NM_000975	Hs.388664	NP_000966
5824	0.033283	activated RNA polymerase II transcription cofactor 4 (PC4), mRNA /cds=(57,440) /gb=NM_006713 /gi=19923783 /ug=Hs.349506 /len=1336	NM_006713	Hs.349506	NP_006704
5827	0.010701	PHKB gene (exon 25)	X84930		
5870	0.035141	Similar to cyclin K, clone MGC:9113 IMAGE:3907416, mRNA, complete cds /cds=(110,1174) /gb=BC015935 /gi=16198507 /ug=Hs.375192 /len=1925	BC015935	Hs.375192	
5899	0.006684	Fas (TNFRSF6) associated factor 1 (FAF1), transcript variant 1, mRNA /cds=(454,2406) /gb=NM_007051 /gi=19528653 /ug=Hs.25821 /len=2610	NM_007051	Hs.25821	NP_572051
5918	0.026643	Mus musculus mitochondrion, complete genome	NC_001569		
5928	0.021147	ubiquitin-conjugating enzyme E2B (RAD6 (UBE2B), mRNA /cds=(422,880) /gb=NM_003337 /gi=4507770 /ug=Hs.811 /len=2591	NM_003337	Hs.811	NP_003328
5934	0.006762	enthoprotin (ENTH), mRNA /cds=(102,1979) /gb=NM_014666 /gi=7661967 /ug=Hs.132853 /len=3336	NM_014666	Hs.132853	NP_055481
5937	0.045762	mitogen-activated protein kinase 9 (MAPK9), transcript variant 3, mRNA /cds=(50,1198) /gb=NM_139069 /gi=21237741 /ug=Hs.246857 /len=1947	NM_139069	Hs.246857	NP_620709
5938	0.013819	chaperonin containing TCP1, subunit 3 (gamma) (CCT3), mRNA /cds=(1,1635) /gb=NM_005998 /gi=5174726 /ug=Hs.1708 /len=1901	NM_005998	Hs.1708	NP_005989
5939	0.012175	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 S. cerevisiae) (BTAF1), mRNA /cds=(118,5667) /gb=NM_003972 /gi=27477069 /ug=Hs.180930 /len=6345	NM_003972	Hs.180930	NP_003963
5959	0.013819	germline T-cell receptor beta chain	U66061		
5971	0.008779	UI-E-CI1-abg-f-09-0-UI.r1 UI-E-CI1 cDNA clone UI-E-CI1-abg-f-09-0-UI 5', mRNA sequence /clone=UI-E-CI1-abg-f-09-0-UI /clone_end=5' /gb=BM691540 /gi=19004798 /ug=Hs.172047 /len=1039	BM691540	Hs.172047	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5974	0.015649	KIAA0266 gene product (KIAA0266), mRNA /cds=(734,3034) /gb=NM_021645 /gi=11063982 /ug=Hs.127376 /len=5585	NM_021645	Hs.127376	NP_067677
5976	0.045762	ox06a01.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:1655496 3' similar to gb:M86849 GAP JUNCTION BETA-2 PROTEIN mRNA sequence /clone=IMAGE:1655496 /clone_end=3' /gb=AI033469 /gi=3254422 /ug=Hs.386279 /len=551	AI033469	Hs.386279	
6004	0.048172	UDP-glucose pyrophosphorylase 2 (UGP2), mRNA /cds=(85,1611) /gb=NM_006759 /gi=13027637 /ug=Hs.77837 /len=1832	NM_006759	Hs.77837	NP_006750
6006	0.018779	ribosomal protein L23a (RPL23A), mRNA /cds=(22,492) /gb=NM_000984 /gi=17105393 /ug=Hs.419463 /len=546	NM_000984	Hs.419463	NP_000975
6009	4.63E-04	methylmalonyl Coenzyme A mutase (MUT), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,2329) /gb=NM_000255 /gi=4557766 /ug=Hs.155212 /len=2798	NM_000255	Hs.155212	NP_000246
6027	0.025168	mesenchyme homeo box 2 (growth arrest specific homeo box) (MEOX2), mRNA /cds=(182,1093) /gb=NM_005924 /gi=21396478 /ug=Hs.77858 /len=2284	NM_005924	Hs.77858	NP_005915
6028	0.043451	protein-tyrosine kinase, trkB	X75958		NP_006171
6034	0.026643	NRAS-related gene (D1S155E), mRNA /cds=(428,2824) /gb=NM_007158 /gi=20070240 /ug=Hs.69855 /len=4076	NM_007158	Hs.69855	NP_009089
6037	0.006234	splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(156,821) /gb=NM_003016 /gi=4506898 /ug=Hs.73965 /len=1879	NM_003016	Hs.73965	NP_003007
6042	0.007162	laminin, gamma 1 (formerly LAMB2) (LAMC1), mRNA /cds=(300,5129) /gb=NM_002293 /gi=9845497 /ug=Hs.432855 /len=7923	NM_002293	Hs.432855	NP_002284
6068	0.048172	mitochondrial ribosomal protein L27 (MRPL27), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA /cds=(32,316) /gb=NM_148571 /gi=22547130 /ug=Hs.7736 /len=2472	NM_148571	Hs.7736	NP_683412

Spot	p-value	Description	Gene Accession No.	Unig ne Accession No.	Protein Accession No.
6069	0.022422	stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4 (SERP1), mRNA /cds=(316,516) /gb=NM_014445 /gi=19923408 /ug=Hs.76698 /len=2488	NM_014445	Hs.76698	NP_055260
6083	0.033283	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA /cds=(9,536) /gb=NM_002495 /gi=4505368 /ug=Hs.10758 /len=668	NM_002495	Hs.10758	NP_002486
6106	0.009383	EST (ym17h04.s1 clone 48282 3')	H11657		
6139	0.015649	cofilin 1 (non-muscle) (CFL1), mRNA /cds=(52,552) /gb=NM_005507 /gi=5031634 /ug=Hs.180370 /len=1059	NM_005507	Hs.180370	NP_005498
6159	0.045762	general transCRiption factor 2-I (GTF2I)	AF038968		NP_127496
6182	0.028189	signal sequence receptor, gamma (translocon-associated protein gamma) (SSR3), mRNA /cds=(57,614) /gb=NM_007107 /gi=6005883 /ug=Hs.28707 /len=3061	NM_007107	Hs.28707	NP_009038
6185	0.001721	chloride intracellular channel 4 (CLIC4), mRNA /cds=(198,959) /gb=NM_013943 /gi=7330334 /ug=Hs.25035 /len=4318	NM_013943	Hs.25035	NP_039234
6205	0.039115	jumping translocation breakpoint (JTB), mRNA /cds=(433,873) /gb=NM_006694 /gi=5729888 /ug=Hs.6396 /len=1040	NM_006694	Hs.6396	NP_006685
6262	0.018779	UDP-glucose ceramide glucosyltransferase-like 2 (UGCG2), mRNA /cds=(72,4622) /gb=NM_020121 /gi=11386200 /ug=Hs.22983 /len=4848	NM_020121	Hs.22983	NP_064506
6322	0.006684	ubiquitin specific protease 9 (USP9Y)	XM_000563		
6341	0.005811	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 (ADAMTS1), mRNA /cds=(294,3146) /gb=NM_006988 /gi=11038653 /ug=Hs.8230 /len=4459	NM_006988	Hs.8230	NP_008919
6403	0.004687	glyceronephosphate O-acyltransferase (GNPAT), mRNA /cds=(158,2200) /gb=NM_014236 /gi=7657133 /ug=Hs.12482 /len=2470	NM_014236	Hs.12482	NP_055051
6428	0.028189	serologically defined colon cancer antigen 1 (SDCCAG1), mRNA /cds=(183,1271) /gb=NM_004713 /gi=4759077 /ug=Hs.388584 /len=2078	NM_004713	Hs.388584	NP_004704
6429	0.033283	ubiquitin A-52 residue ribosomal protein fusion product 1 (UBA52), mRNA /cds=(39,425) /gb=NM_003333 /gi=15451941 /ug=Hs.5308 /len=515	NM_003333	Hs.5308	NP_003324

Spot	p-value	Description	Gene Accession No.	Unigen Accession No.	Protein Accession No.
6442	0.025168	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), mRNA /cds=(115,1677) /gb=NM_004566 /gi=4758899 /ug=Hs.195471 /len=4322	NM_004566	Hs.195471	NP_004557
6529	0.00767	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA /cds=(95,1048) /gb=NM_020529 /gi=10092618 /ug=Hs.81328 /len=1550	NM_020529	Hs.81328	NP_065390
6543	0.045762	general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), mRNA /cds=(161,1807) /gb=NM_005316 /gi=19923304 /ug=Hs.89578 /len=2989	NM_005316	Hs.89578	NP_005307
6565	0.002995	PTK9 protein tyrosine kinase 9 (PTK9), mRNA /cds=(61,1113) /gb=NM_002822 /gi=4506274 /ug=Hs.82643 /len=3000	NM_002822	Hs.82643	NP_002813
6566	0.019933	RAB11A, member RAS oncogene family (RAB11A), mRNA /cds=(104,754) /gb=NM_004663 /gi=20149549 /ug=Hs.75618 /len=2474	NM_004663	Hs.75618	NP_004654
6570	0.002773	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), mRNA /cds=(25,753) /gb=NM_003574 /gi=20070155 /ug=Hs.9006 /len=1390	NM_003574	Hs.9006	NP_003565
6577	0.012175	ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=NM_004152 /gi=9845504 /ug=Hs.281960 /len=986	NM_004152	Hs.281960	NP_004143
6583	0.045762	KIAA0170 gene product (KIAA0170), mRNA /cds=(14,6283) /gb=NM_014641 /gi=7661965 /ug=Hs.433653 /len=6940	NM_014641	Hs.433653	NP_055456
6592	0.00767	methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,1111) /gb=NM_006636 /gi=13699869 /ug=Hs.154672 /len=2154	NM_006636	Hs.154672	NP_006627
6593	0.019933	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae) (NHP2L1), mRNA /cds=(95,481) /gb=NM_005008 /gi=4826859 /ug=Hs.182255 /len=1475	NM_005008	Hs.182255	NP_004999
6600	0.043451	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone) (GNRH1), mRNA /cds=(1075,1353) /gb=NM_000825 /gi=19923125 /ug=Hs.82963 /len=1512	NM_000825	Hs.82963	NP_000816

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6603	0.001133	tm68a09.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2163256 3', mRNA sequence /clone=IMAGE:2163256 /clone_end=3' /gb=AI498805 /gi=4390787 /ug=Hs.436349 /len=460	AI498805	Hs.436349	
6612	0.037084	high-mobility group box 1 (HMGB1), mRNA /cds=(77,724) /gb=NM_002128 /gi=20149538 /ug=Hs.6727 /len=1207	NM_002128	Hs.6727	NP_002119
6618	0.022422	eukaryotic translation elongation factor 1 gamma (EEF1G), mRNA /cds=(38,1351) /gb=NM_001404 /gi=25453475 /ug=Hs.256184 /len=1429	NM_001404	Hs.256184	NP_001395
6623	0.048172	attractin (ATRIN), transcript variant 1, mRNA /cds=(80,4369) /gb=NM_139321 /gi=21450860 /ug=Hs.194019 /len=8645	NM_139321	Hs.194019	NP_647538
6630	0.005038	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase) (NDUFS6), mRNA /cds=(11,385) /gb=NM_004553 /gi=4758791 /ug=Hs.49767 /len=547	NM_004553	Hs.49767	NP_004544
6633	0.019933	HSPCO34 protein (LOC51668), mRNA /cds=(58,402) /gb=NM_016126 /gi=7706382 /ug=Hs.46967 /len=598	NM_016126	Hs.46967	NP_057210
6650	0.043451	tetratricopeptide repeat domain 1 (TTC1), mRNA /cds=(51,929) /gb=NM_003314 /gi=4507710 /ug=Hs.7733 /len=1407	NM_003314	Hs.7733	NP_003305
6651	0.028189	tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10), mRNA /cds=(96,941) /gb=NM_003810 /gi=23510439 /ug=Hs.83429 /len=1776	NM_003810	Hs.83429	NP_003801
6654	0.017682	pM5 protein (PM5), mRNA /cds=(1,3669) /gb=NM_014287 /gi=10947030 /ug=Hs.439182 /len=4182	NM_014287	Hs.439182	NP_055102
6666	0.01471	tigger transposable element derived 1 (TIGD1), mRNA /cds=(635,2410) /gb=NM_145702 /gi=22209000 /ug=Hs.351348 /len=2448	NM_145702	Hs.351348	NP_663748
6683	0.021147	lamin A/C (LMNA), transcript variant 1, mRNA /cds=(213,2207) /gb=NM_170707 /gi=27436945 /ug=Hs.377973 /len=3181	NM_170707	Hs.377973	NP_733822
6708	0.043451	erythroid differentiation-related factor 1	AF040247		
6715	0.022422	KIAA0076 gene product (KIAA0076), mRNA /cds=(87,5183) /gb=NM_014780 /gi=7661893 /ug=Hs.51039 /len=5253	NM_014780	Hs.51039	NP_055595
6722	0.025168	syndecan 1 (SDC1), mRNA /cds=(253,1185) /gb=NM_002997 /gi=21359855 /ug=Hs.82109 /len=2484	NM_002997	Hs.82109	NP_002988

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Prot in Accession No.
6734	0.031506	PAI-1 mRNA-binding protein (PAI-RBP1), mRNA /cds=(86,1249) /gb=NM_015640 /gi=7661625 /ug=Hs.165998 /len=2201	NM_015640	Hs.165998	NP_056455
6750	0.033283	ADP-ribosylation-like factor 6 interacting protein 4 (ARL6IP4), mRNA /cds=(63,719) /gb=NM_016638 /gi=7706183 /ug=Hs.103561 /len=952	NM_016638	Hs.103561	NP_061164
6752	0.01471	tumor endothelial marker 6 (TEM6), mRNA /cds=(93,3710) /gb=NM_022748 /gi=17511208 /ug=Hs.12210 /len=6702	NM_022748	Hs.12210	NP_073585
6755	0.012975	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 (SLC25A3), nuclear gene encoding mitochondrial protein, transcript variant 1b, mRNA /cds=(49,1134) /gb=NM_002635 /gi=4505774 /ug=Hs.78713 /len=1330	NM_002635	Hs.78713	NP_005879
6760	0.023762	2-hydroxyphytanoyl-CoA lyase (HPCL2), mRNA /cds=(100,1836) /gb=NM_012260 /gi=6912417 /ug=Hs.63290 /len=1976	NM_012260	Hs.63290	NP_036392
6772	0.029809	hypothetical protein FLJ22301 (FLJ22301), mRNA /cds=(696,2054) /gb=NM_024836 /gi=13376246 /ug=Hs.181406 /len=2952	NM_024836	Hs.181406	NP_079112
6794	0.037084	chromosome 13 open reading frame 12 (C13orf12), mRNA /cds=(76,501) /gb=NM_015932 /gi=21361533 /ug=Hs.279813 /len=1352	NM_015932	Hs.279813	NP_057016
6796	0.007162	hypothetical protein, clone 2746033 (HSA272196), mRNA /cds=(39,593) /gb=NM_018405 /gi=24475639 /ug=Hs.8179 /len=861	NM_018405	Hs.8179	NP_060875
6813	0.039115	constitutive photomorphogenic protein (COP1), mRNA /cds=(1,2196) /gb=NM_022457 /gi=21359962 /ug=Hs.105737 /len=2196	NM_022457	Hs.105737	NP_071902
6829	0.023762	transforming growth factor, alpha (TGFA), mRNA /cds=(32,514) /gb=NM_003236 /gi=4507460 /ug=Hs.170009 /len=4119	NM_003236	Hs.170009	NP_003227
6835	0.012975	mRNA for KIAA0191 gene, partial cds. /cds=(1,4553) /gb=D83776 /gi=1228034 /ug=Hs.12413 /len=5203	D83776	Hs.12413	
6846	0.035141	mitogen-activated protein kinase kinase 7 (MAP3K7), transcript variant A, mRNA /cds=(306,2045) /gb=NM_003188 /gi=21735560 /ug=Hs.7510 /len=2912	NM_003188	Hs.7510	NP_663306

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6851	0.013819	Similar to expressed sequence AW111961, clone IMAGE:5268751, mRNA /gb=BC041839 /gi=27693117 /ug=Hs.237642 /len=3713	BC041839	Hs.237642	
6861	0.005811	mRNA; cDNA DKFZp434A012 (from clone DKFZp434A012) /gb=AL096752 /gi=5419888 /ug=Hs.306327 /len=2248	AL096752	Hs.306327	
6880	0.031506	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1), nuclear gene encoding mitochondrial protein, mRNA /cds=(463,702) /gb=NM_001864 /gi=18105034 /ug=Hs.421621 /len=783	NM_001864	Hs.421621	NP_001855
6881	0.006684	uncharacterized hematopoietic stem/progenitor cells protein MDS029 (MDS029), mRNA /cds=(112,438) /gb=NM_018464 /gi=8923929 /ug=Hs.43549 /len=636	NM_018464	Hs.43549	NP_060934
6894	0.009383	Werner helicase interacting protein (WHIP), transcript variant 1, mRNA /cds=(192,2189) /gb=NM_020135 /gi=18426901 /ug=Hs.236828 /len=2670	NM_020135	Hs.236828	NP_569079
6920	0.017682	thioredoxin (TXN), mRNA /cds=(64,381) /gb=NM_003329 /gi=4507744 /ug=Hs.432922 /len=501	NM_003329	Hs.432922	NP_003320
6935	0.048172	FtsJ 3 (E. coli) (FTSJ3), mRNA /cds=(72,2615) /gb=NM_017647 /gi=17017990 /ug=Hs.257486 /len=2999	NM_017647	Hs.257486	NP_060117
6941	0.039115	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2 (SMARCC2), transcript variant 1, mRNA /cds=(33,3677) /gb=NM_003075 /gi=21237804 /ug=Hs.236030 /len=4039	NM_003075	Hs.236030	NP_620706
6969	0.010023	oligophrenin 1 (OPHN1), mRNA /cds=(638,3046) /gb=NM_002547 /gi=4505506 /ug=Hs.128824 /len=7350 (=FLJ11206)	NM_002547	Hs.128824	NP_002538
6972	0.035141	similar to zinc finger protein (LOC91172), mRNA (=FLJ12859,=FLJ11645)	XM_036627		
6974	0.045762	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa (NDUFAB1), mRNA /cds=(25,495) /gb=NM_005003 /gi=4826851 /ug=Hs.5556 /len=663	NM_005003	Hs.5556	NP_004994
6989	0.012175	transmembrane 9 superfamily member 1 (TM9SF1), mRNA /cds=(35,1855) /gb=NM_006405 /gi=21361314 /ug=Hs.91586 /len=2138	NM_006405	Hs.91586	NP_006396

Spot	p-value	Description	Gene Accession No.	Unig ne Accession No.	Protein Accession No.
7005	0.005811	clone MGC:24133 IMAGE:4693393, mRNA, complete cds /cds=(61,528) /gb=BC017973 /gi=22450811 /ug=Hs.288010 /len=946	BC017973	Hs.288010	NP_777556
7022	0.019933	ribosomal protein S29 (RPS29), mRNA /cds=(31,201) /gb=NM_001032 /gi=13904868 /ug=Hs.539 /len=346	NM_001032	Hs.539	NP_001023
7033	0.029809	vacuolar protein sorting 35 (yeast) (VPS35), mRNA /cds=(48,2438) /gb=NM_018206 /gi=17999540 /ug=Hs.264190 /len=2707	NM_018206	Hs.264190	NP_060676
7042	0.047799	mRNA for KIAA0261 gene, partial cds. /cds=(1,3866) /gb=D87450 /gi=1665788 /ug=Hs.154978 /len=6155	D87450	Hs.154978	
7043	0.009383	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), mRNA /cds=(556,1788) /gb=NM_000430 /gi=6031206 /ug=Hs.77318 /len=5581	NM_000430	Hs.77318	NP_000421
7048	0.012975	twisted gastrulation 1 (Drosophila) (TWSG1), mRNA /cds=(106,777) /gb=NM_020648 /gi=21314788 /ug=Hs.247302 /len=3693	NM_020648	Hs.247302	NP_065699
7068	3.16E-04	KIAA1128 protein (KIAA1128), mRNA /cds=(553,2253) /gb=NM_018999 /gi=24308130 /ug=Hs.81897 /len=7248	NM_018999	Hs.81897	NP_061872
7097	0.037084	translocating chain-associating membrane protein (TRAM), mRNA /cds=(92,1216) /gb=NM_014294 /gi=19923404 /ug=Hs.4147 /len=2722	NM_014294	Hs.4147	NP_055109
7098	0.039115	inactive progesterone receptor, 23 kD (TEBP), mRNA /cds=(107,589) /gb=NM_006601 /gi=23308578 /ug=Hs.278270 /len=1490	NM_006601	Hs.278270	NP_006592
7102	0.010023	survival of motor neuron protein interacting protein 1 (SIP1), mRNA /cds=(84,926) /gb=NM_003616 /gi=4506960 /ug=Hs.102456 /len=1285	NM_003616	Hs.102456	NP_003607
7107	0.00767	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function) (ENPP4), mRNA /cds=(49,1410) /gb=NM_014936 /gi=7662357 /ug=Hs.54037 /len=4312	NM_014936	Hs.54037	NP_055751
7127	0.026643	actin-related protein 10 (S. cerevisiae) (ACTR10), mRNA /cds=(81,1334) /gb=NM_018477 /gi=8923711 /ug=Hs.274369 /len=1621	NM_018477	Hs.274369	NP_060947

Spot	p-value	Description	Gen Accession No.	Unig ne Accession No.	Protein Accession No.
7143	0.041237	benzodiazapine receptor (peripheral) (BZRP), nuclear gene encoding mitochondrial protein, transcript variant PBR, mRNA /cds=(88,597) /gb=NM_000714 /gi=21536444 /ug=Hs.202 /len=848	NM_000714	Hs.202	NP_009295
7166	0.01471	transducer of ERBB2, 1 (TOB1), mRNA /cds=(36,1073) /gb=NM_005749 /gi=22035666 /ug=Hs.178137 /len=1830	NM_005749	Hs.178137	NP_005740
7175	0.029809	AGENCOURT_6853421 NIH_MGC_99 cDNA clone IMAGE:5926418 5', mRNA sequence /clone=IMAGE:5926418 /clone_end=5' /gb=BQ064669 /gi=19893520 /ug=Hs.380699 /len=969	BQ064669	Hs.380699	
7176	0.012175	tumor protein, translationally-controlled 1 (TPT1), mRNA /cds=(95,613) /gb=NM_003295 /gi=4507668 /ug=Hs.401448 /len=830	NM_003295	Hs.401448	NP_003286
7178	0.005412	supervillin (SVIL), transcript variant 2, mRNA /cds=(754,7398) /gb=NM_021738 /gi=11496981 /ug=Hs.154567 /len=8300	NM_021738	Hs.154567	NP_068506
7187	0.015649	collagen, type V, alpha 1 (COL5A1), mRNA /cds=(383,5899) /gb=NM_000093 /gi=16554578 /ug=Hs.146428 /len=6496	NM_000093	Hs.146428	NP_000084
7201	0.043451	glutathione peroxidase 1 (GPX1), mRNA /cds=(319,924) /gb=NM_000581 /gi=10834975 /ug=Hs.76686 /len=1134	NM_000581	Hs.76686	NP_000572
7234	0.00104	chemokine-like factor 1 (CKLF1), mRNA /cds=(148,606) /gb=NM_016951 /gi=10092593 /ug=Hs.15159 /len=689	NM_016951	Hs.15159	NP_058647
7240	0.023762	block of proliferation 1 (BOP1), mRNA /cds=(43,2283) /gb=NM_015201 /gi=21389316 /ug=Hs.30736 /len=2396	NM_015201	Hs.30736	NP_056016
7243	6.11E-04	calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2), transcript variant 1, mRNA /cds=(830,2596) /gb=NM_006549 /gi=27437014 /ug=Hs.108708 /len=5620	NM_006549	Hs.108708	NP_757380
7244	0.011417	Nedd-4-like ubiquitin-protein ligase, clone MGC:17353 IMAGE:3453212, mRNA, complete cds	BC013645.1	Hs.333382	AAH13645.1
7279	0.028189	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB (BDP1), mRNA /cds=(205,6969) /gb=NM_018429 /gi=21281668 /ug=Hs.272808 /len=7207	NM_018429	Hs.272808	NP_060899

Spot	p-value	D scription	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7283	0.048172	HSPC056 protein (HSPC056), mRNA /cds=(145,972) /gb=NM_014154 /gi=7661763 /ug=Hs.422287 /len=2879	NM_014154	Hs.422287	NP_054873
7284	0.033283	GK003 protein (GK003), mRNA /cds=(10,690) /gb=NM_020192 /gi=21281666 /ug=Hs.83313 /len=901	NM_020192	Hs.83313	NP_064577
7285	0.043451	MR4-ET0140-070501-014-g01 ET0140 cDNA, mRNA sequence /gb=BQ331564 /gi=20972721 /ug=Hs.442329 /len=219	BQ331564	Hs.442329	
7288	0.022422	KIAA0800 gene product (KIAA0800), mRNA /cds=(169,4692) /gb=NM_014703 /gi=7662315 /ug=Hs.118738 /len=5984	NM_014703	Hs.118738	NP_055518
7310	0.023762	UI-H-BI2-agp-f-12-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2725031 3', mRNA sequence /clone=IMAGE:2725031 /clone_end=3' /gb=AW292456 /gi=6699092 /ug=Hs.437793 /len=745	AW292456	Hs.437793	
7313	0.048172	translocation protein 1 (TLOC1), mRNA /cds=(613,1812) /gb=NM_003262 /gi=14602425 /ug=Hs.8146 /len=3091	NM_003262	Hs.8146	NP_003253
7319	0.039115	mRNA for KIAA0276 gene, partial cds. /cds=(1,932) /gb=D87466 /gi=1665816 /ug=Hs.240112 /len=4185	D87466	Hs.240112	
7320	0.006684	RNA-binding region (RNP1, RRM) containing 4 (RNPC4), mRNA /cds=(187,1461) /gb=NM_018107 /gi=21361701 /ug=Hs.4997 /len=2442	NM_018107	Hs.4997	NP_060577
7321	0.017682	translocase of inner mitochondrial membrane 17 A (yeast) (TIMM17A), mRNA /cds=(8,523) /gb=NM_006335 /gi=5454119 /ug=Hs.20716 /len=1645	NM_006335	Hs.20716	NP_006326
7322	0.031506	BM-017 (=ALEX3)	AF208859		NP_808817
7331	0.037084	AGENCOURT_8856629 Lupski_sciatic_nerve cDNA clone IMAGE:6200636 5', mRNA sequence /clone=IMAGE:6200636 /clone_end=5' /gb=BQ947179 /gi=22362657 /ug=Hs.356605 /len=1277	BQ947179	Hs.356605	
7343	0.007162	hypothetical protein FLJ12619 (FLJ12619), mRNA /cds=(539,1228) /gb=NM_030939 /gi=21359961 /ug=Hs.7779 /len=2444	NM_030939	Hs.7779	NP_112201
7349	0.005412	dermatopontin (DPT), mRNA /cds=(7,612) /gb=NM_001937 /gi=4755134 /ug=Hs.80552 /len=717	NM_001937	Hs.80552	NP_001928

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7357	0.008208	chromosome 6 open reading frame 33 (C6orf33), mRNA /cds=(165,1229) /gb=NM_133367 /gi=19115959 /ug=Hs.239388 /len=4650	NM_133367	Hs.239388	NP_588608
7360	0.028189	clone IMAGE:5016712, mRNA /gb=BC032119 /gi=22749564 /ug=Hs.400876 /len=1185	BC032119	Hs.400876	
7361	0.037084	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 (SMARCA4), mRNA /cds=(277,5220) /gb=NM_003072 /gi=21071055 /ug=Hs.78202 /len=5681	NM_003072	Hs.78202	NP_003063
7378	0.022422	regulator of G-protein signalling 10 (RGS10), mRNA /cds=(44,547) /gb=NM_002925 /gi=11184225 /ug=Hs.82280 /len=664	NM_002925	Hs.82280	NP_002916
7387	0.037157	ribosomal protein L4 (RPL4), mRNA /cds=(57,1340) /gb=NM_000968 /gi=16579884 /ug=Hs.286 /len=1449	NM_000968	Hs.286	NP_000959
7390	0.045762	peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA /cds=(45,542) /gb=NM_021130 /gi=10863926 /ug=Hs.401787 /len=753	NM_021130	Hs.401787	NP_066953
7414	6.69E-04	tetraspanin similar to TM4SF9 (DC-TM4F2), mRNA /cds=(79,891) /gb=NM_030927 /gi=13569888 /ug=Hs.101395 /len=2556	NM_030927	Hs.101395	NP_112189
7420	0.029809	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) (GALNT1), mRNA /cds=(32,1711) /gb=NM_020474 /gi=13124890 /ug=Hs.80120 /len=3778	NM_020474	Hs.80120	NP_065207
7427	0.003487	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_153649	Hs.85844	NP_705935
7455	0.039115	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) (AGPAT2), mRNA /cds=(67,903) /gb=NM_006412 /gi=6041664 /ug=Hs.209119 /len=1522	NM_006412	Hs.209119	NP_006403
7491	0.019933	chromosome 20 open reading frame 149 (C20orf149), mRNA /cds=(150,494) /gb=NM_024299 /gi=13236523 /ug=Hs.79625 /len=803	NM_024299	Hs.79625	NP_077275
7508	0.012175	mRNA for RCC1-like protein (TD-60 gene) /cds=(236,1804) /gb=AJ421269 /gi=27526612 /ug=Hs.284146 /len=4114	AJ421269	Hs.284146	NP_061185

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Prot in Accession No.
7548	0.015649	methionine adenosyltransferase II, beta (MAT2B), mRNA /cds=(73,1077) /gb=NM_013283 /gi=20127525 /ug=Hs.54642 /len=2054	NM_013283	Hs.54642	NP_037415
7574	0.039115	ubiquitin-conjugating enzyme E2N (UBC13 yeast) (UBE2N), mRNA /cds=(64,522) /gb=NM_003348 /gi=4507792 /ug=Hs.75355 /len=1203	NM_003348	Hs.75355	NP_003339
7576	0.002192	cytochrome P450, family 1, subfamily B, polypeptide 1 (CYP1B1), mRNA /cds=(373,2004) /gb=NM_000104 /gi=13325059 /ug=Hs.154654 /len=5128	NM_000104	Hs.154654	NP_000095
7577	0.00767	chromosome 14 open reading frame 108 (C14orf108), mRNA /cds=(407,1879) /gb=NM_018229 /gi=21361775 /ug=Hs.106210 /len=3088	NM_018229	Hs.106210	NP_060699
7581	0.017682	FK506 binding protein 5 (FKBP5), mRNA /cds=(154,1527) /gb=NM_004117 /gi=17149847 /ug=Hs.7557 /len=3781	NM_004117	Hs.7557	NP_004108
7587	3.83E-04	XPA binding protein 1; putative ATP(GTP)-binding protein (NTPBP), mRNA /cds=(25,1149) /gb=NM_007266 /gi=14149628 /ug=Hs.18259 /len=1829	NM_007266	Hs.18259	NP_009197
7599	0.012975	fibrinogen, B beta polypeptide (FGB), mRNA /cds=(9,1484) /gb=NM_005141 /gi=11761630 /ug=Hs.7645 /len=1918	NM_005141	Hs.7645	NP_005132
7600	0.033283	hypothetical protein MGC45400 (MGC45400), mRNA /cds=(245,598) /gb=NM_153333 /gi=23503246 /ug=Hs.389734 /len=1290	NM_153333	Hs.389734	NP_699164
7618	0.037084	hypothetical protein FLJ11240 (FLJ11240), mRNA /cds=(26,1648) /gb=NM_018368 /gi=8922955 /ug=Hs.339833 /len=1947	NM_018368	Hs.339833	NP_060838
7623	0.009969	growth factor receptor-bound protein 10 (GRB10), mRNA /cds=(782,2548) /gb=NM_005311 /gi=19923302 /ug=Hs.81875 /len=5431	NM_005311	Hs.81875	NP_005302
7637	0.012975	serum response factor (c-fos serum response element-binding transcription factor) (SRF), mRNA /cds=(359,1885) /gb=NM_003131 /gi=4507204 /ug=Hs.155321 /len=4201	NM_003131	Hs.155321	NP_003122
7642	0.048172	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
7694	4.70E-05	cDNA FLJ25013 fis, clone CBL01365. /gb=AK057742 /gi=16553667 /ug=Hs.380091 /len=2200	AK057742	Hs.380091	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7697	0.045762	thioredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) /gb=NM_006472 /gi=5454161 /ug=Hs.179526 /len=2704	NM_006472	Hs.179526	NP_006463
7724	0.003233	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), mRNA /cds=(252,1457) /gb=NM_002546 /gi=22547122 /ug=Hs.81791 /len=2291	NM_002546	Hs.81791	NP_002537
7730	0.001342	MTB (MTB) mRNA, complete cds /cds=(80,265) /gb=AF348994 /gi=28190031 /ug=Hs.333727 /len=408	AF348994	Hs.333727	NP_783321
7731	0.005412	cDNA FLJ14844 fis, clone PLACE1000133, highly similar to TRANSCRIPTION FACTOR BTF3. /cds=(91,567) /gb=AK027750 /gi=14042660 /ug=Hs.93748 /len=2203	AK027750	Hs.93748	
7753	0.017682	SAC1 suppressor of actin mutations 1-like (yeast) (SACM1L), mRNA /cds=(70,1833) /gb=NM_014016 /gi=7662337 /ug=Hs.5867 /len=3572	NM_014016	Hs.5867	NP_054735
7807	0.011417	poly(A) polymerase gamma (PAPOLG), mRNA /cds=(232,2442) /gb=NM_022894 /gi=16306567 /ug=Hs.146123 /len=4252	NM_022894	Hs.146123	NP_075045
7839	0.023762	EST(xc43h04.x1 NCI_CGAP_Co20 clone IMAGE:2587063 3' gb:M99436 TRANSDUCIN-LIKE ENHANCER PROTEIN 2)	AW081723		NP_003251
7873	0.002024	BX098638 Soares fetal liver spleen 1NFLS cDNA clone IMAGp998G14405, mRNA sequence /clone=IMAGp998G14405 IMAGE:208165 /gb=BX098638 /gi=27829530 /ug=Hs.435496 /len=438	BX098638	Hs.435496	
7908	0.031506	EST EST43399 Fetal brain I cDNA 3' end	AA338448		NP_112577
7941	0.00767	EST (EST370348 MAGE resequences, MAGE cDNA)	AW958278		NP_112420
7951	0.008208	EST (am59f03.x1 Johnston frontal	AI124626		
7968	0.031506	low density lipoprotein receptor-related protein 5 (LRP5), mRNA /cds=(49,4896) /gb=NM_002335 /gi=4505018 /ug=Hs.6347 /len=5100	NM_002335	Hs.6347	NP_002326
7985	0.035141	SH3-domain GRB2-like 3 (SH3GL3), mRNA /cds=(493,1560) /gb=NM_003027 /gi=20070145 /ug=Hs.80315 /len=2015	NM_003027	Hs.80315	NP_003018

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7991	0.033283	hypothetical protein FLJ20425 (LYAR), mRNA /cds=(189,1328) /gb=NM_017816 /gi=8923397 /ug=Hs.425427 /len=1598	NM_017816	Hs.425427	NP_060286
8020	0.023762	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART), mRNA /cds=(79,3111) /gb=NM_000819 /gi=24475881 /ug=Hs.82285 /len=3291	NM_000819	Hs.82285	NP_780294
8054	0.011417	pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence /cds=UNKNOWN/gb=AF334710 /gi=12658438 /ug=Hs.8364 /len=1819	AF334710	Hs.8364	NP_002603
8056	0.00767	ADP-ribosyltransferase (NAD ; poly (ADP-ribose) polymerase) (ADPRT), mRNA /cds=(160,3204) /gb=NM_001618 /gi=11496989 /ug=Hs.177766 /len=3859	NM_001618	Hs.177766	NP_001609
8076	0.041237	hypothetical protein PRO2577 (PRO2577), mRNA /cds=(492,665) /gb=NM_018630 /gi=8924181 /ug=Hs.241576 /len=1032	NM_018630	Hs.241576	
8097	0.027996	mRNA for KIAA1915 protein, partial cds. /cds=(356,2536) /gb=AB067502 /gi=15620888 /ug=Hs.12915 /len=7801	AB067502	Hs.12915	
8191	0.035141	downstream neighbor of SON (DONSON), transcript variant 1, mRNA /cds=(68,1768) /gb=NM_017613 /gi=22035582 /ug=Hs.17834 /len=2189	NM_017613	Hs.17834	NP_665738
8198	0.039115	PHD zinc finger protein XAP135 (XAP135), transcript variant 2, mRNA /cds=(222,1448) /gb=NM_133325 /gi=19747275 /ug=Hs.7759 /len=1583	NM_133325	Hs.7759	NP_579866
8203	0.019933	hypothetical protein FLJ14668 (FLJ14668), mRNA /cds=(59,475) /gb=NM_032822 /gi=14249519 /ug=Hs.334644 /len=1786	NM_032822	Hs.334644	NP_116211
8230	0.01471	mRNA for KIAA0592 protein, partial cds. /cds=(1,4062) /gb=AB011164 /gi=3043707 /ug=Hs.439367 /len=4623	AB011164	Hs.439367	
8272	0.043451	EST(PM4-BT0650-010400-002-a06 BT0650)	BE083882		NP_060487
8308	0.004048	EST(ty24e09.x1 NCI_CGAP_Ut3 clone IMAGE:2280040 3' contains Alu repeat)	AI758800		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8309	0.002773	hypothetical protein FLJ14906 (FLJ14906), mRNA /cds=(131,736) /gb=NM_032859 /gi=14249591 /ug=Hs.183528 /len=2492	NM_032859	Hs.183528	NP_116248
8333	0.035141	EST (fb12g02.x1 zebrafish fin day0 regeneration)	AI384158		
8341	0.019933	EST(we27d09.x1 NCI_CGAP_Lu24 clone IMAGE:2342321 3')	AI797144		NP_002877
8359	0.035141	UI-H-BW1-amn-b-05-0-UI.s1 NCI_CGAP_Sub7 cDNA clone IMAGE:3070401 3', mRNA sequence /clone=IMAGE:3070401 /clone_end=3' /gb=BF513064 /gi=11598243 /ug=Hs.446233 /len=777	BF513064	Hs.446233	
8373	0.035141	NISC_gj17d11.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:3272108 3', mRNA sequence /clone=IMAGE:3272108 /clone_end=3' /gb=CB050438 /gi=27788725 /ug=Hs.435309 /len=534	CB050438	Hs.435309	
8381	0.010023	Tho2 mRNA, complete cds /cds=(1,4437) /gb=AF441770 /gi=20799317 /ug=Hs.16411 /len=4452	AF441770	Hs.16411	
8411	0.017682	UI-1-BB1p-aya-d-12-0-UI.s1 NCI_CGAP_PI6 cDNA clone UI-1-BB1p-aya-d-12-0-UI 3', mRNA sequence /clone=UI-1-BB1p-aya-d-12-0-UI /clone_end=3' /gb=BU754499 /gi=23713459 /ug=Hs.432873 /len=1196	BU754499	Hs.432873	
8435	0.019933	BX099435 NCI_CGAP_Co8 cDNA clone IMAGp998M083951, mRNA sequence /clone=IMAGp998M083951 IMAGE:1559599 /gb=BX099435 /gi=27829993 /ug=Hs.126589 /len=659	BX099435	Hs.126589	
8438	0.017682	mRNA sequence /gb=L26969 /gi=16905391 /ug=Hs.362852 /len=1738	L26969	Hs.362852	
8459	0.003487	zs54b10.r1 NCI_CGAP_GCB1 cDNA clone IMAGE:701275 5', mRNA sequence /clone=IMAGE:701275 /clone_end=5' /gb=AA287780 /gi=1933461 /ug=Hs.369808 /len=497	AA287780	Hs.369808	
8472	0.037084	cDNA FLJ14188 fis, clone NT2RP2005980. /gb=AK024250 /gi=10436579 /ug=Hs.288671 /len=2289	AK024250	Hs.288671	
8480	0.031506	ribosomal protein L37a (RPL37A), mRNA /cds=(36,314) /gb=NM_000998 /gi=16306561 /ug=Hs.296290 /len=392	NM_000998	Hs.296290	NP_000989
8486	0.043451	cDNA, 3' end /clone=IMAGE:1935382 /clone_end=3' /gb=AI340092 /gi=4077019 /ug=Hs.327321 /len=361	AI340092	Hs.327321	NP_002370

Spot	p-value	D scription	Gene Accession No.	Unigene Acc ssion No.	Protein Accession No.
8492	0.003233	EST CM2-BT0857-021100-470-g06 BT0857 Homo sapiens cDNA	BF745663		
8514	0.041237	mRNA; cDNA DKFZp451B1818 (from clone DKFZp451B1818) /gb=AL832623 /gi=21733198 /ug=Hs.77554 /len=6240	AL832623	Hs.77554	
8516	0.039115	EST (MR1-SN0033-100400-001-a10 SN0033)	AW867013		
8529	0.004357	EST (602645742F1 NIH_MGC_76 clone IMAGE:4767299 5')	BG618375		
8530	0.045762	UI-E-EJ0-ahq-g-22-0-UI.s1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahq-g-22-0-UI.3', mRNA sequence /clone=UI-E-EJ0-ahq-g- 22-0-UI /clone_end=3' /gb=BM674631 /gi=18984529 /ug=Hs.444500 /len=1272	BM674631	Hs.444500	
8546	0.045762	EST(hc98c08.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2908046 3' similar to TR:O14792 O14792 HEPARAN SULFATE 3-O- SULFOTRANSFERASE-1 PRECURSOR)	AW340546		NP_005105
8547	0.019933	cDNA FLJ36837 fis, clone ASTRO2011422. /gb=AK094156 /gi=21753158 /ug=Hs.36475 /len=3302	AK094156	Hs.36475	
8557	0.018779	UI-H-ED0-awy-a-01-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5825160 3', mRNA sequence /clone=IMAGE:5825160 /clone_end=3' /gb=BQ017647 /gi=19752924 /ug=Hs.124747 /len=1445	BQ017647	Hs.124747	
8560	0.012175	ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500	NM_000991	Hs.356371	NP_000982
8564	0.039115	EST(cDNA clone IMAGE:2569171 3')	AW073383		
8595	0.017682	ribosomal protein L3 (RPL3), mRNA /cds=(27,1238) /gb=NM_000967 /gi=16507968 /ug=Hs.119598 /len=1311	NM_000967	Hs.119598	NP_000958
8606	0.011736	hypothetical protein DKFZp451G182 (DKFZp451G182), mRNA /cds=(99,4049) /gb=NM_153610 /gi=23957703 /ug=Hs.50794 /len=4678	NM_153610	Hs.50794	NP_705838
8646	0.001585	cDNA FLJ39413 fis, clone PLACE6015729. /gb=AK096732 /gi=21756291 /ug=Hs.194339 /len=1957	AK096732	Hs.194339	
8669	0.005412	cDNA FLJ10190 fis, clone HEMBA1004753. /gb=AK001052 /gi=7022081 /ug=Hs.274546 /len=1318	AK001052	Hs.274546	
8673	0.012175	jun1.P1.D7 conorm cDNA 3', mRNA sequence /clone_end=3' /gb=AI535800 /gi=4449935 /ug=Hs.369112 /len=480	AI535800	Hs.369112	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8675	0.002372	UI-H-EI0-ayo-a-20-0-UI.s1 NCI_CGAP_EI0 cDNA clone IMAGE:5841307 3', mRNA sequence /clone=IMAGE:5841307 /clone_end=3' /gb=BQ004581 /gi=19729481 /ug=Hs.412459 /len=1095	BQ004581	Hs.412459	
8738	0.041237	tb26b01.x1 NCI_CGAP_Kid12 cDNA clone IMAGE:2055433 3' similar to contains Alu repetitive element;, mRNA sequence /clone=IMAGE:2055433 /clone_end=3' /gb=AI308217 /gi=4002852 /ug=Hs.177064 /len=421	AI308217	Hs.177064	
8746	0.018779	tg02e02.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2107610 3', mRNA sequence /clone=IMAGE:2107610 /clone_end=3' /gb=AI380429 /gi=4190282 /ug=Hs.172445 /len=478	AI380429	Hs.172445	
8769	0.033283	EST(adult brain Danio rerio cDNA clone 4966301 5' similar to SW:RLA1_CHICK P18660 60S ACIDIC RIBOSOMAL PROTEIN P1. ;contains element MER22 repetitive element ;)	BI429083		
8771	0.035141	mitochondrion, complete genome	NC_001807		
8781	0.011417	cDNA: FLJ20933 fis, clone ADSE01388. /gb=AK024586 /gi=10436898 /ug=Hs.296757 /len=1567	AK024586	Hs.296757	
8788	0.012975	ESTs, cDNA /gb=AW978555 /gi=8169822 /ug=Hs.92448 /len=754	AW978555	Hs.92448	
8828	0.037084	cDNA FLJ13443 fis, clone PLACE1002853	AK023505		NP_078968
8837	0.003487	no significant match	SEQ.ID.No.39		
8838	0.048172	No significant match	SEQ.ID.No.45		
8840	0.019933	No significant match	SEQ.ID.No.54		
8856	0.003233	control			
8874	0.026411	No significant match. (ORF:+1:256~491[237])	SEQ.ID.No.26		
8946	0.018779	hypothetical protein FLJ33282 (FLJ33282), mRNA /cds=(225,1523) /gb=NM_152388 /gi=22748830 /ug=Hs.346509 /len=2078	NM_152388	Hs.346509	
8949	0.029809	tx18g05.x1 NCI_CGAP_Ut4 cDNA clone IMAGE:2269592 3', mRNA sequence /clone=IMAGE:2269592 /clone_end=3' /gb=AI612954 /gi=4622121 /ug=Hs.187303 /len=205	AI612954	Hs.187303	
8967	0.032562	hypothetical protein FLJ13231 (FLJ13231), mRNA /cds=(134,1255) /gb=NM_023073 /gi=12751482 /ug=Hs.156148 /len=2642	NM_023073	Hs.156148	NP_075561

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8972	0.023762	EST (ym20a08.r1 Soares infant brain 1NIB IMAGE:48353 5')	H15948		
8981	0.006234	AV737351 CB cDNA clone CBLALE11 5', mRNA sequence /clone=CBLALE11 /clone_end=5' /gb=AV737351 /gi=10854932 /ug=Hs.444989 /len=511	AV737351	Hs.444989	
8988	0.019933	hypothetical protein FLJ36674 (FLJ36674), mRNA /cds=(26,484) /gb=NM_173622 /gi=27734737 /ug=Hs.164595 /len=2236	NM_173622	Hs.164595	NP_775893
8990	0.028189	hypothetical protein FLJ39514 (FLJ39514), mRNA /cds=(121,2040) /gb=NM_152540 /gi=22749126 /ug=Hs.48565 /len=2221	NM_152540	Hs.48565	NP_689753
9061	0.037084	cDNA FLJ33960 fis, clone CTONG2018843. /gb=AK091279 /gi=21749612 /ug=Hs.126465 /len=2849	AK091279	Hs.126465	
9072	0.035141	clone MGC:20469 IMAGE:4554554, mRNA, complete cds /cds=(208,1149) /gb=BC012182 /gi=15082546 /ug=Hs.82508 /len=1862	BC012182	Hs.82508	
9096	0.041237	C1q and tumor necrosis factor related protein 7 (C1QTNF7), mRNA /cds=(234,1103) /gb=NM_031911 /gi=21314748 /ug=Hs.153714 /len=3959	NM_031911	Hs.153714	NP_114117
9106	0.023762	yz39f06.s1 Morton Fetal Cochlea cDNA clone IMAGE:285443 3', mRNA sequence /clone=IMAGE:285443 /clone_end=3' /gb=N66393 /gi=1218518 /ug=Hs.102754 /len=618	N66393	Hs.102754	
9108	3.48E-04	UI-H-EI0-aye-c-17-0-UI.s1 NCI_CGAP_EI0 cDNA clone UI-H-EI0-aye-c-17-0-UI 3', mRNA sequence /clone=UI-H-EI0-aye-c-17-0-UI /clone_end=3' /gb=CA447385 /gi=24811805 /ug=Hs.420740 /len=812	CA447385	Hs.420740	
9174	0.012975	UI-E-EJ0-ahs-e-16-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahs-e-16-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahs-e-16-0-UI /clone_end=5' /gb=BM714718 /gi=19027976 /ug=Hs.446458 /len=1136	BM714718	Hs.446458	
9244	0.021147	Mus musculus mitochondrion, complete genome	NC_001569		
9266	0.018779	clone FLB2932 mRNA sequence /gb=AF138859 /gi=7340965 /ug=Hs.274405 /len=2990	AF138859	Hs.274405	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9274	0.001585	mRNA; cDNA DKFZp586G2120 (from clone DKFZp586G2120); complete cds /cds=(19,2604) /gb=AL136924/gi=12053342 /ug=Hs.62349 /len=4137	AL136924	Hs.62349	NP_061866
9275	0.003758	ESTs, cDNA, 5' end /clone=IMAGE:3857750 /clone_end=5' /gb=BF035134 /gi=10742846 /ug=Hs.195789 /len=847	BF035134	Hs.195789	
9310	0.001585	No significant match	SEQ.ID.No.71		
9311	0.018779	Novel, ORF+1(73~201)	SEQ.ID.No.75		
9315	0.037084	No significant match	SEQ.ID.No.89		
9372	0.012175	chromosome 17 open.reading frame 35 (C17orf35), mRNA /cds=(259,837) /gb=NM_003876 /gi=4505900 /ug=Hs.15196 /len=1211	NM_003876	Hs.15196	NP_003867
9399	0.002773	NPD002 protein (NPD002), mRNA /cds=(89,1954) /gb=NM_014049 /gi=21361496 /ug=Hs.7010 /len=2494	NM_014049	Hs.7010	NP_054768
9407	0.011417	adenylate kinase 3 like 1 (AK3L1), mRNA /cds=(141,824) /gb=NM_016282 /gi=19923436 /ug=Hs.43436 /len=2642	NM_016282	Hs.43436	NP_057366
9417	0.00767	Siah-interacting protein (SIP), mRNA /cds=(118,804) /gb=NM_014412 /gi=7656951 /ug=Hs.27258 /len=2435	NM_014412	Hs.27258	NP_055227
9457	0.022422	serine/threonine kinase 17a (apoptosis-inducing) (STK17A); mRNA /cds=(118,1362) /gb=NM_004760 /gi=4758191 /ug=Hs.9075 /len=2641	NM_004760	Hs.9075	NP_004751
9459	0.010023	ubiquinol-cytochrome c reductase binding protein (UQCRB), mRNA /cds=(54,389) /gb=NM_006294 /gi=20070231 /ug=Hs.131255 /len=965	NM_006294	Hs.131255	NP_006285
9473	0.011417	mRNA; cDNA DKFZp564D152 (from clone DKFZp564D152); complete cds /cds=(99,1415) /gb=AL136629 /gi=12052783 /ug=Hs.278479 /len=3229	AL136629	Hs.278479	
9485	0.012975	mRNA; cDNA DKFZp434K1412 (from clone DKFZp434K1412) /gb=AL137753 /gi=6808455 /ug=Hs.12144 /len=5448	AL137753	Hs.12144	
9486	0.048172	neural precursor cell expressed, developmentally down-regulated 5 (NEDD5), mRNA /cds=(259,1344) /gb=NM_004404 /gi=4758157 /ug=Hs.155595 /len=3433	NM_004404	Hs.155595	NP_004395
9489	0.015649	similar to putative (H. sapiens) (LOC129641), mRNA	XM_059369		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9492	0.048653	601846634F1 NIH_MGC_55 cDNA clone IMAGE:4077632 5', mRNA sequence /clone=IMAGE:4077632 /clone_end=5' /gb=BF214729 /gi=11108315 /ug=Hs.446581 /len=835	BF214729	Hs.446581	
9498	0.048172	PFTAIRES protein kinase 1 (PFTK1), mRNA /cds=(145,1500) /gb=NM_012395 /gi=6912583 /ug=Hs.57856 /len=4957	NM_012395	Hs.57856	NP_036527
9511	0.028189	emopamil binding related protein, delta8-delta7 sterol isomerase related protein (EBRP), mRNA /cds=(53,673) /gb=NM_032565 /gi=14211872 /ug=Hs.433278 /len=931	NM_032565	Hs.433278	NP_115954
9513	0.035141	hypothetical gene supported by AY007122 (LOC92719), mRNA	XM_046853		
9530	0.004048	hypothetical protein FLJ10856 (FLJ10856), mRNA /cds=(148,1233) /gb=NM_018247 /gi=8922719 /ug=Hs.108530 /len=3720	NM_018247	Hs.108530	NP_060717
9547	0.048172	mitochondrion, complete genome	NC_001807		
9548	0.033283	ubiquitin specific protease 1 (USP1), mRNA /cds=(246,2603) /gb=NM_003368 /gi=21361109 /ug=Hs.35086 /len=3379	NM_003368	Hs.35086	NP_003359
9561	0.037084	phosphatidylinositol transfer protein, beta (PITPNB), mRNA /cds=(40,855) /gb=NM_012399 /gi=19923401 /ug=Hs.7370 /len=2906	NM_012399	Hs.7370	NP_036531
9595	0.001459	hypothetical protein MGC4701 (MGC4701), mRNA /cds=(149,1585) /gb=NM_024511 /gi=24308290 /ug=Hs.421054 /len=1686	NM_024511	Hs.421054	NP_078787
9596	0.001867	vimentin (VIM), mRNA /cds=(123,1523) /gb=NM_003380 /gi=4507894 /ug=Hs.297753 /len=1851	NM_003380	Hs.297753	NP_000995
9610	0.017682	nuclear DNA-binding protein (C1D), transcript variant 1, mRNA /cds=(64,489) /gb=NM_006333 /gi=27894371 /ug=Hs.15164 /len=1200	NM_006333	Hs.15164	NP_775269
9648	0.025168	Similar to RIKEN cDNA 1500009M05 gene, clone MGC:40370 IMAGE:5105935, mRNA, complete cds /cds=(45,452) /gb=BC032300 /gi=21619026 /ug=Hs.295953 /len=1617	BC032300	Hs.295953	
9712	0.026643	w154c05.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2428712 3', mRNA sequence /clone=IMAGE:2428712 /clone_end=3' /gb=AI864553 /gi=5528660 /ug=Hs.371597 /len=474	AI864553	Hs.371597	

Sp t	p-value	Description	Gen Accession No.	Unigene Accession No.	Protein Accession No.
9721	0.045762	EST(yj01e06.r1 clone 147490 5')	R81297		NP_057707
9730	0.035141	601862578F1 NIH_MGC_53 cDNA clone IMAGE:4082082 5', mRNA sequence /clone=IMAGE:4082082 /clone_end=5' /gb=BF207870 /gi=11101456 /ug=Hs.396179 /len=756	BF207870	Hs.396179	
9769	0.043451	AGENCOURT_6445786 NIH_MGC_92 cDNA clone IMAGE:5587250 5', mRNA sequence /clone=IMAGE:5587250 /clone_end=5' /gb=BM468951 /gi=18517993 /ug=Hs.275340 /len=967	BM468951	Hs.275340	
9774	0.031506	cDNA FLJ36605 fis, clone TRACH2015316, highly similar to VIMENTIN. /cds=(631,1317) /gb=AK093924 /gi=21752883 /ug=Hs.379100 /len=2665	AK093924	Hs.379100	
9833	0.004687	AGENCOURT_6861057 NIH_MGC_99 cDNA clone IMAGE:5931113 5', mRNA sequence /clone=IMAGE:5931113 /clone_end=5' /gb=BQ066467 /gi=19895513 /ug=Hs.446485 /len=1029	BQ066467	Hs.446485	
9886	0.005811	mRNA; cDNA DKFZp451F1910 (from clone DKFZp451F1910) /gb=AL833265 /gi=21733898 /ug=Hs.332030 /len=5254	AL833265	Hs.332030	
9921	0.033283	hypothetical protein FLJ10477 (FLJ10477), mRNA /cds=(232,873) /gb=NM_018105 /gi=8922445 /ug=Hs.7432 /len=2167	NM_018105	Hs.7432	NP_060575
9965	0.039115	hypothetical protein DKFZp434K1421 (DKFZP434K1421), mRNA /cds=(29,1705) /gb=NM_032141 /gi=14149806 /ug=Hs.374609 /len=2547	NM_032141	Hs.374609	NP_115517
9972	0.035141	caldesmon 1 (CALD1), transcript variant 1, mRNA /cds=(230,2611) /gb=NM_033138 /gi=15149460 /ug=Hs.325474 /len=3610	NM_033138	Hs.325474	NP_149347
10011	0.045762	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein), clone MGC:9025 IMAGE:3880116, mRNA, complete cds (BC018163.1)	BC018163	Hs.348024	NP_002872
10054	0.028189	similar to hypothetical protein FLJ10883 (LOC115294), mRNA /cds=(98,1171) /gb=NM_052937 /gi=24308385 /ug=Hs.60293 /len=3967	NM_052937	Hs.60293	NP_443169
10080	0.015649	hypothetical protein DKFZp761N0624 (DKFZp761N0624), mRNA /cds=(113,1444) /gb=NM_032295 /gi=14150046 /ug=Hs.21893 /len=2973	NM_032295	Hs.21893	NP_115671

Spot	p-value	Description	Gene Accession No.	Unigen Accession No.	Protein Accession No.
10100	0.025168	hypothetical protein FLJ22662 (FLJ22662), mRNA /cds=(66,1586) /gb=NM_024829 /gi=13376231 /ug=Hs.178470 /len=1707	NM_024829	Hs.178470	NP_079105
10143	0.043451	phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA /cds=(207,4604) /gb=NM_007366 /gi=19923388 /ug=Hs.171945 /len=5633	NM_007366	Hs.171945	NP_031392
10146	0.037084	EST qz90a06.x1 Soares_pregnant_uterus_NbHPU cDNA clone IMAGE:2041810 3'	AI493872		NP_008878
10151	0.006684	cDNA FLJ36605 fis, clone TRACH2015316, highly similar to VIMENTIN. /cds=(631,1317) /gb=AK093924 /gi=21752883 /ug=Hs.379100 /len=2665	AK093924	Hs.379100	
10205	0.003193	EST (ql74f05.s1 NCI_CGAP_Kid3 cDNA clone IMAGE:1535361 3')	AA919165		
10208	0.004048	cDNA FLJ33503 fis, clone BRAMY2004521. /cds=(367,750) /gb=AK090822 /gi=21749052 /ug=Hs.356719 /len=2339	AK090822	Hs.356719	NP_787089
10228	0.004357	hypothetical protein FLJ10342 (FLJ10342), mRNA /cds=(534,1145) /gb=NM_018064 /gi=14149717 /ug=Hs.101514 /len=1506	NM_018064	Hs.101514	NP_060534
10247	0.002773	vimentin (VIM) gene	M18895		
10277	0.039115	likely ortholog of mouse embryonic epithelial gene 1 (EEG1), mRNA /cds=(319,1794) /gb=NM_017611 /gi=18252046 /ug=Hs.274453 /len=2630	NM_017611	Hs.274453	NP_060081
10315	0.035141	EST (MR0-HT0407-010200-008-g12 HT0407)	BE159321		
10323	0.006234	mRNA; cDNA DKFZp434K1115 (from clone DKFZp434K1115); complete cds /cds=(97,2877) /gb=AL136764 /gi=12053044 /ug=Hs.42676 /len=4868	AL136764	Hs.42676	
10351	0.021147	EST (IL2-UM0076-070400-061-F10 UM0076)	AW802800		
10358	0.033283	cDNA, 5' end /clone=IMAGE:4148900 /clone_end=5' /gb=BF342391 /gi=11289392 /ug=Hs.30469 /len=803	BF342391	Hs.30469	NP_055313
10385	0.045762	chondroitin sulfate GalNAcT-2 (GALNAcT-2), mRNA /cds=(336,1964) /gb=NM_018590 /gi=24429591 /ug=Hs.180758 /len=3745	NM_018590	Hs.180758	NP_061060
10392	0.012175	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994

Spot	p-value	D scription	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10430	0.017682	EST(ha63a03.x1 NCI_CGAP_Pan1 cDNA clone IMAGE:2878348 3')	AW338626		NP_006826
10432	0.010023	UI-H-BW0-ajd-b-12-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2731343 3', mRNA sequence /clone=IMAGE:2731343 /clone_end=3' /gb=AW297162 /gi=6703808 /ug=Hs.438076 /len=690	AW297162	Hs.438076	
10456	0.045762	mRNA; cDNA DKFZp451D112 (from clone DKFZp451D112); complete cds /cds=(316,4719) /gb=AL831962 /gi=21732493 /ug=Hs.202949 /len=5391	AL831962	Hs.202949	
10503	0.003487	thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556	NM_021109	Hs.75968	NP_066932
10536	0.005658	nascent-polypeptide-associated complex alpha polypeptide (NACA), mRNA /cds=(26,673) /gb=NM_005594 /gi=5031930 /ug=Hs.32916 /len=797	NM_005594	Hs.32916	NP_005585
10565	0.048172	clone IMAGE:5284350, mRNA /gb=BC037924 /gi=23138690 /ug=Hs.143061 /len=2659	BC037924	Hs.143061	
10566	0.023762	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
10601	0.004048	EST(cDNA clone IMAGE:3566688 3')	BF110315		NP_002154
10627	0.013819	602584221F1 NIH_MGC_76 cDNA clone IMAGE:4712140 5', mRNA sequence /clone=IMAGE:4712140 /clone_end=5' /gb=BG564543 /gi=13572195 /ug=Hs.105449 /len=981	BG564543	Hs.105449	
10632	0.010701	UI-H-EI1-aze-g-21-0-UI.s1 NCI_CGAP_EI1 cDNA clone IMAGE:5847596 3', mRNA sequence /clone=IMAGE:5847596 /clone_end=3' /gb=BQ003542 /gi=19728442 /ug=Hs.190642 /len=1086	BQ003542	Hs.190642	
10660	0.023762	BX111472 Soares_senescent_fibroblasts_NbHSF cDNA clone IMAGp998B18737, mRNA sequence /clone=IMAGp998B18737; IMAGE:3251 69 /gb=BX111472 /gi=27878522 /ug=Hs.56025 /len=714	BX111472	Hs.56025	
10697	0.021147	EST(PM0-HT0913-100401-013-c08 HT0913 cDNA, MRNA sequence)	BG998053		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10771	0.039257	HUM515D03B Clontech placenta polyA mRNA (#6518) cDNA clone GEN-515D03 5', mRNA sequence /clone=GEN-515D03 /clone_end=5' /gb=D58893 /gi=968527 /ug=Hs.335953 /len=365	D58893	Hs.335953	
10779	0.01471	EST (ADB cDNA clone ADBAKA02 5')	AV704531		
10780	0.037084	hypothetical protein FLJ10300 (FLJ10300), mRNA /cds=(1710,3359) /gb=NM_018051 /gi=21361686 /ug=Hs.42233 /len=3785	NM_018051	Hs.42233	NP_060521
10793	0.041237	im56f03.y1 HR85 islet cDNA clone IMAGE:6039292 5', mRNA sequence /clone=IMAGE:6039292 /clone_end=5' /gb=CA773752 /gi=26011160 /ug=Hs.380642 /len=630	CA773752	Hs.380642	
10794	0.002773	FSDH region gene 1 (FRG1), mRNA /cds=(192,968) /gb=NM_004477 /gi=4758403 /ug=Hs.203772 /len=1042	NM_004477	Hs.203772	NP_004468
10798	0.016639	EST (ta16g05.x1 NCI_CGAP_Lym5 IMAGE:2044280 3')	AI471814		
10843	0.025168	EST (QV0-ST0236-171299-075-c08 ST0236 cDNA)	AW816517		
10852	0.011417	EST yb28f09.s1 Stratagene fetal spleen #937205) H.sapiens cDNA clone IMAGE:72521 3'	T51639		
10853	6.69E-04	EST(z189c05.r1 Soares testis NHT clone 729512 5')	AA398038		NP_004632
10862	0.003758	mitochondrion, complete genome	NC_001807		
10864	0.016639	EST (ab81d11.s1 Stratagene fetal retina 937202 IMAGE:853365 3')	AA663308		
10888	2.60E-05	UI-H-DH0-aui-j-10-0-UI.s1 NCI_CGAP_DH0 cDNA clone IMAGE:5871081 3', mRNA sequence /clone=IMAGE:5871081 /clone_end=3' /gb=BM994461 /gi=19719362 /ug=Hs.434057 /len=2059	BM994461	Hs.434057	
10897	0.029809	hypothetical protein FLJ25534 (FLJ25534), mRNA /cds=(297,1145) /gb=NM_153234 /gi=23397511 /ug=Hs.23197 /len=2550	NM_153234	Hs.23197	NP_694966
10912	0.028189	cDNA FLJ34675 fis, clone LIVER2001608. /gb=AK091994 /gi=21750487 /ug=Hs.380100 /len=1725	AK091994	Hs.380100	
10950	0.011417	cDNA FLJ38913 fis, clone NT2NE2008017. /gb=AK096232 /gi=21755673 /ug=Hs.50094 /len=2555	AK096232	Hs.50094	NP_835224
10991	0.028189	ribosomal protein L12 (RPL12), mRNA /cds=(89,586) /gb=NM_000976 /gi=15431291 /ug=Hs.405042 /len=632	NM_000976	Hs.405042	NP_000967

Spot	p-value	Description	Gen Accession No.	Unigene Accession No.	Protein Accession No.
10996	0.028189	BX118052 Soares breast 2NbHBst cDNA clone IMAGp998C21252, mRNA sequence /clone=IMAGp998C21252, IMAGE:158156 /gb=BX118052 /gi=27840946 /ug=Hs.32250 /len=612	BX118052	Hs.32250	
11003	0.002372	cDNA FLJ14832 fis, clone OVARC1001169. /gb=AK027738 /gi=14042638 /ug=Hs.235860 /len=2350	AK027738	Hs.235860	
11011	0.007162	EST(cDNA clone IMAGE:2686869 3')	AW197394		
11016	0.033283	mitochondrion, complete genome	NC_001807		
11030	0.048172	ESTs, cDNA, 3' end /clone=IMAGE:2308223 /clone_end=3' /gb=AI671885 /gi=4851616 /ug=Hs.110855 /len=593	AI671885	Hs.110855	
11032	0.017682	nj38c05.s1 NCI_CGAP_AA1 cDNA clone IMAGE:994760 3' similar to gb:M62424 THROMBIN RECEPTOR PRECURSOR mRNA sequence /clone=IMAGE:994760 /clone_end=3' /gb=AA548630 /gi=2318912 /ug=Hs.105848 /len=555	AA548630	Hs.105848	
11033	0.021147	FLJ30661 fis, clone DFNES2000526 /cds=UNKNOWN /gb=AK055223 /gi=16549904 /ug=Hs.265540 /len=2514	AK055223	Hs.265540	NP_057178
11046	0.017682	wc25f11.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2316237 3', mRNA sequence /clone=IMAGE:2316237 /clone_end=3' /gb=AI678258 /gi=4888440 /ug=Hs.174257 /len=585	AI678258	Hs.174257	
11085	0.008208	EST(cDNA clone IMAGE:2126419 3')	AI435109		
11136	0.016639	clone IMAGE:3138608, mRNA /cds=UNKNOWN /gb=BC007266 /gi=13938277 /ug=Hs.334566 /len=1635	BC007266	Hs.334566	
11138	0.045762	nn90a10.s1 NCI_CGAP_Br2 cDNA clone IMAGE:1098426 3', mRNA sequence /clone=IMAGE:1098426 /clone_end=3' /gb=AA614814 /gi=2467010 /ug=Hs.270700 /len=404	AA614814	Hs.270700	
11148	0.019933	ij23g01.x1 Melton Normalized Islet 4 N4-HIS 1 cDNA clone IMAGE:6135721 3', mRNA sequence /clone=IMAGE:6135721 /clone_end=3' /gb=BQ100789 /gi=20133773 /ug=Hs.372964 /len=568	BQ100789	Hs.372964	
11169	0.018775	nad13a08.x1 NCI_CGAP_Lu24 cDNA clone IMAGE:3365271 3', mRNA sequence /clone=IMAGE:3365271 /clone_end=3' /gb=BF439728 /gi=11452245 /ug=Hs.257883 /len=202	BF439728	Hs.257883	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Prot in Accession No.
11218	0.007162	chromosome 3q clone CTD-2650N22, WORKING DRAFT SEQUENCE, 5 unordered pieces	AC108668		
11243	0.029809	apoA polymorphism Kringle IV gene, exons 1 and 2	L14005		
11256	0.045762	cDNA FLJ31919 fis, clone NT2RP7004964. /gb=AK056481 /gi=16551895 /ug=Hs.400872 /len=4013	AK056481	Hs.400872	
11266	9.20E-05	B-cell translocation gene 1, anti-proliferative (BTG1), mRNA /cds=(309,824) /gb=NM_001731 /gi=4502472 /ug=Hs.77054 /len=1783	NM_001731	Hs.77054	NP_001722
11275	0.031506	glucose phosphate isomerase (GPI), mRNA /cds=(104,1780) /gb=NM_000175 /gi=18201904 /ug=Hs.406458 /len=2075	NM_000175	Hs.406458	NP_000166
11299	0.039115	ATX1 antioxidant protein 1 (yeast) (ATOX1), mRNA /cds=(114,320) /gb=NM_004045 /gi=4757803 /ug=Hs.279910 /len=502	NM_004045	Hs.279910	NP_004036
11305	0.010023	tousled-like kinase 2 (TLK2), mRNA /cds=(147,2396) /gb=NM_006852 /gi=11140818 /ug=Hs.57553 /len=3327	NM_006852	Hs.57553	NP_006843
11321	0.039115	transient receptor potential cation channel, subfamily C, member 1 (TRPC1), mRNA /cds=(138,2417) /gb=NM_003304 /gi=27545448 /ug=Hs.250687 /len=4085	NM_003304	Hs.250687	NP_003295
11331	0.017682	cell cycle progression 8 protein (CPR8), mRNA /cds=(13,1140) /gb=NM_004748 /gi=4758047 /ug=Hs.82506 /len=1856	NM_004748	Hs.82506	NP_004739
11335	0.023762	COX11 cytochrome c oxidase assembly protein (yeast) (COX11), nuclear gene encoding mitochondrial protein, mRNA /cds=(48,878) /gb=NM_004375 /gi=17921983 /ug=Hs.241515 /len=2717	NM_004375	Hs.241515	NP_004366
11353	0.005412	mRNA; cDNA DKFZp434E2321 (from clone DKFZp434E2321); partial cds /cds=(1,1051) /gb=AL133619 /gi=6599234 /ug=Hs.29383 /len=3447	AL133619	Hs.29383	
11365	6.45E-05	Rho-specific guanine-nucleotide exchange factor 164 kDa (P164RHOGEF), mRNA /cds=(16,6207) /gb=NM_014786 /gi=21361457 /ug=Hs.45180 /len=7540	NM_014786	Hs.45180	NP_055601
11402	0.033283	cytochrome c, somatic (CYCS), mRNA /cds=(61,378) /gb=NM_018947 /gi=21361707 /ug=Hs.169248 /len=3990	NM_018947	Hs.169248	NP_061820

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11422	0.048172	CGI-45 protein (CGI-45), mRNA /cds=(194,1321) /gb=NM_015999 /gi=21361518 /ug=Hs.5298 /len=2108	NM_015999	Hs.5298	NP_057083
11446	0.021147	ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=NM_004152 /gi=9845504 /ug=Hs.281960 /len=986	NM_004152	Hs.281960	NP_004143
11479	0.033283	B lymphocyte activation-related protein BC-2048	AAL26788		
11482	0.013819	clone IMAGE:5271722, mRNA /gb=BC038786 /gi=24270905 /ug=Hs.190456 /len=1535	BC038786	Hs.190456	
11498	0.048653	clone MGC:16614 IMAGE:4111344, mRNA, complete cds /cds=(258,998) /gb=BC009313 /gi=14424569 /ug=Hs.373515 /len=2052	BC009313	Hs.193700	
11503	0.045762	hypothetical protein DKFZp564K0822 (DKFZP564K0822), mRNA /cds=(10,528) /gb=NM_030796 /gi=13540577 /ug=Hs.4750 /len=2789	NM_030796	Hs.4750	NP_110423
11519	0.008208	mRNA; cDNA DKFZp761O0611 (from clone DKFZp761O0611) /gb=AL834155 /gi=21739631 /ug=Hs.22969 /len=4502	AL834155	Hs.22969	
11539	0.041237	mRNA for KIAA1327 protein, partial cds. /cds=(1,5417) /gb=AB037748 /gi=20521883 /ug=Hs.106204 /len=6687	AB037748	Hs.106204	
11608	0.029809	EST(MR0-HT0407-140300-013-h01 HT0407)	BE159552		NP_003751
11615	0.048172	mRNA for KIAA0261 gene, partial cds. /cds=(1,3866) /gb=D87450 /gi=1665788 /ug=Hs.154978 /len=6155	D87450	Hs.154978	
11616	0.030757	EST qz49d11.x1 NCI_CGAP_Kid11 IMAGE:2030229 3'	AI493076		
11634	0.003233	hypothetical protein FLJ12118 (FLJ12118), mRNA /cds=(24,1718) /gb=NM_024537 /gi=13375694 /ug=Hs.381043 /len=1843	NM_024537	Hs.381043	NP_078813
11691	0.023762	cDNA sequence cDNA sequence DKFZp434D0935 (from clone cDNA sequence DKFZp434D0935)	AL117502		NP_149107
11700	0.031506	EST(qh83b09.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:1853561 3')	AI243681		NP_004727
11702	0.023762	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
11720	0.035141	mRNA for KIAA1509 protein, partial cds. /cds=(1,3983) /gb=AB040942 /gi=7959278 /ug=Hs.201500 /len=5283	AB040942	Hs.201500	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11783	0.015649	cDNA FLJ20709 fis, clone KAIA1124, highly similar to D86324 mRNA for CMP-N-acetylneuraminic acid. /gb=AK000716 /gi=7020978 /ug=Hs.24697 /len=3488	AK000716	Hs.24697	
11784	0.004687	sperm associated antigen 9 (SPAG9), transcript variant 1, mRNA /cds=(79,4002) /gb=NM_003971 /gi=27436919 /ug=Hs.129872 /len=4663	NM_003971	Hs.129872	NP_758853
11788	0.019933	Bardet-Biedl syndrome 2 (BBS2), mRNA /cds=(422,2587) /gb=NM_031885 /gi=22208996 /ug=Hs.332633 /len=2978	NM_031885	Hs.332633	NP_114091
11797	0.013819	UI-E-C10-aae-d-12-0-UI.s1 UI-E-C10 cDNA clone UI-E-C10-aae-d-12-0-UI 3', mRNA sequence /clone=UI-E-C10-aae-d-12-0-UI /clone_end=3' /gb=BM663444 /gi=18968780 /ug=Hs.395779 /len=1260	BM663444	Hs.395779	
11811	0.039115	FLJ11481 fis, clone HEMBA1001803 /cds=UNKNOWN /gb=AK021543 /gi=10432744 /ug=Hs.135159 /len=1539	AK021543	Hs.135159	
11816	0.019933	likely ortholog of rat V-1 protein (V-1), mRNA /cds=(229,585) /gb=NM_145808 /gi=21956644 /ug=Hs.21321 /len=3770	NM_145808	Hs.21321	NP_665807
11822	0.006234	protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C), mRNA /cds=(89,1633) /gb=NM_002719 /gi=4506022 /ug=Hs.171734 /len=4064	NM_002719	Hs.171734	NP_848703
11830	0.035141	DKFZp564P2064_s1 564 (synonym: hfbr2) cDNA clone DKFZp564P2064 3', mRNA sequence /clone=DKFZp564P2064 /clone_end=3' /gb=AL037172 /gi=5406623 /ug=Hs.328612 /len=682	AL037172	Hs.328612	
11839	0.015649	proteasome (prosome, macropain) 26S subunit, ATPase, 2 (PSMC2), mRNA /cds=(71,1372) /gb=NM_002803 /gi=24430152 /ug=Hs.61153 /len=1545	NM_002803	Hs.61153	NP_002794
11851	0.041237	mitochondrion, complete genome	NC_001807		
11860	0.009383	FOXJ2 forkhead factor (FHX), mRNA /cds=(490,2214) /gb=NM_018416 /gi=8923841 /ug=Hs.120844 /len=4873	NM_018416	Hs.120844	NP_060886
11865	0.039115	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA /cds=(407,1972) /gb=NM_000944 /gi=19923130 /ug=Hs.272458 /len=4425	NM_000944	Hs.272458	NP_000935

Spot	p-value	D scription	Gene Accession No.	Unigen Accession No.	Protein Accession No.
11875	0.045762	general transcription factor IIIC, polypeptide 3, 102kDa (GTF3C3), mRNA /cds=(94,2754) /gb=NM_012086 /gi=6912397 /ug=Hs.90847 /len=2961	NM_012086	Hs.90847	NP_036218
11876	0.047799	immediate early response 3 (IER3), transcript variant long, mRNA /cds=(30,611) /gb=NM_052815 /gi=16554596 /ug=Hs.76095 /len=1345	NM_052815	Hs.76095	NP_434702
11897	0.037084	hypothetical protein FLJ20701 (FLJ20701), mRNA /cds=(39,938) /gb=NM_017933 /gi=8923631 /ug=Hs.424598 /len=2284	NM_017933	Hs.424598	NP_060403
11921	0.028189	hypothetical protein DKFZp762O076 (DKFZp762O076), mRNA /cds=(77,850) /gb=NM_018710 /gi=24308164 /ug=Hs.21621 /len=2266	NM_018710	Hs.21621	NP_061180
11927	0.005038	CCR4-NOT transcription complex, subunit 8 (CNOT8), mRNA /cds=(245,1123) /gb=NM_004779 /gi=24496777 /ug=Hs.26703 /len=2489	NM_004779	Hs.26703	NP_004770
11938	0.022422	BTA1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 S. cerevisiae) (BTA1), mRNA /cds=(118,5667) /gb=NM_003972 /gi=27477069 /ug=Hs.180930 /len=6345	NM_003972	Hs.180930	NP_003963
11939	0.043451	tyrosine 3-monooxygenase/tryptophan 5- monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747	NM_012479	Hs.25001	NP_036611
11963	0.022422	proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813 /gi=5802981 /ug=Hs.75969 /len=2061	NM_006813	Hs.75969	NP_006804
11979	0.003594	chromosome 20 open reading frame 6 (C20orf6), mRNA /cds=(109,2664) /gb=NM_016649 /gi=22507381 /ug=Hs.88820 /len=3216	NM_016649	Hs.88820	NP_057733
12079	0.023762	EST nj89e12.s1 NCI_CGAP_Pr11 cDNA clone IMAGE:999694	AA552262		
12085	0.033283	retinoic acid induced 14 (RAI14), mRNA /cds=(112,3054) /gb=NM_015577 /gi=13470085 /ug=Hs.15165 /len=4925	NM_015577	Hs.15165	NP_056392
12123	0.031506	UI-H-BI0-aaa-f-10-0-UI.s1 NCI_CGAP_Sub1 cDNA clone IMAGE:2708874 3', mRNA sequence /clone=IMAGE:2708874 /clone_end=3' /gb=AW014102 /gi=5862859 /ug=Hs.304671 /len=654	AW014102	Hs.304671	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12231	0.01471	EST (UI-H-BI3-akf-b-05-0-UI.s1 NCI_CGAP_Sub5 clone IMAGE:2734017 3')	AW449060		NP_061174
12257	0.033283	EST390958 MAGE resequences, MAGP cDNA, mRNA sequence /gb=AW978849 /gi=8170126 /ug=Hs.124977 /len=678	AW978849	Hs.124977	
12259	0.048172	EST (Similar to pleckstrin homology, Sec7 and coiled/coil domains 3, clone MGC:5340 IMAGE:2984886, complete cds /cds=(3,542) /gb=BC008191 /gi=14198262 /ug=Hs.7984 /len=3720)	BC008191	Hs.7984	NP_004218
12297	0.026643	hypothetical protein MGC10744 (MGC10744), mRNA /cds=(77,184) /gb=NM_032354 /gi=14150156 /ug=Hs.25092 /len=1212	NM_032354	Hs.25092	NP_115730
12320	0.037084	EST(EST178403 Colon carcinoma (HCC) cell line cDNA 5' end similar to similar to ribosomal protein L30)	AA307521		NP_000980
12346	0.048172	selenoprotein H (SELH), mRNA /cds=(243,611) /gb=NM_170746 /gi=25014108 /ug=Hs.290874 /len=834	NM_170746	Hs.290874	NP_734467
12352	0.021147	UI-H-BI2-ahm-d-05-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2727224 3', mRNA sequence /clone=IMAGE:2727224 /clone_end=3' /gb=AW293452 /gi=6700088 /ug=Hs.16228 /len=634	AW293452	Hs.16228	
12355	0.021147	cDNA FLJ36238 fis, clone THYMU2001422. /gb=AK093557 /gi=21752458 /ug=Hs.345588 /len=2269	AK093557	Hs.345588	
12371	0.041237	ESTs, cDNA, 5' end /clone=BMFBFE06 /clone_end=5' /gb=AV756341 /gi=10914189 /ug=Hs.244273 /len=766	AV756341	Hs.244273	
12375	0.037157	UI-H-DT0-avk-p-22-0-UI.s1 NCI_CGAP_DT0 cDNA clone IMAGE:5880837 3', mRNA sequence /clone=IMAGE:5880837 /clone_end=3' /gb=BM996358 /gi=19721259 /ug=Hs.433458 /len=838	BM996358	Hs.433458	
12395	0.007162	SH3-domain binding protein 4 (SH3BP4), mRNA /cds=(336,3227) /gb=NM_014521 /gi=7657561 /ug=Hs.17667 /len=5145	NM_014521	Hs.17667	NP_055336
12399	0.001721	UI-E-CK1-afh-b-14-0-UI.r1 UI-E-CK1 cDNA clone UI-E-CK1-afh-b-14-0-UI 5', mRNA sequence /clone=UI-E-CK1-afh-b-14-0-UI /clone_end=5' /gb=BM702699 /gi=19015957 /ug=Hs.446508 /len=1088	BM702699	Hs.446508	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12412	0.001133	cDNA / IL3-NT0294-060401-533-D04 NT0294	BI041924		
12430	0.004687	mRNA; cDNA DKFZp686J19116 (from clone DKFZp686J19116) /gb=AL833458 /gi=21734100 /ug=Hs.428760 /len=3297	AL833458	Hs.428760	
12431	0.043451	ESTs, cDNA /gb=AW993259 /gi=8253410 /ug=Hs.113105 /len=678	AW993259	Hs.113105	
12432	0.037084	BX102166 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGp998H154200, mRNA sequence /clone=IMAGp998H154200; IMAGE:1655102 /gb=BX102166 /gi=27845155 /ug=Hs.131494 /len=724	BX102166	Hs.131494	
12435	0.045762	clone IMAGE:5263531, mRNA /gb=BC037740 /gi=22902216 /ug=Hs.18016 /len=5036	BC037740	Hs.18016	
12439	0.048653	cDNA FLJ12048 fis, clone HEMBB1001990. /gb=AK022110 /gi=10433433 /ug=Hs.289044 /len=1805	AK022110	Hs.289044	
12465	0.022422	ESTs, cDNA, 5' end /clone=IMAGE:3922401 /clone_end=5' /gb=BE894201 /gi=10356330 /ug=Hs.176376 /len=916	BE894201	Hs.176376	
12484	0.04068	qa50a08.x1 Soares_NhHMPu_S1 cDNA clone IMAGE:1690166 3', mRNA sequence /clone=IMAGE:1690166 /clone_end=3' /gb=AI123569 /gi=3539335 /ug=Hs.117060 /len=773	AI123569	Hs.117060	
12501	0.015649	EST(cDNA clone IMAGE:4693130 5')	BG539987		NP_005397
12513	0.00767	AGENCOURT_8841454 Lupski_sciatic_nerve cDNA clone IMAGE:6199422 5', mRNA sequence /clone=IMAGE:6199422 /clone_end=5' /gb=BQ924341 /gi=22339372 /ug=Hs.442591 /len=930	BQ924341	Hs.442591	
12514	0.041237	DCBCQH10 DCB cDNA, mRNA sequence /gb=BU198777 /gi=22717083 /ug=Hs.50273 /len=867	BU198777	Hs.50273	
12574	1.92E-04	UI-H-ED0-awx-b-15-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5824814 3', mRNA sequence /clone=IMAGE:5824814 /clone_end=3' /gb=BQ020068 /gi=19755345 /ug=Hs.396278 /len=1351	BQ020068	Hs.396278	
12580	0.035141	No significant match	SEQ.ID.No.34		
12609	0.010265	Similar to hypothetical protein FLJ31322, clone IMAGE:5296647, mRNA /gb=BC045189 /gi=28277118 /ug=Hs.350001 /len=2971	BC045189	Hs.350001	NP_787112

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12656	0.035141	hypothetical protein DKFZp564B1162 (DKFZP564B1162), mRNA /cds=(661,2628) /gb=NM_031305 /gi=13775229 /ug=Hs.93589 /len=4593	NM_031305	Hs.93589	NP_112595
12664	0.010023	hypothetical protein FLJ12888 (FLJ12888), mRNA /cds=(333,2210) /gb=NM_024945 /gi=13376426 /ug=Hs.284137 /len=3413	NM_024945	Hs.284137	NP_079221
12695	0.025168	mitochondrion, complete genome	NC_001807		
12720	0.012975	mRNA; cDNA DKFZp667O1616 (from clone DKFZp667O1616) /gb=AL713722 /gi=19584452 /ug=Hs.365655 /len=1773	AL713722	Hs.365655	
12725	2.60E-04	EST(CM3-BN0151-130400-146-f01_1 BN0151)	BE008220		
12734	0.023762	mRNA for FLJ00201 protein. /cds=(1,2119) /gb=AK074129 /gi=18676605 /ug=Hs.353001 /len=4443	AK074129	Hs.353001	
12739	0.022422	xn86b03.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2701325 3', mRNA sequence /clone=IMAGE:2701325 /clone_end=3' /gb=AW195867 /gi=6475097 /ug=Hs.370978 /len=571	AW195867	Hs.370978	
12743	0.041237	EST (RC3-BN0036-090200-011-h11 BN0036 cDNA)	AW994082		
12750	0.019933	mRNA; cDNA DKFZp667H216 (from clone DKFZp667H216) /gb=AL833204 /gi=21733834 /ug=Hs.356145 /len=3782	AL833204	Hs.356145	
12794	0.039115	ribosomal protein L12 (RPL12), mRNA /cds=(89,586) /gb=NM_000976 /gi=15431291 /ug=Hs.405042 /len=632	NM_000976	Hs.405042	NP_000967
12797	0.026643	EST(xu17f02.x1 NCI_CGAP_Co14 cDNA clone IMAGE:2800443 3')	AW272306		NP_002201
12798	0.015649	UI-H-DF0-bem-a-10-0-UI.s1: NCI_CGAP_DF0 cDNA clone UI-H-DF0-bem-a-10-0-UI 3', mRNA sequence /clone=UI-H-DF0-bem-a-10-0-UI /clone_end=3' /gb=CA425521 /gi=24788247 /ug=Hs.411829 /len=1131	CA425521	Hs.411829	
12835	0.013819	AGENCOURT_8856629 Lupski_sciatic_nerve cDNA clone IMAGE:6200636 5', mRNA sequence /clone=IMAGE:6200636 /clone_end=5' /gb=BQ947179 /gi=22362657 /ug=Hs.356605 /len=1277	BQ947179	Hs.356605	
12843	0.008208	cDNA clone IMAGE:123789 3' similar to contains Alu repetitive element; contains THR repetitive element ; Soares fetal liver spleen 1NFLS	R01434		
12847	0.041237	EST(cDNA clone IMAGE:4472298 5')	BG251774		NP_598001

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12848	0.006762	cDNA: FLJ23165 fis, clone LNG09846. /gb=AK026818 /gi=10439763 /ug=Hs.279898 /len=2117	AK026818	Hs.279898	
12871	0.048172	wg97c03.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2379172 3' similar to contains L1.b1 L1 repetitive element ;, mRNA sequence /clone=IMAGE:2379172 /clone_end=3' /gb=AI762342 /gi=5178009 /ug=Hs.304298 /len=531	AI762342	Hs.304298	
12882	0.026643	DKFZp564A2463 (from clone DKFZp564A2463) /cds=UNKNOWN /gb=AL137573 /gi=6808283 /ug=Hs.43143 /len=1320	AL137573	Hs.43143	
12891	0.045762	cDNA FLJ38472 fis, clone FEBRA2022148. /gb=AK095791 /gi=21755125 /ug=Hs.50150 /len=2454	AK095791	Hs.50150	
12892	0.004048	ESTs, cDNA, 5' end /clone=IMAGE:1554245 /clone_end=5' /gb=AI792925 /gi=5340641 /ug=Hs.137097 /len=585	AI792925	Hs.137097	
12898	0.025168	603395193F1 NIH_MGC_90 cDNA clone IMAGE:5405278 5', mRNA sequence /clone=IMAGE:5405278 /clone_end=5' /gb=BI871283 /gi=16044958 /ug=Hs.443147 /len=845	BI871283	Hs.443147	
12907	0.045762	UI-E-EO0-ahy-j-09-0-UI.r1 UI-E-EO0 cDNA clone UI-E-EO0-ahy-j-09-0-UI 5', mRNA sequence /clone=UI-E-EO0-ahy-j- 09-0-UI /clone_end=5' /gb=BM722772 /gi=19043589 /ug=Hs.433569 /len=1166	BM722772	Hs.433569	
12961	0.028189	yp92f09.r1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:194921 5', mRNA sequence /clone=IMAGE:194921 /clone_end=5' /gb=R91059 /gi=958599 /ug=Hs.330761 /len=430	R91059	Hs.330761	
13007	0.023762	EST(cDNA clone GKCAHD03 5')	AV696986		NP_072179
13042	0.033283	EST(cDNA clone IMAGE:4717063 5')	BG569807		
13065	0.003487	control			
13109	0.025168	cDNA FLJ13752 fis, clone PLACE3000352. /gb=AK023814 /gi=10435863 /ug=Hs.144871 /len=3904	AK023814	Hs.144871	
13110	5.57E-04	hypothetical protein P1 p373c6 (P1P373C6), mRNA /cds=(254,1891) /gb=NM_019110 /gi=17738284 /ug=Hs.44720 /len=2316	NM_019110	Hs.44720	NP_061983

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13127	0.035141	brain abundant, membrane attached signal protein 1 (BASP1), mRNA /cds=(53,736) /gb=NM_006317 /gi=5453749 /ug=Hs.79516 /len=1486	NM_006317	Hs.79516	NP_006308
13139	0.035141	chromosome 1 open reading frame 8 (C1orf8), mRNA /cds=(251,1222) /gb=NM_004872 /gi=27545320 /ug=Hs.416495 /len=1709	NM_004872	Hs.416495	NP_004863
13151	0.039115	cell division cycle associated 4 (CDCA4), transcript variant 1, mRNA /cds=(164,889) /gb=NM_017955 /gi=22027508 /ug=Hs.34045 /len=2171	NM_017955	Hs.34045	NP_663747
13160	0.011417	retinoid X receptor, beta (RXRB), mRNA /cds=(180,1781) /gb=NM_021976 /gi=27436942 /ug=Hs.79372 /len=2892	NM_021976	Hs.79372	NP_068811
13161	0.00767	hypothetical protein FLJ10035 (FLJ10035), mRNA /cds=(251,1132) /gb=NM_030803 /gi=24475809 /ug=Hs.16390 /len=2404	NM_030803	Hs.16390	NP_110430
13188	0.001867	hypothetical protein PRO2013 (PRO2013), mRNA /cds=(136,381) /gb=NM_021243 /gi=24308272 /ug=Hs.238205 /len=876	NM_021243	Hs.238205	
13193	0.048172	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA), mRNA /cds=(210,1139) /gb=NM_002715 /gi=4506016 /ug=Hs.91773 /len=2181	NM_002715	Hs.91773	NP_002706
13206	0.005412	spinal cord-derived growth factor-B (SCDGF-B), transcript variant 1, mRNA /cds=(176,1288) /gb=NM_025208 /gi=15451919 /ug=Hs.112885 /len=3808	NM_025208	Hs.112885	NP_149126
13207	0.002024	ARP8 actin-related protein 8 (yeast) (ACTR8), mRNA /cds=(5,1129) /gb=NM_022899 /gi=12597636 /ug=Hs.124219 /len=2797	NM_022899	Hs.124219	NP_075050
13225	0.017682	hypothetical protein MGC4276 similar to CG8198 (MGC4276), mRNA /cds=(70,462) /gb=NM_030940 /gi=24475709 /ug=Hs.177776 /len=1978	NM_030940	Hs.177776	NP_112202
13227	0.033283	cysteine dioxygenase, type I (CDO1), mRNA /cds=(255,857) /gb=NM_001801 /gi=4502754 /ug=Hs.3229 /len=1556	NM_001801	Hs.3229	NP_001792
13302	0.025168	nuclear pore complex protein (NUP107), mRNA /cds=(116,2893) /gb=NM_020401 /gi=9966880 /ug=Hs.236204 /len=3131	NM_020401	Hs.236204	NP_065134

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13304	0.029809	wl27d01.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2426113 3', mRNA sequence /clone=IMAGE:2426113 /clone_end=3' /gb=AI866216 /gi=5530323 /ug=Hs.413738 /len=133	AI866216	Hs.413738	
13309	0.01471	nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA /cds=(217,3171) /gb=NM_000901 /gi=4505198 /ug=Hs.1790 /len=5749	NM_000901	Hs.1790	NP_000892
13319	0.004357	cDNA FLJ33540 fis, clone BRAMY2007613. /gb=AK090859 /gi=21749098 /ug=Hs.21213 /len=2030	AK090859	Hs.21213	
13357	0.005811	mRNA; cDNA DKFZp451B1418 (from clone DKFZp451B1418) /gb=AL832622 /gi=21733197 /ug=Hs.446489 /len=5612	AL832622	Hs.446489	
13425	0.025168	EST(wk79e07.x1 NCI_CGAP_Pan1 clone IMAGE:2421636 3')	AI813780		
13453	0.035141	mesoderm induction early response 1 (MIR1), mRNA /cds=(234,1844) /gb=NM_020948 /gi=24308260 /ug=Hs.222746 /len=4972	NM_020948	Hs.222746	NP_065999
13457	0.045762	translin (TSN), mRNA /cds=(236,922) /gb=NM_004622 /gi=20302160 /ug=Hs.75066 /len=3408	NM_004622	Hs.75066	NP_004613
13459	0.039115	N-ethylmaleimide-sensitive factor (NSF), mRNA /cds=(61,2295) /gb=NM_006178 /gi=11079227 /ug=Hs.108802 /len=3960	NM_006178	Hs.108802	NP_006169
13467	0.010701	EST(zt04d06.r1 NCI_CGAP_GCB1 clone IMAGE:712139 5')	AA280235		NP_005728
13469	0.029809	clone IMAGE:5299642, mRNA /gb=BC041913 /gi=27469540 /ug=Hs.17132 /len=2227	BC041913	Hs.17132	
13501	0.007162	likely ortholog of mouse WD-40-repeat-containing protein with a SOCS box 2 (WSB2), mRNA /cds=(66,1280) /gb=NM_018639 /gi=20149658 /ug=Hs.136644 /len=2610	NM_018639	Hs.136644	NP_061109
13513	0.015649	EST(PM3-SN0020-270300-001-h08 SN0020)	AW865025		NP_115668
13520	0.031506	EST(tz32c11.x1 NCI_CGAP_Ut2 clone IMAGE:2290292 3')	AI631079		NP_079436
13522	0.021147	mRNA; cDNA DKFZp451O1818 (from clone DKFZp451O1818) /gb=AL832650 /gi=21733226 /ug=Hs.12396 /len=4870	AL832650	Hs.12396	
13530	7.32E-04	synaptic nuclei expressed gene 1 (SYNE-1), transcript variant beta, mRNA /cds=(121,10086) /gb=NM_015293 /gi=19526752 /ug=Hs.192102 /len=10742	NM_015293	Hs.192102	NP_598411

Spot	p-value	D description	Gene Accession No.	Unigen Accession No.	Protein Accession No.
13562	0.041237	AGENCOURT_6653840 NIH_MGC_116 cDNA clone IMAGE:5761286 5', mRNA sequence /clone=IMAGE:5761286 /clone_end=5' /gb=BM924828 /gi=19375207 /ug=Hs.181174 /len=1422	BM924828	Hs.181174	
13599	0.00767	mRNA; cDNA DKFZp313E1012 (from clone DKFZp313E1012) /gb=AL832661 /gi=21733237 /ug=Hs.94694 /len=3233	AL832661	Hs.94694	
13601	0.001234	similar to rat myomegalin (LOC64182), mRNA /cds=(336,1268) /gb=NM_022359 /gi=21314705 /ug=Hs.333512 /len=1717	NM_022359	Hs.333512	NP_071754
13602	0.003758	UI-1-BC1p-asi-a-02-0-UI.s1 NCI_CGAP_P13 cDNA clone UI-1-BC1p-asi-a-02-0-UI 3', mRNA sequence /clone=UI-1-BC1p-asi-a-02-0-UI /clone_end=3' /gb=BQ011545 /gi=19736446 /ug=Hs.361171 /len=1143	BQ011545	Hs.361171	
13615	0.018779	mRNA full length insert cDNA clone EUROIMAGE 1476475 /gb=AJ420560 /gi=17066424 /ug=Hs.93231 /len=1346	AJ420560	Hs.93231	
13619	0.014281	FLJ30633 fis, clone CTONG2002418, weakly similar to Homo sapiens scaffold attachment factor B (SAF-B) mRNA (AK055195.1)	AK055195	Hs.331328	NP_079031
13642	0.031506	calpastatin (CAST), transcript variant 2, mRNA /cds=(155,2215) /gb=NM_173060 /gi=27765084 /ug=Hs.359682 /len=4296	NM_173060	Hs.359682	NP_775085
13665	0.003758	ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA /cds=(22,459) /gb=NM_003350 /gi=12025664 /ug=Hs.79300 /len=1535	NM_003350	Hs.79300	NP_003341
13670	0.048172	hypothetical protein FLJ11506 (FLJ11506), mRNA /cds=(16,963) /gb=NM_024666 /gi=20070334 /ug=Hs.77703 /len=2774	NM_024666	Hs.77703	NP_078942
13729	0.023762	EH-domain containing 1 (EHD1), mRNA /cds=(247,1851) /gb=NM_006795 /gi=5803008 /ug=Hs.155119 /len=3508	NM_006795	Hs.155119	NP_006786
13731	0.022422	diacylglycerol O-acyltransferase homolog 2 (mouse) (DGAT2), mRNA /cds=(777,1670) /gb=NM_032564 /gi=14211870 /ug=Hs.334305 /len=2713	NM_032564	Hs.334305	NP_115953
13768	0.021586	likely ortholog of mouse hypoxia induced gene 1 (HIG1), mRNA /cds=(93,374) /gb=NM_014056 /gi=7661619 /ug=Hs.7917 /len=1362	NM_014056	Hs.7917	NP_054775
13786	0.011417	mitochondrion, complete genome	NC_001807		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13795	0.045762	hypothetical protein FLJ21302 (FLJ21302), mRNA /cds=(91,1203) /gb=NM_022901 /gi=12597640 /ug=Hs.128071 /len=3160	NM_022901	Hs.128071	NP_075052
13797	0.037084	603041572T1 NIH_MGC_116 cDNA clone IMAGE:5163112 3', mRNA sequence /clone=IMAGE:5163112 /clone_end=3' /gb=BI517954 /gi=15342746 /ug=Hs.398211 /len=964	BI517954	Hs.398211	
13835	0.013819	mRNA for KIAA1078 protein, partial cds. /cds=(1,4098) /gb=AB029001 /gi=20521755 /ug=Hs.23585 /len=6740	AB029001	Hs.23585	
13945	0.018779	EST(tx88e11.x1 NCI_CGAP_Ut4 clone IMAGE:2276684 3' contains Alu repeat)	AI690725		
13961	0.021147	Novel	SEQ.ID.No.90		
13986	0.019933	phosphodiesterase 6D, cGMP-specific, rod, delta (PDE6D), mRNA /cds=(151,603) /gb=NM_002601 /gi=4505670 /ug=Hs.48291 /len=1131	NM_002601	Hs.48291	NP_002592
14059	0.045762	EST (cDNA clone IMAGE:2490676 3')	AI972954		NP_000996
14076	0.023762	hypothetical protein FLJ22611 (FLJ22611), mRNA /cds=(295,1923) /gb=NM_032226 /gi=24308321 /ug=Hs.27774 /len=2821	NM_032226	Hs.27774	NP_115602
14111	0.039115	hypothetical protein MGC3121 (MGC3121), mRNA /cds=(179,1936) /gb=NM_024031 /gi=13128979 /ug=Hs.293629 /len=2063	NM_024031	Hs.293629	NP_076936
14122	0.033283	602152950F1 NIH_MGC_81 cDNA clone IMAGE:4293853 5', mRNA sequence /clone=IMAGE:4293853 /clone_end=5' /gb=BF673050 /gi=11946945 /ug=Hs.208558 /len=830	BF673050	Hs.208558	
14129	0.035141	zu07g05.s1 Soares_testis_NHT cDNA clone IMAGE:731192 3' similar to P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ;, mRNA sequence /clone=IMAGE:731192 /clone_end=3' /gb=AA417352 /gi=2077434 /ug=Hs.445851 /len=519	AA417352	Hs.445851	
14132	0.00767	EST (ie64h03.x1 Homo sapiens cDNA, 3' end/clone_end=3' /gb=BI963813 /gi=16338218 /ug=Hs.349015/len=555)	BI963813	Hs.349015	NP_116159
14163	0.016639	EST(AV657608 GLC cDNA clone GLCFDF10 3')	AV657608		
14219	0.041237	cDNA FLJ37978 fis, clone CTONG2010348. /gb=AK095297 /gi=21754529 /ug=Hs.381207 /len=3284	AK095297	Hs.381207	
14249	0.043451	mitochondrion, complete genome	NC_001807		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14266	0.028189	EST, cDNA /clone=IMAGE:1266535 /gb=AA729300 /gi=2750659 /ug=Hs.325555 /len=173	AA729300	Hs.325555	
14268	0.037084	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta (CAMK2D), transcript variant 1, mRNA /cds=(505,1941) /gb=NM_172127 /gi=26667185 /ug=Hs.111460 /len=4098	NM_172127	Hs.111460	NP_742126
14294	0.035141	decorin (DCN), transcript variant A1, mRNA /cds=(200,1279) /gb=NM_001920 /gi=19743844 /ug=Hs.433989 /len=1751	NM_001920	Hs.433989	NP_598014
14295	0.011417	cDNA: FLJ22765 fis, clone KAIA1180. /gb=AK026418 /gi=10439279 /ug=Hs.163986 /len=1994	AK026418	Hs.163986	
14375	8.74E-04	ESTs, cDNA, 3' end /clone=IMAGE:2402646 /clone_end=3' /gb=AI768858 /gi=5235367 /ug=Hs.157149 /len=562	AI768858	Hs.157149	NP_066012
14386	0.004357	UI-E-EJ0-aik-i-20-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-aik-i-20-0-UI 5', mRNA sequence /clone=UI-E-EJ0-aik-i-20-0-UI /clone_end=5' /gb=BM727413 /gi=19048746 /ug=Hs.112619 /len=1667	BM727413	Hs.112619	
14387	0.016639	likely ortholog of rat V-1 protein (V-1), mRNA /cds=(229,585) /gb=NM_145808 /gi=21956644 /ug=Hs.21321 /len=3770	NM_145808	Hs.21321	NP_665807
14417	0.019933	proteasome (prosome, macropain) subunit, alpha type, 4 (PSMA4), mRNA /cds=(137,922) /gb=NM_002789 /gi=23110940 /ug=Hs.251531 /len=1189	NM_002789	Hs.251531	NP_002780
14453	0.023762	No significant match, ORF+1(16~273)	SEQ.ID.No.41		
14455	0.004357	No significant match, ORF+3(135~404)	SEQ.ID.No.50		
14504	0.021586	No significant match (ORF:none)	SEQ.ID.No.22		
14521	0.036435	HSC15D092 normalized infant brain cDNA cDNA clone c-15d09 3', mRNA sequence /clone=c-15d09 /clone_end=3' /gb=Z39248 /gi=562440 /ug=Hs.27328 /len=352	Z39248	Hs.27328	
14524	0.001721	EST (wa75f06.x1 Soares_NFL_T_GBC_S1	AI685268		
14546	4.21E-04	EST (601819273F1 NIH_MGC_58 cDNA clone IMAGE:4051098 5')	BF130672		NP_003655
14549	0.036435	UI-H-BI3-alq-c-04-0-UI.s1 NCI_CGAP_Sub5 cDNA clone IMAGE:3068166 3', mRNA sequence /clone=IMAGE:3068166 /clone_end=3' /gb=BF512182 /gi=11597361 /ug=Hs.196953 /len=864	BF512182	Hs.196953	

Spot	p-valu	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14560	0.017682	TRAM-like protein (KIAA0057), mRNA /cds=(76,1188) /gb=NM_012288 /gi=6912449 /ug=Hs.153954 /len=6974	NM_012288	Hs.153954	NP_036420
14614	0.019094	EST(yq95a02.r1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:203498 5' similar to contains Alu repetitive element)	H56096		
14637	0.01471	hypothetical protein PRO1331 (PRO1331), mRNA /cds=(423,617) /gb=NM_030778 /gi=13562115 /ug=Hs.301824 /len=1634	NM_030778	Hs.301824	NP_110405
14704	0.043451	qz33c01.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2028672 3', mRNA sequence /clone=IMAGE:2028672 /clone_end=3' /gb=AI262059 /gi=3870262 /ug=Hs.386784 /len=229	AI262059	Hs.386784	
14833	0.013819	EST380251 MAGE resequences, MAGJ cDNA, mRNA sequence /gb=AW968281 /gi=8158016 /ug=Hs.319460 /len=689	AW968281	Hs.319460	
14837	0.026643	EST(RC4-CT0322-261299-011-h03 CT0322 Homo sapiens cDNA, mRNA sequence)	AW857814		
14842	0.008208	mitochondrion, complete genome	NC_001807		
14864	0.018779	cDNA FLJ31594 fis, clone NT2RI2002507	AK056156		NP_006818
14934	0.007918	No significant match (ORF:+1:1~102[102])	SEQ.ID.No.59		
14942	0.005811	EST, cDNA /gb=AW360966 /gi=6865616 /ug=Hs.6653 /len=661	AW360966	Hs.6653	NP_055942
14948	0.048172	EST(Fetal Cochlea Homo sapiens cDNA clone IMAGE:2537435 5')	BI497119		NP_006826

TABLE 3C					
Genes Corresponding To Differentially Expressed Genes in Figure 10-Allergies					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
167	0.041383	corticotropin releasing hormone binding protein (CRHBP), mRNA /cds=(94,1062) /gb=NM_001882 /gi=5921997 /ug=Hs.115617 /len=1295	NM_001882	Hs.115617	NP_001873
169	0.041383	nuclear protein double minute 1 (MDM1), mRNA /cds=(93,2237) /gb=NM_017440 /gi=24586654 /ug=Hs.12871 /len=2942	NM_017440	Hs.12871	NP_064513
170	0.04789	Duffy blood group (FY), mRNA /cds=(495,1511) /gb=NM_002036 /gi=4503818 /ug=Hs.183 /len=1559	NM_002036	Hs.183	NP_002027
178	0.025981	zinc finger protein 161 (ZNF161), mRNA /cds=(42,1592) /gb=NM_007146 /gi=6005967 /ug=Hs.223754 /len=2306	NM_007146	Hs.223754	NP_009077
179	0.04789	ubiquitin specific protease 9, X chromosome (fat facets-like Drosophila) (USP9X), transcript variant 1, mRNA /cds=(60,7751) /gb=NM_004652 /gi=11641424 /ug=Hs.77578 /len=8171	NM_004652	Hs.77578	NP_068706
205	0.01859	mRNA for KIAA0268 gene, partial cds. /cds=(1,3582) /gb=D87742 /gi=1665824 /ug=Hs.241552 /len=5976	D87742	Hs.241552	
248	0.04789	hemoglobin, beta (HBB), mRNA /cds=(51,494) /gb=NM_000518 /gi=28302128 /ug=Hs.155376 /len=626	NM_000518	Hs.155376	NP_000509
252	0.01859	hypothetical protein HSPC177 (HSPC177), mRNA /cds=(80,739) /gb=NM_016410 /gi=20127557 /ug=Hs.36237 /len=1434	NM_016410	Hs.36237	NP_057494
278	0.041383	coatomer protein complex, subunit gamma (COPG), mRNA /cds=(76,2700) /gb=NM_016128 /gi=21359909 /ug=Hs.266914 /len=3075	NM_016128	Hs.266914	NP_663768
313	0.020961	FLI-LRR associated protein-1	AF045573		NP_032541
324	0.030485	phosphoprotein enriched in astrocytes 15 (PEA15), mRNA /cds=(194,586) /gb=NM_003768 /gi=21359835 /ug=Hs.194673 /len=2486	NM_003768	Hs.194673	NP_003759
355	0.025981	double-stranded RNA-binding nuclear protein NFAR-1	AF167569		NP_703194
394	0.04789	FLJ11874 fis, clone HEMBA1007073 /cds=UNKNOWN /gb=AK021936 /gi=10433239 /ug=Hs.367819 /len=2737	AK021936	Hs.367819	
419	0.035601	SYNCRIP	AB035725		NP_062770
429	0.025981	NPD009 protein (NPD009), mRNA /cds=(1327,1677) /gb=NM_020686 /gi=24476005 /ug=Hs.283675 /len=2514	NM_020686	Hs.283675	NP_065737

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
458	0.025981	zinc finger protein 354B (ZNF354B), mRNA /cds=(180,2018) /gb=NM_058230 /gi=17530790 /ug=Hs.325804 /len=2140	NM_058230	Hs.325804	NP_478137
460	0.035601	sorting nexin 3 (SNX3), transcript variant 3, mRNA /cds=(326,667) /gb=NM_152828 /gi=23111042 /ug=Hs.12102 /len=1559	NM_152828	Hs.12102	NP_690041
549	0.011794	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 (GNB2L1), mRNA /cds=(96,1049) /gb=NM_006098 /gi=24475893 /ug=Hs.5662 /len=1093	NM_006098	Hs.5662	NP_006089
589	0.025981	AGENCOURT_6640990 NIH_MGC_68 cDNA clone IMAGE:5735856 5', mRNA sequence /clone=IMAGE:5735856 /clone_end=5' /gb=BM907553 /gi=19357932 /ug=Hs.424427 /len=645	BM907553	Hs.424427	
625	0.030485	fragile X mental retardation 1 (FMR1), mRNA /cds=(220,2118) /gb=NM_002024 /gi=4503764 /ug=Hs.89764 /len=4362	NM_002024	Hs.89764	NP_002015
633	0.044987	A kinase (PRKA) anchor protein 13 (AKAP13), transcript variant 2, mRNA /cds=(214,8655) /gb=NM_007200 /gi=21493028 /ug=Hs.301946 /len=10156	NM_007200	Hs.301946	NP_658913
648	0.044987	HLA class-I (HLA-A26) heavy chain, complete cds (clone cMIY-1)	D32129		NP_002107
658	0.001504	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 /len=1705	NM_006855	Hs.250696	NP_057839
662	0.022033	insulin-like growth factor binding protein 5 (IGFBP5), mRNA /cds=(752,1570) /gb=NM_000599 /gi=10834981 /ug=Hs.380833 /len=1722	NM_000599	Hs.380833	NP_000590
693	0.04789	ubiquitin-conjugating enzyme E2L 3 (UBE2L3), mRNA /cds=(16,480) /gb=NM_003347 /gi=4507788 /ug=Hs.108104 /len=2845	NM_003347	Hs.108104	NP_003338
700	0.022033	major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA /cds=(65,829) /gb=NM_019111 /gi=18641378 /ug=Hs.409805 /len=1237	NM_019111	Hs.409805	NP_061984
709	0.019692	ATP synthase, H transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O), mRNA /cds=(37,678) /gb=NM_001697 /gi=4502302 /ug=Hs.433960 /len=772	NM_001697	Hs.433960	NP_001688
721	0.025981	mitochondrion, complete genome	NC_001807		

Spot	p-value	Description	Gen Accession No.	Unigene Accession No.	Protein Accession No.
726	0.01081	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747	NM_012479	Hs.25001	NP_036611
765	0.041383	peripheral myelin protein 22 (PMP22), transcript variant 1, mRNA /cds=(209,691) /gb=NM_000304 /gi=24430161 /ug=Hs.103724 /len=1828	NM_000304	Hs.103724	NP_696997
771	0.04789	zinc finger protein (ZFD25) (62% aa)	AB027251		NP_057304
772	0.04789	acid sphingomyelinase (ASM) gene, exons a, and alternative a (3' end), b and c (5' end).	M59917		
806	0.035601	ring finger protein 19 (RNF19), mRNA /cds=(318,2834) /gb=NM_015435 /gi=19923421 /ug=Hs.48320 /len=4357	NM_015435	Hs.48320	NP_056250
807	0.025981	KIAA0102 gene product (KIAA0102), mRNA /cds=(308,679) /gb=NM_014752 /gi=7661907 /ug=Hs.77665 /len=1370	NM_014752	Hs.77665	NP_055567
808	0.035601	PIX1 mRNA (ORF)	AF037219		NP_570854
809	0.01859	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) (MCCC1), mRNA /cds=(133,2310) /gb=NM_020166 /gi=13518227 /ug=Hs.47649 /len=2528	NM_020166	Hs.47649	NP_064551
815	0.022033	SnRNP assembly defective 1 (SAD1), mRNA /cds=(493,1467) /gb=NM_006590 /gi=5730024 /ug=Hs.12820 /len=2166	NM_006590	Hs.12820	NP_006581
829	0.022033	zinc finger protein 103 (mouse) (ZFP103), mRNA /cds=(923,2980) /gb=NM_005667 /gi=5031824 /ug=Hs.155968 /len=3423	NM_005667	Hs.155968	NP_005658
844	0.013024	sorting nexin 2 (SNX2), mRNA /cds=(50,1609) /gb=NM_003100 /gi=23111037 /ug=Hs.11183 /len=2091	NM_003100	Hs.11183	NP_003091
846	0.04789	LAG1 longevity assurance 2 (S. cerevisiae) (LASS2), mRNA /cds=(50,742) /gb=NM_013384 /gi=9937997 /ug=Hs.285976 /len=1646	NM_013384	Hs.285976	NP_071358
847	0.01859	peroxisomal biogenesis factor 3 (PEX3), mRNA /cds=(64,1185) /gb=NM_003630 /gi=4505726 /ug=Hs.7277 /len=1979	NM_003630	Hs.7277	NP_003621
865	0.025981	mitochondrion, complete genome	NC_001807		
869	0.008919	receptor associated protein 80 (RAP80), mRNA /cds=(110,2269) /gb=NM_016290 /gi=21361592 /ug=Hs.7889 /len=2516	NM_016290	Hs.7889	NP_057374
873	0.04789	dynactin 4 (p62) (DCTN4), mRNA /cds=(22,1404) /gb=NM_016221 /gi=19923450 /ug=Hs.328865 /len=3837	NM_016221	Hs.328865	NP_057305
874	0.025981	proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813 /gi=5802981 /ug=Hs.75969 /len=2061	NM_006813	Hs.75969	NP_006804

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
877	0.035601	ring finger protein 11 (RNF11), mRNA /cds=(128,592) /gb=NM_014372 /gi=7657519 /ug=Hs.96334 /len=2529	NM_014372	Hs.96334	NP_055187
878	0.04789	protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA /cds=(30,2372) /gb=NM_002835 /gi=18375651 /ug=Hs.62 /len=3161	NM_002835	Hs.62	NP_002826
894	0.04789	splicing factor, arginine/serine-rich 11 (SFRS11), mRNA /cds=(125,1579) /gb=NM_004768 /gi=23111060 /ug=Hs.433581 /len=2775	NM_004768	Hs.433581	NP_004759
896	0.022033	hypothetical protein FLJ32949 (FLJ32949), mRNA /cds=(1,2277) /gb=NM_173812 /gi=27883873 /ug=Hs.125472 /len=2277	NM_173812	Hs.125472	NP_776173
901	0.04789	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2 (STAM2), mRNA /cds=(351,1928) /gb=NM_005843 /gi=21265030 /ug=Hs.17200 /len=3928	NM_005843	Hs.17200	NP_005834
904	0.041383	tumor susceptibility gene 101 (TSG101), mRNA /cds=(127,1299) /gb=NM_006292 /gi=18765712 /ug=Hs.118910 /len=1550	NM_006292	Hs.118910	NP_006283
906	0.041383	transaldolase 1 (TALDO1), mRNA /cds=(51,1064) /gb=NM_006755 /gi=5803186 /ug=Hs.77290 /len=1319	NM_006755	Hs.77290	NP_006746
909	0.00388	integral membrane protein Tmp21-l (p23)	AJ004913		NP_006818
910	0.041383	CD9 antigen (p24) (CD9), mRNA /cds=(112,798) /gb=NM_001769 /gi=21237762 /ug=Hs.1244 /len=1246	NM_001769	Hs.1244	NP_001760
923	0.003097	eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa (EIF3S3), mRNA /cds=(6,1064) /gb=NM_003756 /gi=4503514 /ug=Hs.58189 /len=1280	NM_003756	Hs.58189	NP_003747
947	0.041383	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein (ID4), mRNA /cds=(370,855) /gb=NM_001546 /gi=19923138 /ug=Hs.34853 /len=2389	NM_001546	Hs.34853	NP_001537
968	0.04789	translin (TSN), mRNA /cds=(236,922) /gb=NM_004622 /gi=20302160 /ug=Hs.75066 /len=3408	NM_004622	Hs.75066	NP_004613
1030	0.030485	px19-like protein (PX19), mRNA /cds=(177,836) /gb=NM_013237 /gi=7019508 /ug=Hs.279529 /len=1217	NM_013237	Hs.279529	NP_037369
1034	0.041383	N-myristoyltransferase 2 (NMT2), mRNA /cds=(47,1543) /gb=NM_004808 /gi=4758815 /ug=Hs.122647 /len=2838	NM_004808	Hs.122647	NP_004799
1058	0.025981	Williams-Beuren syndrome chromosome region 1 (WBSCR1), transcript variant 1, mRNA /cds=(9,755) /gb=NM_022170 /gi=11559922 /ug=Hs.180900 /len=2546	NM_022170	Hs.180900	NP_114381

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Prot in Accession No.
1209	0.04789	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6) (MPP6), mRNA /cds=(300,1922) /gb=NM_016447 /gi=21361597 /ug=Hs.108931 /len=2201	NM_016447	Hs.108931	NP_057531
1318	0.038534	SH3-domain binding protein 5 (BTK-associated) (SH3BP5), mRNA /cds=(64,1341) /gb=NM_004844 /gi=4759057 /ug=Hs.109150 /len=2570	NM_004844	Hs.109150	NP_004835
1385	0.032841	hypothetical protein FLJ11267 (FLJ11267), mRNA /cds=(292,771) /gb=NM_019607 /gi=9624987 /ug=Hs.165741 /len=1817	NM_019607	Hs.165741	NP_062553
1409	0.035601	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2 (KDEL2), mRNA /cds=(13,651) /gb=NM_006854 /gi=8051609 /ug=Hs.372755 /len=1153	NM_006854	Hs.372755	NP_006845
1437	0.01859	SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA /cds=(373,1902) /gb=NM_000346 /gi=4557852 /ug=Hs.2316 /len=3936	NM_000346	Hs.2316	NP_000337
1441	0.041383	RE1-silencing transCRiption factor (REST)	NM_005612		NP_005603
1445	0.008919	nuclear receptor coactivator 6 (NCOA6), mRNA /cds=(2755,8760) /gb=NM_014071 /gi=7661975 /ug=Hs.159613 /len=9301	NM_014071	Hs.159613	NP_054790
1448	0.035601	retinoic acid repressible protein (RARG-1), mRNA /cds=(33,806) /gb=NM_016167 /gi=15743546 /ug=Hs.106346 /len=896	NM_016167	Hs.106346	NP_057251
1482	0.007315	ATP synthase, H transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=NM_006886 /gi=21327678 /ug=Hs.177530 /len=417	NM_006886	Hs.177530	NP_008817
1505	0.04789	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa (TAF9), transcript variant 1, mRNA /cds=(159,953) /gb=NM_003187 /gi=21166375 /ug=Hs.60679 /len=1153	NM_003187	Hs.60679	NP_057367
1557	0.04789	MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047 /ug=Hs.446594 /len=530	BF814502	Hs.446594	
1574	0.030485	similar to triple functional domain (PTPRF interacting) (LOC115557), mRNA /cds=(331,1755) /gb=NM_133483 /gi=19311007 /ug=Hs.61581 /len=2166	NM_133483	Hs.61581	NP_597840

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1579	0.030485	chromosome 14 open reading frame 108 (C14orf108), mRNA /cds=(407,1879) /gb=NM_018229 /gi=21361775 /ug=Hs.106210 /len=3088	NM_018229	Hs.106210	NP_060699
1598	0.007315	troponin I, skeletal, slow (TNNI1), mRNA /cds=(74,637) /gb=NM_003281 /gi=21361554 /ug=Hs.84673 /len=1108	NM_003281	Hs.84673	NP_003272
1599	0.015602	protein XP_037672 (aa, 58%)	XP_037672		
1618	0.04789	mRNA for KIAA0570 protein, partial cds. /cds=(480,10718) /gb=AB011142 /gi=20521084 /ug=Hs.180948 /len=11269	AB011142	Hs.180948	
1646	0.041383	testis derived transcript (3 LIM domains) (TES), transcript variant 1, mRNA /cds=(182,1447) /gb=NM_015641 /gi=23238186 /ug=Hs.165986 /len=2766	NM_015641	Hs.165986	NP_690042
1647	0.041383	asporin (LRR class 1) (ASP), mRNA /cds=(228,1373) /gb=NM_017680 /gi=16596677 /ug=Hs.10760 /len=2466	NM_017680	Hs.10760	NP_060150
1683	0.01859	mitochondrion, complete genome	NC_001807		
1687	0.004826	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein) (DBI), mRNA /cds=(20,334) /gb=NM_020548 /gi=24475624 /ug=Hs.78888 /len=556	NM_020548	Hs.78888	NP_065438
1723	0.035601	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) (CD59), mRNA /cds=(50,436) /gb=NM_000611 /gi=20127410 /ug=Hs.278573 /len=1946	NM_000611	Hs.278573	NP_000602
1793	0.01081	nuclear receptor subfamily 4, group A, member 1 (NR4A1), transcript variant 1, mRNA /cds=(315,2111) /gb=NM_002135 /gi=27894342 /ug=Hs.1119 /len=2699	NM_002135	Hs.1119	NP_775181
1836	0.00388	hypothetical protein FLJ23445 (FLJ23445), mRNA /cds=(44,658) /gb=NM_025075 /gi=13376622 /ug=Hs.288151 /len=963	NM_025075	Hs.288151	NP_079351
1883	0.030485	cytochrome c oxidase subunit VIIb (COX7B), nuclear gene encoding mitochondrial protein, mRNA /cds=(91,333) /gb=NM_001866 /gi=18105038 /ug=Hs.432170 /len=456	NM_001866	Hs.432170	NP_001857
1999	0.041383	chromosome 20 open reading frame 40 (C20orf40), mRNA /cds=(208,396) /gb=NM_014054 /gi=7661709 /ug=Hs.105379 /len=417	NM_014054	Hs.105379	NP_054773
2070	0.041383	myotubular myopathy 1 (MTM1), mRNA /cds=(55,1866) /gb=NM_000252 /gi=4557895 /ug=Hs.75302 /len=3411	NM_000252	Hs.75302	NP_000243

Spot	p-value	D scription	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2088	0.013024	hypothetical protein LOC51257 (LOC51257), mRNA /cds=(352,1092) /gb=NM_016496 /gi=24475980 /ug=Hs.132744 /len=1614	NM_016496	Hs.132744	NP_057580
2141	0.025981	transcription factor 12 (HTF4, helix-loop- helix transcription factors 4) (TCF12), mRNA /cds=(214,2262) /gb=NM_003205 /gi=4585865 /ug=Hs.21704 /len=4202	NM_003205	Hs.21704	NP_003196
2175	0.035601	clone IMAGE:4799018, mRNA /gb=BC045722 /gi=28277129 /ug=Hs.153527 /len=2587	BC045722	Hs.153527	
2210	0.04789	CGI-09 protein (CGI-09), mRNA /cds=(73,1566) /gb=NM_015939 /gi=19923474 /ug=Hs.128791 /len=2272	NM_015939	Hs.128791	NP_057023
2212	0.01081	chromosome 21 open reading frame 4 (C21orf4), mRNA /cds=(159,635) /gb=NM_006134 /gi=8659558 /ug=Hs.284142 /len=750	NM_006134	Hs.284142	NP_006125
2230	0.022033	PMS1 postmeiotic segregation increased 1 (S. cerevisiae) (PMS1), mRNA /cds=(81,2879) /gb=NM_000534 /gi=11496979 /ug=Hs.111749 /len=3121	NM_000534	Hs.111749	NP_000525
2273	0.030485	Pirin (PIR), mRNA /cds=(231,1103) /gb=NM_003662 /gi=4505822 /ug=Hs.424966 /len=1318	NM_003662	Hs.424966	NP_003653
2278	0.022033	latent transforming growth factor beta binding protein 1 (LTBP1), mRNA /cds=(91,4275) /gb=NM_000627 /gi=4557730 /ug=Hs.241257 /len=5075	NM_000627	Hs.241257	NP_000618
2339	0.035601	chemokine (C-C motif) receptor 5 (CCR5), mRNA /cds=(358,1416) /gb=NM_000579 /gi=4502638 /ug=Hs.54443 /len=3655	NM_000579	Hs.54443	NP_000570
2399	0.04789	mitochondrion, complete genome	NC_001807		
2473	0.030485	Pseudoautosomal GTP-binding protein-like (PGPL), mRNA /cds=(330,1541) /gb=NM_012227 /gi=6912587 /ug=Hs.372587 /len=1867	NM_012227	Hs.372587	NP_036359
2499	0.04789	dynein, cytoplasmic, light intermediate polypeptide 1 (DNCL1), mRNA /cds=(81,1652) /gb=NM_016141 /gi=7705852 /ug=Hs.266483 /len=2487	NM_016141	Hs.266483	NP_057225
2507	0.025981	cDNA FLJ13552 fis, clone PLACE1007218. /gb=AK023614 /gi=10435594 /ug=Hs.204945 /len=1850	AK023614	Hs.204945	
2550	0.004826	uncharacterized bone marrow protein BM042 (BM042) (=cDNA sequence DKFZp761A1124)	NM_018458		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2557	0.01859	leucine-rich PPR-motif containing (LRPPRC), mRNA /cds=(46,3867) /gb=NM_133259 /gi=18959201 /ug=Hs.182490 /len=4782	NM_133259	Hs.182490	NP_573566
2617	0.035601	collagen, type I, alpha 1 (COL1A1), mRNA /cds=(120,4514) /gb=NM_000088 /gi=14719826 /ug=Hs.172928 /len=5921	NM_000088	Hs.172928	NP_000079
2680	0.04789	SEC63, endoplasmic reticulum translocon component (S. cerevisiae (SEC63L), mRNA /cds=(133,2415) /gb=NM_007214 /gi=14591934 /ug=Hs.31575 /len=3368	NM_007214	Hs.31575	NP_009145
2698	0.005961	topoisomerase (DNA) II alpha 170kDa (TOP2A), mRNA /cds=(127,4722) /gb=NM_001067 /gi=19913405 /ug=Hs.156346 /len=5698	NM_001067	Hs.156346	NP_001058
2799	0.015602	glia maturation factor, beta (GMFB), mRNA /cds=(98,526) /gb=NM_004124 /gi=4758441 /ug=Hs.151413 /len=4131	NM_004124	Hs.151413	NP_004115
2829	0.022033	mitochondrion, complete genome	NC_001807		
2865	0.030485	nudix (nucleoside diphosphate linked moiety X)-type motif 4 (NUDT4), mRNA /cds=(191,736) /gb=NM_019094 /gi=24432097 /ug=Hs.355399 /len=3652	NM_019094	Hs.355399	NP_061967
2866	0.00388	translation initiation factor IF2 (IF2), mRNA /cds=(142,3804) /gb=NM_015904 /gi=15451891 /ug=Hs.158688 /len=4170	NM_015904	Hs.158688	NP_056988
2940	0.01859	hypothetical protein FLJ20421 (FLJ20421), mRNA /cds=(284,1363) /gb=NM_017813 /gi=8923391 /ug=Hs.378857 /len=1668	NM_017813	Hs.378857	NP_060283
3005	0.013024	likely ortholog of mouse Paneth cell enhanced expression (HCLA-ISO), mRNA /cds=(1152,2198) /gb=NM_030937 /gi=24475708 /ug=Hs.143601 /len=2943	NM_030937	Hs.143601	NP_112199
3015	0.022033	mitochondrion, complete genome	NC_001807		
3050	0.035601	DnaJ (Hsp40) subfamily B, member 9 (DNAJB9), mRNA /cds=(203,874) /gb=NM_012328 /gi=9558754 /ug=Hs.6790 /len=2371	NM_012328	Hs.6790	NP_036460
3051	0.030485	clone MGC:45564 IMAGE:4384472, mRNA, complete cds /cds=(188,1123) /gb=BC036746 /gi=22477830 /ug=Hs.132230 /len=3767	BC036746	Hs.132230	
3056	0.041383	biglycan (BGN), mRNA /cds=(145,1251) /gb=NM_001711 /gi=19718760 /ug=Hs.821 /len=2367	NM_001711	Hs.821	NP_001702
3088	0.01859	sulfotransferase family, cytosolic, 1C, member 2 (SULT1C2), mRNA /cds=(330,1238) /gb=NM_006588 /gi=5730070 /ug=Hs.312644 /len=2143	NM_006588	Hs.312644	NP_006579

Spot	p-value	D scription	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3143	0.01081	hypothetical protein FLJ20671 (FLJ20671), mRNA /cds=(43,465) /gb=NM_017924 /gi=19923511 /ug=Hs.180201 /len=2855	NM_017924	Hs.180201	NP_060394
3173	0.035601	hypothetical protein FLJ11730 (FLJ11730), mRNA /cds=(33,608) /gb=NM_022756 /gi=20149668 /ug=Hs.17118 /len=1558	NM_022756	Hs.17118	NP_073593
3181	0.022033	protein phosphatase 2A, regulatory subunit B' (PR 53) (PPP2R4), mRNA /cds=(190,1161) /gb=NM_021131 /gi=10880986 /ug=Hs.400740 /len=2661	NM_021131	Hs.400740	NP_821070
3187	0.04789	clone IMAGE:5229459, mRNA /gb=BC044229 /gi=28277403 /ug=Hs.266263 /len=2044	BC044229	Hs.266263	
3208	0.041383	Sry-related HMG-box protein (SOX18) mRNA, complete cds	AF270652		NP_060889
3243	0.022033	FK506 binding protein 11, 19 kDa (FKBP11), mRNA /cds=(73,678) /gb=NM_016594 /gi=7706130 /ug=Hs.24048 /len=727	NM_016594	Hs.24048	NP_057678
3247	0.04789	602410168F1 NIH_MGC_92 cDNA clone IMAGE:4538560 5', mRNA sequence /clone=IMAGE:4538560 /clone_end=5' /gb=BG394022 /gi=13287470 /ug=Hs.421597 /len=1059	BG394022	Hs.421597	
3264	0.025981	TEA domain family member 4 (TEAD4), mRNA /cds=(164,1468) /gb=NM_003213 /gi=4507426 /ug=Hs.94865 /len=1670	NM_003213	Hs.94865	NP_003204
3265	0.04789	hypothetical protein similar to actin related protein 2/3 complex, subunit 5 (MGC3038), mRNA /cds=(87,548) /gb=NM_030978 /gi=13569955 /ug=Hs.315164 /len=1041	NM_030978	Hs.315164	NP_112240
3273	0.013024	golgi reassembly stacking protein 2, 55kDa (GORASP2), mRNA /cds=(52,1524) /gb=NM_015530 /gi=20127538 /ug=Hs.6880 /len=2424	NM_015530	Hs.6880	NP_056345
3288	0.041383	cyclin G2 (CCNG2), mRNA /cds=(136,1170) /gb=NM_004354 /gi=4757935 /ug=Hs.79069 /len=2044	NM_004354	Hs.79069	NP_004345
3335	0.041383	signal sequence receptor, gamma (translocon-associated protein gamma) (SSR3), mRNA /cds=(57,614) /gb=NM_007107 /gi=6005883 /ug=Hs.28707 /len=3061	NM_007107	Hs.28707	NP_009038
3361	0.025981	integrin, beta 8 (ITGB8), mRNA /cds=(681,2990) /gb=NM_002214 /gi=4504778 /ug=Hs.355722 /len=3789	NM_002214	Hs.355722	NP_002205
3371	0.022033	KIAA0372 gene product (KIAA0372), mRNA /cds=(298,4992) /gb=NM_014639 /gi=7662077 /ug=Hs.170098 /len=5704	NM_014639	Hs.170098	NP_055454

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3456	0.041383	ionized calcium binding adapter molecule 2 (IBA2), mRNA /cds=(89,541) /gb=NM_031426 /gi=13899240 /ug=Hs.4944 /len=3381	NM_031426	Hs.4944	NP_113614
3492	0.013024	UI-H-BI2-ags-a-03-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2725156 3', mRNA sequence /clone=IMAGE:2725156 /clone_end=3' /gb=AW292521 /gi=6699157 /ug=Hs.227074 /len=685	AW292521	Hs.227074	
3518	0.04789	hypothetical protein FLJ23548 (FLJ23548), mRNA /cds=(204,713) /gb=NM_024590 /gi=13375780 /ug=Hs.22895 /len=1871	NM_024590	Hs.22895	NP_078866
3555	0.04789	cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple) (COMP), mRNA /cds=(26,2299) /gb=NM_000095 /gi=4557482 /ug=Hs.1584 /len=2439	NM_000095	Hs.1584	NP_000086
3592	0.041383	solute carrier family 30 (zinc transporter), member 5 (SLC30A5), mRNA /cds=(202,2499) /gb=NM_022902 /gi=20070322 /ug=Hs.129445 /len=2952	NM_022902	Hs.129445	NP_076960
3644	0.025981	hypothetical protein FLJ20343 (FLJ20343), mRNA /cds=(19,1524) /gb=NM_017775 /gi=22547158 /ug=Hs.252692 /len=2784	NM_017775	Hs.252692	NP_060245
3657	0.005961	oxysterol binding protein-like 5 (OSBPL5), transcript variant 1, mRNA /cds=(117,2756) /gb=NM_020896 /gi=22035607 /ug=Hs.112034 /len=3873	NM_020896	Hs.112034	NP_663613
3702	0.035601	ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794 /ug=Hs.418650 /len=801	NM_002032	Hs.418650	NP_002023
3719	0.015602	putative ribonuclease III (RNASE3L), mRNA /cds=(246,4370) /gb=NM_013235 /gi=21359821 /ug=Hs.49163 /len=4764	NM_013235	Hs.49163	NP_037367
3804	0.041383	thymidine kinase 1, soluble (TK1), mRNA /cds=(58,762) /gb=NM_003258 /gi=4507518 /ug=Hs.105097 /len=1421	NM_003258	Hs.105097	NP_003249
3861	0.00388	basigin (BSG), mRNA /cds=(58,867) /gb=NM_001728 /gi=4502458 /ug=Hs.74631 /len=1638	NM_001728	Hs.74631	NP_001719
3911	0.015602	mitochondrion, complete genome	NC_001807		
3979	0.001929	TGFB inducible early growth response (TIEG), mRNA /cds=(124,1566) /gb=NM_005655 /gi=5032176 /ug=Hs.82173 /len=2899	NM_005655	Hs.82173	NP_005646
4004	0.022033	bromodomain containing 2 (BRD2), mRNA /cds=(1702,4107) /gb=NM_005104 /gi=12408641 /ug=Hs.75243 /len=4693	NM_005104	Hs.75243	NP_005095

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4020	0.022033	CASP8 associated protein 2 (CASP8AP2), mRNA /cds=(197,6145) /gb=NM_012115 /gi=16306505 /ug=Hs.122843 /len=6782	NM_012115	Hs.122843	NP_036247
4054	0.022033	histamine N-methyltransferase (HNMT), mRNA /cds=(253,1131) /gb=NM_006895 /gi=5901969 /ug=Hs.81182 /len=1667	NM_006895	Hs.81182	NP_008826
4064	0.035601	ubiquitin-like 5 (UBL5), mRNA /cds=(66,287) /gb=NM_024292 /gi=13236509 /ug=Hs.13836 /len=413	NM_024292	Hs.13836	NP_077268
4100	0.04789	splicing factor 30, survival of motor neuron-related (SPF30), mRNA /cds=(193,909) /gb=NM_005871 /gi=21361283 /ug=Hs.79968 /len=2033	NM_005871	Hs.79968	NP_005862
4114	0.04789	cullin 2 (CUL2)	AF126404		NP_003582
4119	0.041383	reverse transcriptase homolog - human retrotransposon L1	I38588		
4121	0.022033	natural killer cell enhancing factor (NKEFA)	L19184		NP_002565
4125	0.008919	for protein disulfide isomerase-related (PDIR), mRNA /cds=(57,1616) /gb=NM_006810 /gi=5803120 /ug=Hs.76901 /len=1693	NM_006810	Hs.76901	NP_006801
4138	0.008919	mRNA; cDNA DKFZp451M092 (from clone DKFZp451M092) /gb=AL713650 /gi=19584326 /ug=Hs.336425 /len=3645	AL713650	Hs.336425	
4219	0.030485	ATP citrate lyase (ACLY), mRNA /cds=(85,3402) /gb=NM_001096 /gi=4501864 /ug=Hs.174140 /len=4297	NM_001096	Hs.174140	NP_001087
4225	0.007315	Parkinson disease (autosomal recessive, early onset) 7 (PARK7), mRNA /cds=(21,590) /gb=NM_007262 /gi=6005748 /ug=Hs.10958 /len=842	NM_007262	Hs.10958	NP_009193
4238	0.04789	cytokine SDF-1-beta (=L36033)	U16752		NP_000600
4271	0.01859	ras gene family, member E (ARHE), mRNA /cds=(141,875) /gb=NM_005168 /gi=21361257 /ug=Hs.6838 /len=2685	NM_005168	Hs.6838	NP_005159
4340	0.04789	heat shock 90kDa protein 1, beta (HSPCB), mRNA /cds=(85,2259) /gb=NM_007355 /gi=20149593 /ug=Hs.74335 /len=2567	NM_007355	Hs.74335	NP_031381
4390	0.013024	ataxia telangiectasia and Rad3 related (ATR), mRNA /cds=(106,8040) /gb=NM_001184 /gi=20143978 /ug=Hs.77613 /len=8265	NM_001184	Hs.77613	NP_001175
4402	0.01081	putative homeodomain transcription factor 1 (PHTF1), mRNA /cds=(32,2320) /gb=NM_006608 /gi=5729975 /ug=Hs.123637 /len=2806	NM_006608	Hs.123637	NP_006599

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4421	0.041383	sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA /cds=(46,2430) /gb=NM_005065 /gi=19923668 /ug=Hs.181300 /len=7885	NM_005065	Hs.181300	NP_005056
4432	0.01081	dentin matrix acidic	NM_004407		NP_004398
4438	0.022033	trypsin-like serine protease (TLSP) gene	AF164623		
4506	0.041383	chronic myelogenous leukemia tumor antigen 66 (CML66), mRNA /cds=(233,1984) /gb=NM_032869 /gi=23618845 /ug=Hs.195870 /len=2288	NM_032869	Hs.195870	NP_116258
4518	0.00388	leptin receptor (ORF)	U66496		NP_002294
4520	0.01859	centrosome-associated protein 350 (CAP350), mRNA /cds=(168,9521) /gb=NM_014810 /gi=18378734 /ug=Hs.92200 /len=11740	NM_014810	Hs.92200	NP_055625
4531	0.04789	erythrocyte membrane protein band 4.1-like 2 (EPB41L2), mRNA /cds=(45,3062) /gb=NM_001431 /gi=4503578 /ug=Hs.7857 /len=4336	NM_001431	Hs.7857	NP_001422
4608	0.030485	MacGAP protein (MacGAP), mRNA /cds=(23,1879) /gb=NM_033515 /gi=15723375 /ug=Hs.178705 /len=3305	NM_033515	Hs.178705	NP_277050
4614	0.01859	sperm antigen-36	AF187554		
4619	0.04789	IMP (inosine monophosphate) dehydrogenase 2 (IMPDH2), mRNA /cds=(48,1592) /gb=NM_000884 /gi=4504688 /ug=Hs.75432 /len=1654	NM_000884	Hs.75432	NP_000875
4641	0.015602	major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA /cds=(63,863) /gb=NM_002124 /gi=4504410 /ug=Hs.375570 /len=1182	NM_002124	Hs.375570	NP_002115
4678	0.041383	hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA /cds=(49,2259) /gb=NM_000414 /gi=4504504 /ug=Hs.75441 /len=2593	NM_000414	Hs.75441	NP_000405
4710	0.008919	vinculin (VCL), transcript variant meta-VCL, mRNA /cds=(86,3490) /gb=NM_014000 /gi=7669549 /ug=Hs.75350 /len=5341	NM_014000	Hs.75350	NP_054706
4738	0.015602	hypothetical protein (KIAA1439)	AB037860		NP_005586
4746	0.035601	snail 2 (Drosophila) (SNAI2), mRNA /cds=(165,971) /gb=NM_003068 /gi=24497625 /ug=Hs.93005 /len=2101	NM_003068	Hs.93005	NP_003059
4823	0.01859	SH3-domain GRB2-like endophilin B2 (SH3GLB2), mRNA /cds=(147,1334) /gb=NM_020145 /gi=24431995 /ug=Hs.30002 /len=2039	NM_020145	Hs.30002	NP_064530
4834	0.022033	mitochondrion, complete genome	NC_001807		

Spot	p-value	D scription	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4848	0.041383	aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 2, mRNA /cds=(61,7308) /gb=NM_013227 /gi=6995993 /ug=Hs.2159 /len=7434	NM_013227	Hs.2159	NP_037359
4853	0.025981	clone 24571 mRNA sequence /gb=AF070564 /gi=3387932 /ug=Hs.421200 /len=1487	AF070564	Hs.421200	
4885	0.004826	clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992	AF001542	Hs.356442	
4887	0.035601	mRNA; cDNA DKFZp434N079 (from clone DKFZp434N079) /gb=AL133591 /gi=6599179 /ug=Hs.141480 /len=1965	AL133591	Hs.141480	
4916	0.025981	collagen, type X, alpha 1(Schmid metaphyseal chondrodysplasia) (COL10A1), mRNA /cds=(97,2139) /gb=NM_000493 /gi=18105031 /ug=Hs.179729 /len=3285	NM_000493	Hs.179729	NP_000484
4922	0.015602	topoisomerase (DNA) II beta 180kDa (TOP2B), mRNA /cds=(1,4866) /gb=NM_001068 /gi=19913407 /ug=Hs.75248 /len=5189	NM_001068	Hs.75248	NP_001059
4928	0.01859	mitochondrion, complete genome	NC_001807		
4963	0.01081	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,327) /gb=NM_001865 /gi=18105035 /ug=Hs.70312 /len=470	NM_001865	Hs.70312	NP_001856
5001	0.041383	mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053) /gb=AL049265 /gi=4500013 /ug=Hs.71968 /len=2864	AL049265	Hs.71968	
5071	0.003097	cDNA FLJ10004 fis, clone HEMBA1000076. /gb=AK000866 /gi=7021190 /ug=Hs.411490 /len=1974	AK000866	Hs.411490	
5079	1.45E-04	APR-1 protein (MAGEH1), mRNA /cds=(271,930) /gb=NM_014061 /gi=18105051 /ug=Hs.279819 /len=1475	NM_014061	Hs.279819	NP_054780
5138	0.035601	exostoses (multiple) 2 (EXT2), mRNA /cds=(488,2644) /gb=NM_000401 /gi=4557572 /ug=Hs.75334 /len=3781	NM_000401	Hs.75334	NP_000392
5150	0.013024	HSPC039 protein mRNA, complete cds /cds=(81,329) /gb=AF125100 /gi=5106995 /ug=Hs.406542 /len=1583	AF125100	Hs.406542	NP_057181
5222	0.041383	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence	NC_001144		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5225	0.04789	platelet-derived growth factor receptor, beta polypeptide (PDGFRB), mRNA /cds=(357,3677) /gb=NM_002609 /gi=15451788 /ug=Hs.76144 /len=5598	NM_002609	Hs.76144	NP_002600
5235	0.030485	major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA /cds=(63,863) /gb=NM_002124 /gi=4504410 /ug=Hs.375570 /len=1182	NM_002124	Hs.375570	NP_002115
5258	0.004826	testis derived transcript (3 LIM domains) (TES), transcript variant 1, mRNA /cds=(182,1447) /gb=NM_015641 /gi=23238186 /ug=Hs.165986 /len=2766	NM_015641	Hs.165986	NP_690042
5290	0.04789	hypothetical protein FLJ20719 (FLJ20719), mRNA /cds=(402,2213) /gb=NM_017940 /gi=24308174 /ug=Hs.446473 /len=3745	NM_017940	Hs.446473	NP_060410
5294	0.035601	KIAA0063 gene product (KIAA0063), mRNA /cds=(280,888) /gb=NM_014876 /gi=7661887 /ug=Hs.3094 /len=3168	NM_014876	Hs.3094	NP_055691
5301	0.035601	X-box binding protein 1 (XBP1), mRNA /cds=(49,834) /gb=NM_005080 /gi=14110394 /ug=Hs.149923 /len=1836	NM_005080	Hs.149923	NP_005071
5332	0.041383	clone IMAGE:5262128, mRNA, partial cds /cds=(1,1409) /gb=BC035036 /gi=23271542 /ug=Hs.356247 /len=4728	BC035036	Hs.356247	
5363	0.030485	MAD, mothers against decapentaplegic (Drosophila) interacting protein, receptor activation anchor (MADHIP), transcript variant 3, mRNA /cds=(439,4410) /gb=NM_004799 /gi=4759059 /ug=Hs.194716 /len=4839	NM_004799	Hs.194716	NP_015563
5402	0.025981	brain cDNA, clone:QnpA-21421	AB050422		
5431	0.013024	thymine-DNA glycosylase (TDG), mRNA /cds=(400,1632) /gb=NM_003211 /gi=4507422 /ug=Hs.173824 /len=3410	NM_003211	Hs.173824	NP_003202
5432	0.022033	zinc finger protein 202 (ZNF202), mRNA /cds=(11,1957) /gb=NM_003455 /gi=10835040 /ug=Hs.9443 /len=4053	NM_003455	Hs.9443	NP_003446
5434	0.015602	ATP synthase, H transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), mRNA /cds=(98,868) /gb=NM_001688 /gi=21361564 /ug=Hs.81634 /len=1230	NM_001688	Hs.81634	NP_001679
5438	0.035601	mitochondrion, complete genome	NC_001807		
5439	0.030485	hypothetical protein MGC4276 similar to CG8198 (MGC4276), mRNA /cds=(70,462) /gb=NM_030940 /gi=24475709 /ug=Hs.177776 /len=1978	NM_030940	Hs.177776	NP_112202

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5468	0.030485	Deleted in split-hand/split-foot 1 region (DSS1), mRNA /cds=(129,341) /gb=NM_006304 /gi=5453639 /ug=Hs.333495 /len=509	NM_006304	Hs.333495	NP_006295
5628	0.030485	v-fos FBJ murine osteosarcoma viral oncogene (FOS), mRNA /cds=(156,1298) /gb=NM_005252 /gi=6552332 /ug=Hs.25647 /len=2084	NM_005252	Hs.25647	NP_005243
5639	0.022033	mitogen-activated protein kinase 7 (MAPK7), transcript variant 1, mRNA /cds=(355,2805) /gb=NM_139033 /gi=20986500 /ug=Hs.3080 /len=3113	NM_139033	Hs.3080	NP_620603
5676	0.035601	discs, large 7 (Drosophila) (DLG7), mRNA /cds=(218,2758) /gb=NM_014750 /gi=21361644 /ug=Hs.77695 /len=2979	NM_014750	Hs.77695	NP_055565
5701	0.041383	mitochondrion, complete genome	NC_001807		
5743	0.022033	heme-regulated initiation factor 2-alpha kinase (HRI), mRNA /cds=(63,1955) /gb=NM_014413 /gi=11125767 /ug=Hs.258730 /len=2813	NM_014413	Hs.258730	NP_055228
5745	0.035601	clone IMAGE:5299888, mRNA /gb=BC039397 /gi=24659826 /ug=Hs.112237 /len=1338	BC039397	Hs.112237	
5749	0.030485	up-regulated gene 4 (URG4), mRNA /cds=(14,2782) /gb=NM_017920 /gi=19923541 /ug=Hs.5131 /len=3606	NM_017920	Hs.5131	NP_060390
5769	0.025981	cDNA: FLJ21561 fis, clone COL06415. /gb=AK025214 /gi=10437681 /ug=Hs.96918 /len=1641	AK025214	Hs.96918	
5783	0.04789	ATPase inhibitory factor 1 (ATPIF1), mRNA /cds=(52,372) /gb=NM_016311 /gi=20149627 /ug=Hs.241336 /len=515	NM_016311	Hs.241336	NP_835498
5889	0.041383	mRNA for KIAA0640 protein, partial cds. /cds=(1,1813) /gb=AB014540 /gi=3327093 /ug=Hs.153026 /len=4824	AB014540	Hs.153026	NP_055870
5903	0.025981	dinucleotide miCRosatellite HUJII77	M96348		
5920	0.025981	mitochondrion, complete genome	NC_001807		
5928	0.035601	ubiquitin-conjugating enzyme E2B (RAD6 (UBE2B), mRNA /cds=(422,880) /gb=NM_003337 /gi=4507770 /ug=Hs.811 /len=2591	NM_003337	Hs.811	NP_003328
5935	0.004826	MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047 /ug=Hs.446594 /len=530	BF814502	Hs.446594	
5939	0.035601	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 S. cerevisiae) (BTAF1), mRNA /cds=(118,5667) /gb=NM_003972 /gi=27477069 /ug=Hs.180930 /len=6345	NM_003972	Hs.180930	NP_003963

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5975	0.01859	cell-line RPMI 8226 chloride ion current inducer protein I(Cln) gene,	AF232225		
6035	0.013024	BCL2 gene, exon 3 and breakpoint region	AF217803		
6063	0.022033	eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA /cds=(16,1239) /gb=NM_001967 /gi=9945313 /ug=Hs.173912 /len=1864	NM_001967	Hs.173912	NP_001958
6065	0.022033	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa (NDUFC2), mRNA /cds=(151,510) /gb=NM_004549 /gi=19923255 /ug=Hs.193313 /len=2168	NM_004549	Hs.193313	NP_004540
6068	0.035601	mitochondrial ribosomal protein L27 (MRPL27), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA /cds=(32,316) /gb=NM_148571 /gi=22547130 /ug=Hs.7736 /len=2472	NM_148571	Hs.7736	NP_683412
6091	0.041383	cDNA FLJ35150 fis, clone PLACE6010568, moderately similar to mRNA for TU12B1-TY. /gb=AK092469 /gi=21751073 /ug=Hs.425567 /len=1714	AK092469	Hs.425567	
6097	0.004826	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747	NM_012479	Hs.25001	NP_036611
6148	0.00388	zinc finger RNA binding protein (ZFR), mRNA /cds=(44,1300) /gb=NM_016107 /gi=7706372 /ug=Hs.173518 /len=2734	NM_016107	Hs.173518	NP_057191
6238	0.022033	tb97a11.x1 NCI_CGAP_Co16 cDNA clone IMAGE:2062268 3' similar to contains Alu repetitive element; mRNA sequence /clone=IMAGE:2062268 /clone_end=3' /gb=AI343476 /gi=4080682 /ug=Hs.183850 /len=515	AI343476	Hs.183850	
6239	0.008919	Similar to RD RNA-binding protein, clone MGC:2263 IMAGE:3050953, mRNA, complete cds /cds=(34,1035) /gb=BC011600 /gi=15079543 /ug=Hs.356818 /len=2478	BC011600	Hs.356818	
6251	0.035601	interferon-related developmental regulator 1 (IFRD1), mRNA /cds=(220,1581) /gb=NM_001550 /gi=4504606 /ug=Hs.7879 /len=1791	NM_001550	Hs.7879	NP_001541
6266	0.038534	cosmid LL12NCO1-67C6, ETV6 gene, intron 1A, partial sequence	U81831		

Spot	p-value	Description	Gen Accession No.	Unigene Accession No.	Protein Accession No.
6302	0.044987	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) (DTR), mRNA /cds=(262,888) /gb=NM_001945 /gi=4503412 /ug=Hs.799 /len=2360	NM_001945	Hs.799	NP_001936
6347	0.007315	mitochondrion, complete genome	NC_001807		
6348	0.041383	major histocompatibility complex, class I, F (HLA-F), mRNA /cds=(1,1089) /gb=NM_018950 /gi=9665231 /ug=Hs.110309 /len=1188	NM_018950	Hs.110309	NP_061823
6407	0.013024	hypothetical protein LOC51244 (LOC51244), mRNA /cds=(340,1233) /gb=NM_016474 /gi=24475969 /ug=Hs.158006 /len=1614	NM_016474	Hs.158006	NP_057558
6451	0.035601	mRNA; cDNA DKFZp586C1723 (from clone DKFZp586C1723) /gb=AL050192 /gi=4884408 /ug=Hs.80285 /len=1797	AL050192	Hs.80285	
6487	0.035601	tumor protein D52 (TPD52), mRNA /cds=(92,646) /gb=NM_005079 /gi=4827037 /ug=Hs.2384 /len=3247	NM_005079	Hs.2384	NP_005070
6522	0.035601	Rattus norvegicus mitochondrial genome	NC_001665		
6590	0.035601	mRNA for KIAA0981 protein, partial cds. /cds=(1,1738) /gb=AB023198 /gi=4589605 /ug=Hs.158135 /len=5182	AB023198	Hs.158135	
6595	0.04789	H factor 1 (complement) (HF1), mRNA /cds=(74,3769) /gb=NM_000186 /gi=4504374 /ug=Hs.250651 /len=3926	NM_000186	Hs.250651	NP_000177
6598	0.030485	phosphomannomutase 2 (PMM2) gene (5e-10 match)	AF157794		
6616	0.025981	LPS-induced TNF-alpha factor (PIG7), mRNA /cds=(234,920) /gb=NM_004862 /gi=4758913 /ug=Hs.76507 /len=1773	NM_004862	Hs.76507	NP_004853
6619	0.025981	phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA	NM_005019		NP_005010
6657	0.035601	serine hydroxymethyltransferase 2 (mitochondrial) (SHMT2), mRNA /cds=(20,1534) /gb=NM_005412 /gi=24942125 /ug=Hs.75069 /len=2122	NM_005412	Hs.75069	NP_005403
6738	0.035601	ankyrin repeat and SOCS box-containing 3 (ASB3), transcript variant 1, mRNA /cds=(136,1692) /gb=NM_016115 /gi=22208952 /ug=Hs.9893 /len=2214	NM_016115	Hs.9893	NP_665862
6758	0.041383	proteasome (prosome, macropain) 26S subunit, ATPase, 2 (PSMC2), mRNA /cds=(71,1372) /gb=NM_002803 /gi=24430152 /ug=Hs.61153 /len=1545	NM_002803	Hs.61153	NP_002794
6837	0.022033	cDNA FLJ39699 fis, clone SMINT2011567, weakly similar to mRNA for ALEX1. /gb=AK097018 /gi=21756651 /ug=Hs.83530 /len=2257	AK097018	Hs.83530	NP_061880

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6860	0.041383	cDNA: FLJ21440 fis, clone COL04389. /gb=AK025093 /gi=10437540 /ug=Hs.218008 /len=1810	AK025093	Hs.218008	
6865	0.007315	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), mRNA /cds=(91,336) /gb=NM_002489 /gi=4505356 /ug=Hs.50098 /len=518	NM_002489	Hs.50098	NP_002480
6866	0.035601	E1A binding protein p300 (EP300), mRNA /cds=(1200,8444) /gb=NM_001429 /gi=4557556 /ug=Hs.25272 /len=9046	NM_001429	Hs.25272	NP_001420
6970	0.030485	neuroplastoma apoptosis-related RNA-binding protein (CUGBP2) gene, exons 10, 11a, 11b, 12, 13a, 13b, 14, and complete cds, alternatively spliced	AF295068		
6989	0.030485	transmembrane 9 superfamily member 1 (TM9SF1), mRNA /cds=(35,1855) /gb=NM_006405 /gi=21361314 /ug=Hs.91586 /len=2138	NM_006405	Hs.91586	NP_006396
6990	0.04789	mRNA for KIAA1866 protein, partial cds. /cds=(1,2299) /gb=AB058769 /gi=14017948 /ug=Hs.334838 /len=4811	AB058769	Hs.334838	
7052	0.022033	SUMO-1-specific protease (SUSP1), mRNA /cds=(1,3339) /gb=NM_015571 /gi=7662311 /ug=Hs.27197 /len=4210	NM_015571	Hs.27197	NP_056386
7077	0.04789	mitochondrion, complete genome	NC_001807		
7087	0.01859	mitochondrion, complete genome	NC_001807		
7152	0.022033	cellular retinoic acid binding protein 1 (CRABP1), mRNA /cds=(75,488) /gb=NM_004378 /gi=4758051 /ug=Hs.346950 /len=735	NM_004378	Hs.346950	NP_004369
7162	0.041383	protein-O-mannosyltransferase 1 (POMT1), mRNA /cds=(180,2423) /gb=NM_007171 /gi=21361381 /ug=Hs.99654 /len=3150	NM_007171	Hs.99654	NP_009102
7204	0.041383	chromosome 20 open reading frame 98 (C20orf98), mRNA /cds=(134,748) /gb=NM_024958 /gi=13376446 /ug=Hs.286128 /len=2042	NM_024958	Hs.286128	NP_079234
7227	0.015602	cytidine monophosphate kinase CMP mRNA, (=UMP-CMP kinase (LOC51727))	AF259961		NP_057392
7234	0.04789	chemokine-like factor 1 (CKLF1), mRNA /cds=(148,606) /gb=NM_016951 /gi=10092593 /ug=Hs.15159 /len=689	NM_016951	Hs.15159	NP_058647
7235	0.022033	SOCS box-containing WD protein SWiP-1 (WSB1), transcript variant 3, mRNA /cds=(317,1051) /gb=NM_134264 /gi=20143909 /ug=Hs.187991 /len=4243	NM_134264	Hs.187991	NP_599027
7330	0.04789	mitochondrion, complete genome	NC_001807		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7331	0.01859	AGENCOURT_8856629 Lupski_sciatic_nerve cDNA clone IMAGE:6200636 5', mRNA sequence /clone=IMAGE:6200636 /clone_end=5' /gb=BQ947179 /gi=22362657 /ug=Hs.356605 /len=1277	BQ947179	Hs.356605	
7381	0.025981	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa (NDUFAB1), mRNA /cds=(25,495) /gb=NM_005003 /gi=4826851 /ug=Hs.5556 /len=663	NM_005003	Hs.5556	NP_004994
7406	0.01081	hypothetical protein FLJ14511 (FLJ14511), mRNA /cds=(23,1273) /gb=NM_033087 /gi=14861835 /ug=Hs.40919 /len=1835	NM_033087	Hs.40919	NP_149078
7433	0.035601	KIAA1579 protein, partial cds /cds=UNKNOWN /gb=AB046799 /gi=10047232 /ug=Hs.49933 /len=4352 (=FLJ25300)	AB046799	Hs.49933	NP_060681
7462	0.04789	TRAF family member-associated NFKB activator (TANK), transcript variant 1, mRNA /cds=(159,1436) /gb=NM_004180 /gi=19743568 /ug=Hs.146847 /len=2089	NM_004180	Hs.146847	NP_597841
7532	0.035601	a disintegrin and metalloproteinase domain 33 (ADAM33), transcript variant 1, mRNA /cds=(88,2529) /gb=NM_025220 /gi=24041037 /ug=Hs.173716 /len=3594	NM_025220	Hs.173716	NP_694882
7564	0.035601	paired basic amino acid cleaving system 4 (PACE4), transcript variant 1, mRNA /cds=(315,3224) /gb=NM_002570 /gi=20336178 /ug=Hs.170414 /len=4553	NM_002570	Hs.170414	NP_612198
7578	0.035601	hypothetical protein DKFZp586G0123 (DKFZp586G0123), mRNA /cds=(25,315) /gb=NM_013386 /gi=9558726 /ug=Hs.24713 /len=1294	NM_013386	Hs.24713	NP_037518
7583	0.030485	AGENCOURT_8929105 NIH_MGC_40 cDNA clone IMAGE:6484442 5', mRNA sequence /clone=IMAGE:6484442 /clone_end=5' /gb=BQ939558 /gi=22355036 /ug=Hs.405871 /len=1129	BQ939558	Hs.405871	
7611	0.041383	RAB14, member RAS oncogene family (RAB14), mRNA /cds=(184,831) /gb=NM_016322 /gi=19923482 /ug=Hs.5807 /len=4106	NM_016322	Hs.5807	NP_057406
7656	0.01081	cDNA FLJ35517 fis, clone SPLEN2000698. /gb=AK092836 /gi=21751529 /ug=Hs.291804 /len=2536	AK092836	Hs.291804	

Spot	p-value	Description	Gene Accession No.	Unigen Accession No.	Prot in Accession No.
7762	0.015602	Similar to ubiquitin protein ligase E3A papilloma virus E6-associated protein, Angelman syndrome), clone IMAGE:4811444, mRNA /gb=BC040187 /gi=25455694 /ug=Hs.25320 /len=4823	BC040187	Hs.25320	
7763	0.015602	chromosome 21 open reading frame 6 (C21orf6), mRNA /cds=(92,1051) /gb=NM_016940 /gi=8393017 /ug=Hs.34136 /len=1729	NM_016940	Hs.34136	NP_058636
7877	0.030485	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax Drosophila) (MLL5), mRNA /cds=(202,5778) /gb=NM_018682 /gi=23503326 /ug=Hs.333300 /len=6543	NM_018682	Hs.333300	NP_061152
7910	0.004826	hypothetical protein MGC33365 (MGC33365), mRNA /cds=(268,1560) /gb=NM_173552 /gi=27734894 /ug=Hs.288954 /len=4096	NM_173552	Hs.288954	NP_775823
7927	0.008919	UI-H-EZ1-bca-n-05-0-UI.s1 NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-bca-n-05-0-UI 3', mRNA sequence /clone=UI-H-EZ1-bca-n-05-0-UI /clone_end=3' /gb=BQ774356 /gi=21982825 /ug=Hs.43227 /len=1083	BQ774356	Hs.43227	
7953	0.04789	UI-H-DP0-avb-i-09-0-UI.s1 NCI_CGAP_Fs1 cDNA clone IMAGE:5877200 3', mRNA sequence /clone=IMAGE:5877200 /clone_end=3' /gb=BQ020506 /gi=19755784 /ug=Hs.43546 /len=1168	BQ020506	Hs.43546	
8104	0.01859	mRNA; cDNA DKFZp761C169 (from clone DKFZp761C169); partial cds /cds=(997,2475) /gb=AL161991 /gi=7328122 /ug=Hs.71252 /len=3324	AL161991	Hs.71252	NP_075064
8136	0.035601	601661342R1 NIH_MGC_72 cDNA clone IMAGE:3915994 3', mRNA sequence /clone=IMAGE:3915994 /clone_end=3' /gb=BE966653 /gi=11772295 /ug=Hs.330958 /len=703	BE966653	Hs.330958	
8151	0.013024	cDNA: FLJ23115 fis, clone LNG07933. /gb=AK026768 /gi=10439696 /ug=Hs.98728 /len=1917	AK026768	Hs.98728	
8269	0.035601	clone IMAGE:5243705, mRNA /gb=BC043383 /gi=27695948 /ug=Hs.439631 /len=2177	BC043383	Hs.439631	
8278	0.030485	EST(wf82e10.x1 Soares_NFL_T_GBC_S1 clone IMAGE:2362122 3')	AI873423		
8308	0.035601	EST(ty24e09.x1 NCI_CGAP_Ut3 clone IMAGE:2280040 3' contains Alu repeat)	AI758800		

Spot	p-value	Description	Gene Accession No.	Unigen Accession No.	Protein Accession No.
8310	0.002454	phosphatidylinositol-3 phosphate 3-phosphatase adaptor subunit (3PAP), mRNA /cds=(132,2375) /gb=NM_019061 /gi=27477131 /ug=Hs.93872 /len=5064	NM_019061	Hs.93872	NP_061934
8326	0.015602	BX118128 Soares fetal liver spleen 1NFLS cDNA clone IMAGp998L20388, mRNA sequence /clone=IMAGp998L20388;_IMAGE:201763 /gb=BX118128 /gi=27840987 /ug=Hs.15328 /len=783	BX118128	Hs.15328	
8381	0.041383	Tho2 mRNA, complete cds /cds=(1,4437) /gb=AF441770 /gi=20799317 /ug=Hs.16411 /len=4452	AF441770	Hs.16411	
8422	0.008919	cDNA FLJ13792 fis, clone THYRO1000072, weakly similar to MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117). /cds=(9,1337) /gb=AK023854 /gi=10435918 /ug=Hs.154751 /len=2184	AK023854	Hs.154751	
8423	0.025981	ot96g10.s1 Soares_total_fetus_Nb2HF8_9w cDNA clone IMAGE:1624674 3', mRNA sequence /clone=IMAGE:1624674 /clone_end=3' /gb=AA993566 /gi=3180111 /ug=Hs.369984 /len=498	AA993566	Hs.369984	
8431	0.041383	df57g01.y1 Morton Fetal Cochlea cDNA clone IMAGE:2487720 5', mRNA sequence /clone=IMAGE:2487720 /clone_end=5' /gb=AW023610 /gi=5877140 /ug=Hs.370582 /len=458	AW023610	Hs.370582	
8504	0.01081	zinc finger-like protein 9 (ZPR9), mRNA /cds=(130,1563) /gb=NM_033414 /gi=15529977 /ug=Hs.60300 /len=1719	NM_033414	Hs.60300	NP_219482
8505	6.76E-04	EST (hv67h07.x1 NCI_CGAP_Lu24 IMAGE:3178525 3')	BE220163		
8518	0.011207	clone IMAGE:5311197, mRNA /gb=BC042002 /gi=27469533 /ug=Hs.260395 /len=1498	BC042002	Hs.260395	
8519	0.035601	AGENCOURT_6423660 NIH_MGC_67 cDNA clone IMAGE:5580917 5', mRNA sequence /clone=IMAGE:5580917 /clone_end=5' /gb=BM465996 /gi=18515038 /ug=Hs.32990 /len=1594	BM465996	Hs.32990	
8520	0.035601	chromosome 20 open reading frame 52 (C20orf52), mRNA /cds=(164,403) /gb=NM_080748 /gi=18152784 /ug=Hs.401703 /len=602	NM_080748	Hs.401703	NP_542786

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8545	0.04789	as32a11.x1 Barstead aorta HPLRB6 cDNA clone IMAGE:2318876 3', mRNA sequence /clone=IMAGE:2318876 /clone_end=3' /gb=AI707688 /gi=4997464 /ug=Hs.369595 /len=518	AI707688	Hs.369595	
8553	0.008919	EST (we35d08.x1 NCI_CGAP_Lu24 cDNA clone IMAGE:2343087 3' similar to contains L1.t1 L1 repetitive element)	AI701473		
8557	0.041383	UI-H-ED0-awy-a-01-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5825160 3', mRNA sequence /clone=IMAGE:5825160 /clone_end=3' /gb=BQ017647 /gi=19752924 /ug=Hs.124747 /len=1445	BQ017647	Hs.124747	
8572	0.04789	UI-H-EU0-azo-d-01-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE:5851344 3', mRNA sequence /clone=IMAGE:5851344 /clone_end=3' /gb=BQ180851 /gi=20356343 /ug=Hs.436432 /len=1067	BQ180851	Hs.436432	
8577	0.005961	RC5-FT0194-271100-022-B06 FT0194 cDNA, mRNA sequence /gb=BF858635 /gi=12246379 /ug=Hs.270272 /len=590	BF858635	Hs.270272	
8619	0.041383	FLJ11481 fis, clone HEMBA1001803 /cds=UNKNOWN /gb=AK021543 /gi=10432744 /ug=Hs.135159 /len=1539	AK021543	Hs.135159	
8623	0.04789	cDNA FLJ31753 fis, clone NT2RI2007468. /gb=AK056315 /gi=16551681 /ug=Hs.349283 /len=2361	AK056315	Hs.349283	
8647	0.004826	tm62d04.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2162695 3', mRNA sequence /clone=IMAGE:2162695 /clone_end=3' /gb=AI475033 /gi=4328078 /ug=Hs.36915 /len=453	AI475033	Hs.36915	
8649	0.030485	nah90b12.x1 NCI_CGAP_HN19 cDNA clone IMAGE:4257766 similar to P39194 ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY. [1] ;contains Alu repetitive element, mRNA sequence /clone=IMAGE:4257766 /gb=BG272785 /gi=12982288 /ug=Hs.440690 /len=360	BG272785	Hs.440690	
8662	0.030485	ts93d11.x1 NCI_CGAP_GC6 cDNA clone IMAGE:2238837 3', mRNA sequence /clone=IMAGE:2238837 /clone_end=3' /gb=AI631165 /gi=4682495 /ug=Hs.196952 /len=537	AI631165	Hs.196952	
8686	0.01859	mRNA; cDNA DKFZp564P016 (from clone DKFZp564P016) /gb=AL049337 /gi=4500118 /ug=Hs.132571 /len=1938	AL049337	Hs.132571	

Spot	p-value	Description	Gen Accession No.	Unigene Accession No.	Prot in Accession No.
8709	0.002454	clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992	AF001542	Hs.356442	
8710	0.01859	EST(cDNA clone IMAGE:6617359 5')	BU569767		NP_005339
8719	0.041383	clone UWGC:y17c090 from 6p21, complete sequence	AC004188		
8723	0.022033	mRNA; cDNA DKFZp586F071 (from clone DKFZp586F071) /gb=AL050125 /gi=4884333 /ug=Hs.22907 /len=3537	AL050125	Hs.22907	
8749	0.030485	ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794 /ug=Hs.418650 /len=801	NM_002032	Hs.418650	NP_002023
8758	0.013024	ESTs, cDNA, 3' end /clone_end=3' /gb=BM314871 /gi=18049216 /ug=Hs.352487 /len=451	BM314871	Hs.352487	
8780	0.015602	MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047 /ug=Hs.446594 /len=530	BF814502	Hs.446594	
8791	0.005961	tg51b06.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2112275 3', mRNA sequence /clone=IMAGE:2112275 /clone_end=3' /gb=AI419722 /gi=4265653 /ug=Hs.161220 /len=484	AI419722	Hs.161220	
8803	8.90E-04	clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992	AF001542	Hs.356442	
8809	0.01081	cDNA: FLJ23013 fis, clone LNG00740. /gb=AK026666 /gi=10439567 /ug=Hs.372737 /len=1909	AK026666	Hs.372737	
8818	0.04789	Similar to KIAA1753 protein, clone IMAGE:5210724, mRNA /gb=BC033751 /gi=21707446 /ug=Hs.44976 /len=1275	BC033751	Hs.44976	
8859	0.013024	clone IMAGE:5263177, mRNA /gb=BC035116 /gi=23272470 /ug=Hs.19339 /len=4267	BC035116	Hs.19339	
8860	0.022033	clone 23612 mRNA sequence /gb=U90902 /gi=1913880 /ug=Hs.82141 /len=1548	U90902	Hs.82141	
8865	0.030485	cDNA, FLJ12091 fis, clone HEMBB1002582	AK022153		
8901	0.030485	sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA /cds=(46,2430) /gb=NM_005065 /gi=19923668 /ug=Hs.181300 /len=7885	NM_005065	Hs.181300	NP_005056
8924	0.022033	BX112599 Soares fetal liver spleen 1NFLS cDNA clone IMAGp998N15537, mRNA sequence /clone=IMAGp998N15537 IMAGE:248654 /gb=BX112599 /gi=27837735 /ug=Hs.424205 /len=606	BX112599	Hs.424205	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8926	0.01859	clone IMAGE:5001859, mRNA /gb=BC040072 /gi=25303948 /ug=Hs.194051 /len=3016	BC040072	Hs.194051	
8940	0.04789	EST(qp46g11.x1 NCI_CGAP_Co8 clone IMAGE:1926116 3')	AI346632		NP_004646
8972	0.005961	EST (ym20a08.r1 Soares infant brain 1NIB IMAGE:48353 5')	H15948		
9088	0.030485	clone IMAGE:3875308, mRNA, partial cds /cds=UNKNOWN /gb=BC013784 /gi=15489380 /ug=Hs.351379 /len=2872	BC013784	Hs.351379	
9123	0.04789	ESTs, cDNA, 3' end /clone=IMAGE:2730647 /clone_end=3' /gb=AW296700 /gi=6703336 /ug=Hs.335620 /len=451	AW296700	Hs.335620	
9129	0.015602	EST(cDNA.	AW896077		
9141	0.025981	EST384025 MAGE resequences, MAGL cDNA, mRNA sequence /gb=AW972041 /gi=8161782 /ug=Hs.190176 /len=617	AW972041	Hs.190176	
9265	0.022033	clone IMAGE:4052238, mRNA, partial cds /cds=(1,73) /gb=BC014384 /gi=15680102 /ug=Hs.348514 /len=1449	BC014384	Hs.348514	
9270	0.002454	602122561F1 NIH_MGC_56 cDNA clone IMAGE:4279766 5', mRNA sequence /clone=IMAGE:4279766 /clone_end=5' /gb=BF668349 /gi=11942244 /ug=Hs.44731 /len=906	BF668349	Hs.44731	
9302	0.041383	No significant match, ORF-1(1~102,214~317)	SEQ.ID.No.11		
9353	0.04789	No significant match, ORF-2(1~153,226~333)	SEQ.ID.No.97		
9384	0.030485	mitochondrial ribosomal protein L45 (MRPL45), nuclear gene encoding mitochondrial protein, mRNA /cds=(22,942) /gb=NM_032351 /gi=21735611 /ug=Hs.19347 /len=1582	NM_032351	Hs.19347	NP_115727
9454	0.00388	praja 1 (PJA1), mRNA /cds=(295,1662) /gb=NM_022368 /gi=21539662 /ug=Hs.21122 /len=2122	NM_022368	Hs.21122	NP_071763
9489	0.013024	similar to putative (H. sapiens) (LOC129641), mRNA	XM_059369		
9492	0.041383	601846634F1 NIH_MGC_55 cDNA clone IMAGE:4077632 5', mRNA sequence /clone=IMAGE:4077632 /clone_end=5' /gb=BF214729 /gi=11108315 /ug=Hs.446581 /len=835	BF214729	Hs.446581	
9581	3.77E-04	partial steerin-1 gene	AJ251973		
9623	0.030485	KIAA0854 protein (KIAA0854), mRNA /cds=(305,2818) /gb=NM_014943 /gi=7662341 /ug=Hs.30209 /len=4089	NM_014943	Hs.30209	NP_055758

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Prot in Accession No.
9641	0.041383	translocase of inner mitochondrial membrane 17 A (yeast) (TIMM17A), mRNA /cds=(8,523) /gb=NM_006335 /gi=5454119 /ug=Hs.20716 /len=1645	NM_006335	Hs.20716	NP_006326
9674	0.01081	EST(DKFZp564I112 (from clone DKFZp564I112))	AL110136		
9717	0.04789	EST(yu74g03.s1 clone 239572 3' contains Alu repeat)	H81306		
9733	0.01859	hypothetical protein LOC92597 (LOC92597), mRNA /cds=(151,801) /gb=NM_173468 /gi=27735028 /ug=Hs.31422 /len=6956	NM_173468	Hs.31422	NP_775739
9763	0.04789	EST(ze13e01.r1 Soares_fetal_heart_NbHH19WcDNA clone IMAGE:358872 5')	W94505		
9806	0.01081	7k03e02.x1 NCI_CGAP_GC6 cDNA clone IMAGE:3443402 3', mRNA sequence /clone=IMAGE:3443402 /clone_end=3' /gb=BF056273 /gi=10810169 /ug=Hs.188920 /len=572	BF056273	Hs.188920	
9918	0.04789	chromosome 20 open reading frame 108 (C20orf108), mRNA /cds=(41,619) /gb=NM_080821 /gi=18201877 /ug=Hs.352413 /len=3026	NM_080821	Hs.352413	NP_543011
9920	0.015602	hypothetical protein FLJ22419 (FLJ22419), mRNA /cds=(409,1596) /gb=NM_024697 /gi=13375980 /ug=Hs.99256 /len=1674	NM_024697	Hs.99256	NP_078973
9921	0.04789	hypothetical protein FLJ10477 (FLJ10477), mRNA /cds=(232,873) /gb=NM_018105 /gi=8922445 /ug=Hs.7432 /len=2167	NM_018105	Hs.7432	NP_060575
9928	0.008919	LIM domain containing preferred translocation partner in lipoma (LPP), mRNA /cds=(247,2085) /gb=NM_005578 /gi=5031886 /ug=Hs.180398 /len=5656	NM_005578	Hs.180398	NP_005569
9953	0.030485	Fatty acid binding protein 1, liver (Fabp1), mRNA	NM_012556		
10026	0.001162	dishevelled associated activator of morphogenesis 1 (DAAM1), mRNA /cds=(126,3362) /gb=NM_014992 /gi=21071076 /ug=Hs.197751 /len=4256	NM_014992	Hs.197751	NP_055807
10085	0.041383	mRNA for KIAA0931 protein, partial cds. /cds=(1,2205) /gb=AB023148 /gi=4589505 /ug=Hs.173373 /len=6167	AB023148	Hs.173373	
10145	0.025981	EST(fi21a05.x1 Sugano Kawakami zebrafish DRA clone 2601776 3')	AW116880		
10178	0.030485	EST382135 MAGE resequences, MAGK cDNA, mRNA sequence /gb=AW970055 /gi=8159900 /ug=Hs.324815 /len=764	AW970055	Hs.324815	
10238	0.01859	EST(yr06d08.r1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:204495 5')	H58577		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10270	0.04789	yh25h10.s1 Soares placenta Nb2HP cDNA clone IMAGE:130819 3', mRNA sequence /clone=IMAGE:130819 /clone_end=3' /gb=R22183 /gi=776964 /ug=Hs.307975 /len=433	R22183	Hs.307975	
10275	0.04789	EST tn11d09.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2167313 3'	AI560484		NP_852556
10323	0.003097	mRNA; cDNA DKFZp434K1115 (from clone DKFZp434K1115); complete cds /cds=(97,2877) /gb=AL136764 /gi=12053044 /ug=Hs.42676 /len=4868	AL136764	Hs.42676	
10346	0.04789	UI-E-EO1-aiv-e-19-0-UI.s1 UI-E-EO1 cDNA clone UI-E-EO1-aiv-e-19-0-UI 3', mRNA sequence /clone=UI-E-EO1-aiv-e-19-0-UI /clone_end=3' /gb=BU742864 /gi=23689787 /ug=Hs.356716 /len=1044	BU742864	Hs.356716	
10363	0.005961	Similar to RIKEN cDNA 2310026P19 gene, clone MGC:49935 IMAGE:6175382, mRNA, complete cds /cds=(288,3329) /gb=BC043352 /gi=27694113 /ug=Hs.35096 /len=5900	BC043352	Hs.35096	
10407	0.004826	clone IMAGE:125405, mRNA sequence /gb=AF339770 /gi=13507308 /ug=Hs.221635 /len=790	AF339770	Hs.221635	
10451	0.015602	oj03b12.s1 NCI_CGAP_Mel3 cDNA clone IMAGE:1491071 3', mRNA sequence /clone=IMAGE:1491071 /clone_end=3' /gb=AA937379 /gi=3095490 /ug=Hs.137120 /len=403	AA937379	Hs.137120	
10474	0.041383	EST(cDNA clone IMAGE:2505486 3')	AW004819		NP_612487
10530	0.04789	EST383317 MAGE resequences, MAGL cDNA, mRNA sequence /gb=AW971229 /gi=8161074 /ug=Hs.293372 /len=642	AW971229	Hs.293372	
10534	0.013024	hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA /cds=(433,2943) /gb=NM_152588 /gi=22749210 /ug=Hs.396456 /len=4855	NM_152588	Hs.396456	NP_689801
10558	0.025981	ESTs, cDNA /clone=IMAGE:1372579 /gb=AA833868 /gi=2908636 /ug=Hs.156300 /len=495	AA833868	Hs.156300	
10564	0.01081	UI-1-BB1p-akj-h-02-0-UI.s1 NCI_CGAP_PI6 cDNA clone UI-1-BB1p-akj-h-02-0-UI 3', mRNA sequence /clone=UI-1-BB1p-akj-h-02-0-UI /clone_end=3' /gb=BQ021906 /gi=19757184 /ug=Hs.317762 /len=1296	BQ021906	Hs.317762	
10571	0.022033	EST(qv09f01.x1 cDNA, 3' end/clone=IMAGE:1981081 /clone_end=3' /gb=AI274446 /gi=3896714 /ug=Hs.327194 /len=230	AI274446	Hs.327194	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10592	0.030485	EST(cDNA clone IMAGE:3054307 3')	AW575133		NP_005162
10594	0.008919	UI-H-EZ1-bbh-j-15-0-UI.s1 NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-bbh-j-15-0-UI 3', mRNA sequence /clone=UI-H-EZ1-bbh-j-15- 0-UI /clone_end=3' /gb=BQ575990 /gi=21479307 /ug=Hs.445509 /len=1032	BQ575990	Hs.445509	
10596	0.013024	602584296F1 NIH_MGC_76 cDNA clone IMAGE:4712302 5', mRNA sequence /clone=IMAGE:4712302 /clone_end=5' /gb=BG564611 /gi=13572263 /ug=Hs.136470 /len=896	BG564611	Hs.136470	
10597	0.01859	BX106681 Soares_parathyroid_tumor_NbHPA cDNA clone IMAGp998F054235, mRNA sequence /clone=IMAGp998F054235_ IMAGE:16684 84 /gb=BX106681 /gi=27847079 /ug=Hs.293334 /len=605	BX106681	Hs.293334	
10624	0.030485	AGENCOURT_6417307 NIH_MGC_67 cDNA clone IMAGE:5492062 5', mRNA sequence /clone=IMAGE:5492062 /clone_end=5' /gb=BM799896 /gi=19116719 /ug=Hs.304926 /len=913	BM799896	Hs.304926	
10629	0.04789	ac74b05.x5 Stratagene lung (#937210) cDNA clone IMAGE:868305 3' similar to contains Alu repetitive element, mRNA sequence /clone=IMAGE:868305 /clone_end=3' /gb=AI791153 /gi=5338869 /ug=Hs.444952 /len=498	AI791153	Hs.444952	
10633	0.035601	UI-E-CL1-afa-n-02-0-UI.r1 UI-E-CL1 cDNA clone UI-E-CL1-afa-n-02-0-UI 5', mRNA sequence /clone=UI-E-CL1-afa-n-02-0-UI /clone_end=5' /gb=BM696235 /gi=19009493 /ug=Hs.446332 /len=1366	BM696235	Hs.446332	
10637	0.002454	EST(NIH_MGC_71 cDNA clone IMAGE:3909162 5')	BE885396		NP_060114
10642	0.022033	HSC3IC021 normalized infant brain cDNA cDNA clone c-3ic02	F13068		
10669	0.025981	EST(Hippocampus SN pool 1 cDNA clone IMAGE:1948863 similar to contains L1.t2 L1 repetitive element ;)	AI217038		
10675	0.002454	cDNA FLJ11309 fis, clone PLACE1010076. /gb=AK002171 /gi=7023887 /ug=Hs.28005 /len=3232	AK002171	Hs.28005	
10698	0.025981	cDNA FLJ37672 fis, clone BRHIP2012059. /gb=AK094991 /gi=21754166 /ug=Hs.125419 /len=2342	AK094991	Hs.125419	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10733	0.025981	DKFZp434O0813_s1 434 (synonym: htes3) cDNA clone DKFZp434O0813 3', mRNA sequence /clone=DKFZp434O0813 /clone_end=3' /gb=AL040360 /gi=5409314 /ug=Hs.162203 /len=772	AL040360	Hs.162203	
10782	0.025981	EST (cDNA clone IMAGE:120476 3' similar to	T95469		
10788	0.022033	yg45f12.s1 Soares infant brain 1NIB cDNA clone IMAGE:35625 3', mRNA sequence /clone=IMAGE:35625 /clone_end=3' /gb=R45691 /gi=822137 /ug=Hs.268774 /len=574	R45691	Hs.268774	
10798	0.035601	EST (ta16g05.x1 NCI_CGAP_Lym5 IMAGE:2044280 3')	AI471814		
10821	0.035601	601584240F1 NIH_MGC_7 cDNA clone IMAGE:3938912 5', mRNA sequence /clone=IMAGE:3938912 /clone_end=5' /gb=BE798289 /gi=10219487 /ug=Hs.446578 /len=793	BE798289	Hs.446578	
10834	0.025981	EST(EST370510 MAGE resequences, MAGE)	AW958440		NP_061323
10855	0.008919	EST 7h93e02.x1 NCI_CGAP_Co16 cDNA clone IMAGE:3323546 3'	BF064070		
10856	0.01859	clone IMAGE:4138742, mRNA /gb=BC006326 /gi=13937734 /ug=Hs.334571 /len=1666	BC006326	Hs.334571	
10860	0.030485	mitochondrion, complete genome	NC_001807		
10937	0.01859	hypothetical protein MGC16384 (MGC16384), mRNA /cds=(450,602) /gb=NM_053048 /gi=16596689 /ug=Hs.274268 /len=1599	NM_053048	Hs.274268	NP_444276
10954	0.01081	desmin (DES), mRNA /cds=(81,1490) /gb=NM_001927 /gi=18105049 /ug=Hs.279604 /len=2236	NM_001927	Hs.279604	NP_001918
10976	0.04789	in56e04.x1 HR85 islet cDNA clone IMAGE:6126055 3', mRNA sequence /clone=IMAGE:6126055 /clone_end=3' /gb=BU784825 /gi=23830229 /ug=Hs.442971 /len=548	BU784825	Hs.442971	
10999	0.015602	ax37a08.x1 Proliferating Erythroid Cells (LCB:ax library) cDNA clone ax37a08 random, mRNA sequence /clone=ax37a08 /gb=BG943384 /gi=14342756 /ug=Hs.339555 /len=555	BG943384	Hs.339555	
11002	0.013024	AU119153 HEMBA1 cDNA clone HEMBA1005152 5', mRNA sequence /clone=HEMBA1005152 /clone_end=5' /gb=AU119153 /gi=10934388 /ug=Hs.288615 /len=820	AU119153	Hs.288615	

Spot	p-value	D scription	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11013	0.035601	UI-H-FH0-bcl-g-09-0-UI.s1 NCI_CGAP_FH0 cDNA clone UI-H-FH0-bcl-g-09-0-UI 3', mRNA sequence /clone=UI-H-FH0-bcl-g-09-0-UI /clone_end=3' /gb=CA419491 /gi=24782146 /ug=Hs.293327 /len=693	CA419491	Hs.293327	
11014	0.030485	cDNA FLJ14135 fis, clone MAMMA1002728. /gb=AK024197 /gi=10436518 /ug=Hs.289037 /len=1784	AK024197	Hs.289037	
11024	0.04789	hypothetical protein MGC33607 (MGC33607), mRNA /cds=(42,2543) /gb=NM_152775 /gi=22749514 /ug=Hs.41101 /len=2866	NM_152775	Hs.41101	NP_689988
11025	0.01859	EST(cDNA 3'	BM264491		
11031	0.013024	cDNA: FLJ21228 fis, clone COL00739. /gb=AK024881 /gi=10437293 /ug=Hs.306716 /len=1869	AK024881	Hs.306716	
11032	0.01859	nj38c05.s1 NCI_CGAP_AA1 cDNA clone IMAGE:994760 3' similar to gb:M62424 THROMBIN RECEPTOR PRECURSOR mRNA sequence /clone=IMAGE:994760 /clone_end=3' /gb=AA548630 /gi=2318912 /ug=Hs.105848 /len=555	AA548630	Hs.105848	
11048	0.005961	EST(placenta Nb2HP Homo sapiens cDNA clone IMAGE:138431 5' similar to contains Alu repetitive element;)	R68614		
11059	0.01859	UI-E-CQ1-aew-e-07-0-UI.s1 UI-E-CQ1 cDNA clone UI-E-CQ1-aew-e-07-0-UI 3', mRNA sequence /clone=UI-E-CQ1-aew-e-07-0-UI /clone_end=3' /gb=BU728934 /gi=23651308 /ug=Hs.436272 /len=1132	BU728934	Hs.436272	
11063	0.035601	clone alpha_est218/52C1 mRNA sequence. /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992	AF001542	Hs.356442	
11068	0.030485	mRNA; cDNA DKFZp586G1520 (from clone DKFZp586G1520) /gb=AL050148 /gi=4884359 /ug=Hs.31834 /len=3030	AL050148	Hs.31834	
11126	0.01859	full length insert cDNA clone ZD64C04 /gb=AF088052 /gi=3523258 /ug=Hs.384557 /len=831	AF088052	Hs.384557	
11215	0.015602	Novel, ORF+3(39~203)	SEQ.ID.No.53		
11259	0.041383	actin binding LIM protein 1 (ABLIM1), transcript variant ABLIM-I, mRNA /cds=(100,2436) /gb=NM_002313 /gi=21284382 /ug=Hs.158203 /len=7581	NM_002313	Hs.158203	NP_006711
11266	0.035601	B-cell translocation gene 1, anti-proliferative (BTG1), mRNA /cds=(309,824) /gb=NM_001731 /gi=4502472 /ug=Hs.77054 /len=1783	NM_001731	Hs.77054	NP_001722

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11322	0.041383	Hypothetical protein (L1H 3' region) - human (AA=69%)	B34087		
11341	0.041383	similar to rat tricarboxylate carrier-like protein (BA108L7.2), mRNA /cds=(75,1040) /gb=NM_030971 /gi=13569945 /ug=Hs.283844 /len=2735	NM_030971	Hs.283844	NP_112233
11343	0.035601	chromosome 1 open reading frame 33 (C1orf33), mRNA /cds=(32,751) /gb=NM_016183 /gi=18490986 /ug=Hs.274201 /len=1185	NM_016183	Hs.274201	NP_057267
11351	0.04789	type V procollagen alpha 2 chain (COL5A2) gene, exons 34 through 52 and partial cds; and type III procollagen alpha 1 chain (COL3A1) gene, exons 2 through 52	AY016295		
11454	0.025981	similar to protein tyrosine phosphatase, receptor type, E; Protein tyrosine phosphatase, receptor type, epsilon; protein tyrosine phosphatase, receptor type, epsilon polypeptide (H. sapiens) (LOC119466), mRNA	XM_005781		
11465	0.007315	gonadotropin-releasing hormone receptor (GNRHR), mRNA /cds=(1749,2735) /gb=NM_000406 /gi=4504058 /ug=Hs.73064 /len=2735	NM_000406	Hs.73064	NP_000397
11519	0.025981	mRNA; cDNA DKFZp761O0611 (from clone DKFZp761O0611) /gb=AL834155 /gi=21739631 /ug=Hs.22969 /len=4502	AL834155	Hs.22969	
11546	0.04789	EST(PM3-NT0011-120400-001-b03 NT0011)	AW888715		
11551	0.022033	EST(EST64315 Jurkat T-cells VI 5' ribosomal protein S21)	AA355853		NP_114107
11569	0.01859	hypothetical protein DKFZp434K1421 (DKFZP434K1421), mRNA /cds=(29,1705) /gb=NM_032141 /gi=14149806 /ug=Hs.374609 /len=2547	NM_032141	Hs.374609	NP_115517
11585	0.035601	EST (yd08e03.r1 clone 24895 5')	T80443		
11604	0.041383	EST(ae50c06.s1 Stratagene lung carcinoma 937218 clone IMAGE:950314 3' contains Alu repeat)	AA600135		
11637	0.041383	EST(at70b02.x1 Barstead colon HPLRB7 clone IMAGE:2377323 3' contains L1.t3 L1 repeat)	AI832565		
11654	0.025981	clone IMAGE:5260918, mRNA /gb=BC035085 /gi=23958865 /ug=Hs.250448 /len=3052	BC035085	Hs.250448	
11675	0.022033	cDNA FLJ34480 fis, clone HLUNG2004014. /gb=AK091799 /gi=21750255 /ug=Hs.154993 /len=1976	AK091799	Hs.154993	

Spot	p-value	Description	Gene Accession No.	Unig n Accession No.	Protein Accession No.
11683	0.007453	EST (clone IMAGE:1218466 3' similar to contains	AA662478		
11692	0.035601	KIAA0874 protein (KIAA0874), mRNA /cds=(1,6189) /gb=NM_015208 /gi=14140237 /ug=Hs.27973 /len=6189	NM_015208	Hs.27973	NP_056023
11760	0.041383	arrestin, beta 2 (ARRB2), mRNA /cds=(234,1463) /gb=NM_004313 /gi=21626464 /ug=Hs.18142 /len=1941	NM_004313	Hs.18142	NP_004304
11766	0.030485	AV701088 ADA cDNA clone ADAAGB09 5', mRNA sequence /clone=ADAAGB09 /clone_end=5' /gb=AV701088 /gi=10717418 /ug=Hs.419141 /len=652	AV701088	Hs.419141	
11770	0.00388	FLJ33160 fis, clone UTERU2000485 /cds=UNKNOWN /gb=AK057722 /gi=16553641 /ug=Hs.124733 /len=2328	AK057722	Hs.124733	
11800	0.022033	RAN binding protein 2-like 1 (RANBP2L1), transcript variant 1, mRNA /cds=(78,5375) /gb=NM_005054 /gi=19718754 /ug=Hs.179825 /len=7164	NM_005054	Hs.179825	NP_115636
11808	0.035601	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4, cDNA /gb=AW582014 /gi=7257063 /ug=Hs.169986 /len=705	AW582014	Hs.169986	
11823	0.01081	mRNA for KIAA1614 protein, partial cds. /cds=(1,3628) /gb=AB046834 /gi=10047302 /ug=Hs.287381 /len=4143	AB046834	Hs.287381	
11870	0.022033	clone 114 tumor rejection antigen mRNA, complete cds /cds=(3482,3544) /gb=AF445027 /gi=17386079 /ug=Hs.24723 /len=3648	AF445027	Hs.24723	
11876	0.007453	immediate early response 3 (IER3), transcript variant long, mRNA /cds=(30,611) /gb=NM_052815 /gi=16554596 /ug=Hs.76095 /len=1345	NM_052815	Hs.76095	NP_434702
11898	0.00388	intersectin 2 (ITSN2), transcript variant 1, mRNA /cds=(242,5332) /gb=NM_006277 /gi=22325384 /ug=Hs.166184 /len=6092	NM_006277	Hs.166184	NP_671494
11912	0.007315	hypothetical protein MGC40157 (MGC40157), mRNA /cds=(106,498) /gb=NM_152350 /gi=22748758 /ug=Hs.295362 /len=1250	NM_152350	Hs.295362	NP_689563
11913	0.005961	mRNA; cDNA DKFZp434H2019 (from clone DKFZp434H2019) /gb=AL137535 /gi=6808211 /ug=Hs.15806 /len=1974	AL137535	Hs.15806	
11985	0.001504	protocadherin beta 16 (PCDHB16), mRNA /cds=(1156,3486) /gb=NM_020957 /gi=14195604 /ug=Hs.147674 /len=4827	NM_020957	Hs.147674	NP_066008
12004	0.030485	hypothetical L1 protein (third intron of gene TS)	JU0033		JU0033

Spot	p-value	Description	Gene Accession No.	Unigen Accession No.	Protein Accession No.
12057	0.013024	qe17g05.x1 Soares_fetal_lung_NbHL19W cDNA clone IMAGE:1739288 3', mRNA sequence /clone=IMAGE:1739288 /clone_end=3' /gb=AI183765 /gi=3734403 /ug=Hs.146975 /len=382	AI183765	Hs.146975	
12058	0.014488	HPS12_49 testis cDNA library cDNA, mRNA sequence /gb=BM422916 /gi=28192251 /ug=Hs.294041 /len=541	BM422916	Hs.294041	
12061	0.041383	cDNA FLJ36838 fis, clone ASTRO2011426. /gb=AK094157 /gi=21753159 /ug=Hs.407030 /len=2646	AK094157	Hs.407030	
12074	0.038534	EST(as88c04.x1 Barstead colon HPLRB7 clone IMAGE:2335782 3' TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN; contains Alu repeat)	AI735066		
12104	0.009171	helicase-like protein (KIAA2023), mRNA /cds=(399,5378) /gb=NM_173082 /gi=27436872 /ug=Hs.231907 /len=7011	NM_173082	Hs.231907	NP_775105
12109	0.019692	EST(wc45g02.x1 NCI_CGAP_Pr28 clone IMAGE:2321618 3')	AI675688		NP_714916
12120	0.01859	mRNA, cDNA DKFZp761O0611 (from clone DKFZp761O0611) /gb=AL834155 /gi=21739631 /ug=Hs.22969 /len=4502	AL834155	Hs.22969	
12122	0.041383	high-mobility group (nonhistone chromosomal) protein 1-like 10 (HMG1L10), mRNA /cds=(51,686) /gb=NM_172363 /gi=28376645 /ug=Hs.434102 /len=994	NM_172363	Hs.434102	NP_758951
12161	0.04789	EST(hh76d05.y1 NCI_CGAP_GU1 cDNA clone IMAGE:2968713 5' similar to contains L1.t1 L1 repetitive element ;	AW663260		
12182	0.025981	Williams-Beuren Syndrome critical region protein 20 copy B (WBSCR20B), mRNA /cds=(984,1448) /gb=NM_145645 /gi=21717802 /ug=Hs.406306 /len=1634	NM_145645	Hs.406306	NP_663620
12193	0.013024	EST (yd68e02.s1 Soares fetal liver spleen 1NFLS IMAGE:113402 3')	T78464		NP_000436
12213	0.04789	repetitive sequence (ALU SUBFAMILY J)	P39188		
12216	0.025981	exon prediction only (aa 2e-15)	CAB90410		
12244	0.041383	EST(601812732F1 NIH_MGC_54 cDNA clone IMAGE:4047222 5')	BF211120		NP_071942
12246	0.022033	EST (yo20f05.r1 Soares adult brain N2b5HB55Y cDNA clone IMAGE:178497 5')	H46503		
12248	0.002454	EST(yd28g06.r1 Soares fetal liver spleen 1NFLS IMAGE:109594 5')	T82238		
12264	0.025981	clone IMAGE:3909104, mRNA /gb=BC015719 /gi=16041698 /ug=Hs.8852 /len=3169	BC015719	Hs.8852	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12284	0.030485	EST384170 MAGE resequences, MAGL cDNA, mRNA sequence /gb=AW971961 /gi=8161927 /ug=Hs.136340 /len=642	AW971961	Hs.136340	
12290	0.041383	EST(yd74f02.s1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:113979 3' similar to contains Alu repetitive element)	T79796		
12329	0.04789	EST(RC2-CT0298-300100-014-d01 CT0298)	AW604547		NP_000981
12344	0.025981	EST(cDNA clone IMAGE:5303467 5')	BI597128		
12352	0.013024	UI-H-BI2-ahm-d-05-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2727224 3', mRNA sequence /clone=IMAGE:2727224 /clone_end=3' /gb=AW293452 /gi=6700088 /ug=Hs.16228 /len=634	AW293452	Hs.16228	
12369	0.035601	QV3-BN0047-150400-152-h07 BN0047 cDNA, mRNA sequence /gb=AW997115 /gi=8257349 /ug=Hs.274352 /len=686	AW997115	Hs.274352	
12371	0.01081	ESTs, cDNA, 5' end /clone=BMFBFE06 /clone_end=5' /gb=AV756341 /gi=10914189 /ug=Hs.244273 /len=766	AV756341	Hs.244273	
12375	0.01081	UI-H-DT0-avk-p-22-0-UI.s1 NCI_CGAP_DT0 cDNA clone IMAGE:5880837 3', mRNA sequence /clone=IMAGE:5880837 /clone_end=3' /gb=BM996358 /gi=19721259 /ug=Hs.433458 /len=838	BM996358	Hs.433458	
12378	0.013024	cDNA FLJ31274 fis, clone KIDNE2006334. /gb=AK055836 /gi=16550665 /ug=Hs.351722 /len=1817	AK055836	Hs.351722	
12387	0.025981	EST(synonym: hlcc2) cDNA clone DKFZp313J2122 5'	AL598811		NP_006796
12388	0.013024	EST(cDNA clone IMAGE:4398135 5')	BF984363		
12423	0.015602	clone IMAGE:4800262, mRNA /gb=BC040182 /gi=25455679 /ug=Hs.235795 /len=3858	BC040182	Hs.235795	
12425	0.004826	FLJ32080 fis, clone OCBBF2000015 /cds=UNKNOWN /gb=AK056642 /gi=16552101 /ug=Hs.336425 /len=3615	AK056642	Hs.336425	
12426	0.013024	602590145F1 NIH_MGC_76 cDNA clone IMAGE:4724074 5', mRNA sequence /clone=IMAGE:4724074 /clone_end=5' /gb=BG564169 /gi=13571821 /ug=Hs.444093 /len=792	BG564169	Hs.444093	
12429	0.003097	EST(cDNA clone IMAGE:3913767 5')	BE890088		
12430	0.01081	mRNA; cDNA DKFZp686J19116 (from clone DKFZp686J19116) /gb=AL833458 /gi=21734100 /ug=Hs.428760 /len=3297	AL833458	Hs.428760	
12431	0.01859	ESTs, cDNA /gb=AW993259 /gi=8253410 /ug=Hs.113105 /len=678	AW993259	Hs.113105	

Spot	p-value	Description	Gene Accession No.	Unig ne Acc ssion No.	Protein Accession No.
12434	0.015602	EST(cDNA clone HTFABF07 5')	AV731260		
12436	0.035601	UI-H-BW0-ajn-d-08-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2732223 3', mRNA sequence /clone=IMAGE:2732223 /clone_end=3' /gb=AW297946 /gi=6704582 /ug=Hs.444392 /len=807	AW297946	Hs.444392	
12452	0.041383	EST(cDNA clone IMAGE:784142 5')	AA446766		
12457	0.035601	EST (376579 MAGE resequences MAGH)	AW964506		NP_065825
12465	0.015602	ESTs, cDNA, 5' end /clone=IMAGE:3922401 /clone_end=5' /gb=BE894201 /gi=10356330 /ug=Hs.176376 /len=916	BE894201	Hs.176376	
12467	0.013024	EST(cDNA clone IMAGE:2728993 3')	AW292959		
12489	0.01081	MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047 /ug=Hs.446594 /len=530	BF814502	Hs.446594	
12494	0.025981	cDNA FLJ39046 fis, clone NT2RP7010612. /gb=AK096365 /gi=21755841 /ug=Hs.9856 /len=2161	AK096365	Hs.9856	
12505	0.041383	EST(cDNA clone HTBBSD03 5')	AV722328		
12541	0.001504	yb61c11.s1 Stratagene ovary (#937217) cDNA clone IMAGE:75668 3', mRNA sequence /clone=IMAGE:75668 /clone_end=3' /gb=T58438 /gi=660275 /ug=Hs.189678 /len=506	T58438	Hs.189678	
12542	0.01081	ESTs, cDNA /gb=AW797724 /gi=7849594 /ug=Hs.130350 /len=559	AW797724	Hs.130350	
12543	0.041383	EST(cDNA clone CS0DI015YC21 5 prime)	AL545514		NP_003109
12547	0.035601	BX096777 Soares_pregnant_uterus_NbHPU cDNA clone IMAGp998K151202, mRNA sequence /clone=IMAGp998K151202 ; IMAGE:50394 2 /gb=BX096777 /gi=27842974 /ug=Hs.193352 /len=684	BX096777	Hs.193352	
12568	0.022033	EST, cDNA, 3' end /clone=IMAGE:1541875 /clone_end=3' /gb=AA927945 /gi=3076689 /ug=Hs.292141 /len=354	AA927945	Hs.292141	
12574	0.013024	UI-H-ED0-awx-b-15-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5824814 3', mRNA sequence /clone=IMAGE:5824814 /clone_end=3' /gb=BQ020068 /gi=19755345 /ug=Hs.396278 /len=1351	BQ020068	Hs.396278	
12624	3.77E-04	No significant match, ORF+3(156~314)	SEQ.ID.No.77		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12667	0.022033	tq86b01.x1 NCI_CGAP_Ov23 cDNA clone IMAGE:2215657 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element ;, mRNA sequence /clone=IMAGE:2215657 /clone_end=3' /gb=AI567941 /gi=4526393 /ug=Hs.436171 /len=476	AI567941	Hs.436171	
12668	0.035601	hypothetical protein FLJ13110 (FLJ13110), mRNA /cds=(145,750) /gb=NM_022912 /gi=12597656 /ug=Hs.7358 /len=3856	NM_022912	Hs.7358	NP_075063
12669	0.041383	hypothetical protein FLJ31438 (FLJ31438), mRNA /cds=(347,2107) /gb=NM_152385 /gi=22748824 /ug=Hs.24423 /len=2266	NM_152385	Hs.24423	NP_689598
12672	0.04789	hypothetical protein FLJ10254	NP_060511		
12717	0.04789	EST(xx99e02.x1 NCI_CGAP_Lym12 cDNA clone IMAGE:2851802 3' similar to contains Alu repetitive element)	AW515834		NP_387449
12751	0.04789	NISC_gj03b10.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:3270498 3', mRNA sequence /clone=IMAGE:3270498 /clone_end=3' /gb=CB048158 /gi=27786445 /ug=Hs.201018 /len=384	CB048158	Hs.201018	
12771	0.035601	cDNA FLJ37324 fis, clone BRAMY2018279. /gb=AK094643 /gi=21753744 /ug=Hs.12714 /len=2844	AK094643	Hs.12714	
12780	0.013024	clone MGC:16233 IMAGE:3677787, mRNA, complete cds /cds=(85,957) /gb=BC012766 /gi=15215342 /ug=Hs.180428 /len=2845	BC012766	Hs.180428	NP_065195
12798	0.01081	UI-H-DF0-bem-a-10-0-UI.s1 NCI_CGAP_DF0 cDNA clone UI-H-DF0-bem-a-10-0-UI 3', mRNA sequence /clone=UI-H-DF0-bem-a-10-0-UI /clone_end=3' /gb=CA425521 /gi=24788247 /ug=Hs.411829 /len=1131	CA425521	Hs.411829	
12804	0.022033	hypothetical protein FLJ38716 (FLJ38716), mRNA /cds=(266,1354) /gb=NM_152367 /gi=22748790 /ug=Hs.376194 /len=3229	NM_152367	Hs.376194	NP_689580
12838	0.04789	EST(mRNA from cd34 stem cells Homo sapiens cDNA clone CBFBD10)	AF150252		
12846	0.035601	EST, cDNA, 5' end. /clone=DKFZp761D0315 /clone_end=5' /gb=AL137968 /gi=6854648 /ug=Hs.256115 /len=523	AL137968	Hs.256115	
12851	0.041383	FLJ11311 fis, clone PLACE1010102/cds=UNKNOWN /gb=AK002173 /gi=7023889 /ug=Hs.5518 /len=1839	AK002173	Hs.5518	NP_689971

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12879	0.030485	hypothetical protein FLJ22415 (FLJ22415), mRNA /cds=(342,1463) /gb=NM_024769 /gi=13376114 /ug=Hs.135121 /len=2627	NM_024769	Hs.135121	NP_079045
12897	0.01081	EST(cDNA clone IMAGE:6106210 5')	BQ438562		NP_005339
12898	0.022033	603395193F1.NIH_MGC_90 cDNA clone IMAGE:5405278 5', mRNA sequence /clone=IMAGE:5405278 /clone_end=5' /gb=BI871283 /gi=16044958 /ug=Hs.443147 /len=845	BI871283	Hs.443147	
12902	0.04789	ESTs, FLJ25251 fis, clone STM03603 /cds=UNKNOWN /gb=AK057980 /gi=16553972 /ug=Hs.256801 /len=1727	AK057980	Hs.256801	
12903	0.025981	cDNA FLJ33097 fis, clone TRACH2000775. /gb=AK057659 /gi=16553423 /ug=Hs.415317 /len=2977	AK057659	Hs.415317	
12907	0.005961	UI-E-EO0-ahy-j-09-0-UI.r1 UI-E-EO0 cDNA clone UI-E-EO0-ahy-j-09-0-UI 5', mRNA sequence /clone=UI-E-EO0-ahy-j-09-0-UI /clone_end=5' /gb=BM722772 /gi=19043589 /ug=Hs.433569 /len=1166	BM722772	Hs.433569	
12921	0.035601	BX106452 NCI_CGAP_Gas4 cDNA clone IMAGp998N095583, mRNA sequence /clone=IMAGp998N095583 IMAGE:2255816 /gb=BX106452 /gi=27834105 /ug=Hs.200841 /len=458	BX106452	Hs.200841	
12935	0.025981	clone IMAGE:35115, mRNA sequence /gb=AF339818 /gi=13507356 /ug=Hs.326718 /len=1071	AF339818	Hs.326718	
12936	0.022033	clone IMAGE:5263531, mRNA /gb=BC037740 /gi=22902216 /ug=Hs.18016 /len=5036	BC037740	Hs.18016	
12941	0.011207	MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047 /ug=Hs.446594 /len=530	BF814502	Hs.446594	
12973	0.04789	ESTs, cDNA, 3' end /clone=IMAGE:2504343 /clone_end=3' /gb=AW009340 /gi=5858118 /ug=Hs.372482 /len=490	AW009340	Hs.372482	
12975	0.022033	cDNA FLJ38271 fis, clone FCBBF3002782, moderately similar to Leptin receptor. /gb=AK095590 /gi=21754877 /ug=Hs.231895 /len=2435	AK095590	Hs.231895	
12996	0.025981	cDNA FLJ11366 fis, clone HEMBA1000282. /gb=AK021428 /gi=10432610 /ug=Hs.189002 /len=2075	AK021428	Hs.189002	

Spot	p-value	D scription	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13005	0.035601	zx55g04.r1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:446454 5', mRNA sequence /clone=IMAGE:446454 /clone_end=5' /gb=AA203502 /gi=1799213 /ug=Hs.192991 /len=952	AA203502	Hs.192991	
13014	0.041383	cDNA FLJ13334 fis, clone OVARC1001846 /gb=AK023396 /gi=10435315 /ug=Hs.269091 /len=2361	AK023396	Hs.269091	
13015	0.007453	hypothetical protein FLJ31131 (FLJ31131), mRNA /cds=(20,421) /gb=NM_152535 /gi=22749108 /ug=Hs.23853 /len=1970	NM_152535	Hs.23853	
13041	0.004826	AGENCOURT_8351558 NIH_MGC_113 cDNA clone IMAGE:6282273 5', mRNA sequence /clone=IMAGE:6282273 /clone_end=5' /gb=BQ706828 /gi=21845727 /ug=Hs.132759 /len=928	BQ706828	Hs.132759	
13074	0.007453	EST(IL3-NT0280-050201-453-A10_1 NT0280 cDNA, MRNA sequence)	BI040412		
13081	0.041383	Novel	SEQ.ID.No.8		
13128	0.030485	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA /cds=(81,362) /gb=NM_000609 /gi=10834987 /ug=Hs.237356 /len=3541	NM_000609	Hs.237356	NP_000600
13135	0.00388	(clone: SS20B/E6.0) HUMALAD10 alpha- adducin gene, exon 11	L29298		
13161	0.04789	hypothetical protein FLJ10035 (FLJ10035), mRNA /cds=(251,1132) /gb=NM_030803 /gi=24475809 /ug=Hs.16390 /len=2404	NM_030803	Hs.16390	NP_110430
13171	0.04789	hypothetical gene supported by XM_064780 (LOC125750), mRNA	XM_064780		
13194	0.008919	putative serine-rich protein mRNA, partial cds (AF246705.1)	AF246705	Hs.32922	NP_060102
13212	0.004826	hypothetical protein FLJ20060 (FLJ20060), mRNA /cds=(72,2078) /gb=NM_017645 /gi=24431978 /ug=Hs.54617 /len=2884	NM_017645	Hs.54617	NP_060115
13228	0.041383	membrane-spanning 4-domains, subfamily A, member 7 (MS4A7), mRNA /cds=(147,869) /gb=NM_021201 /gi=23110999 /ug=Hs.11090 /len=1257	NM_021201	Hs.11090	NP_067024
13240	0.01859	solute carrier family 38, member 2 (SLC38A2), mRNA /cds=(352,1872) /gb=NM_018976 /gi=21361601 /ug=Hs.298275 /len=4795	NM_018976	Hs.298275	NP_061849
13255	0.04789	FK506 binding protein 7 (FKBP7), mRNA /cds=(96,875) /gb=NM_016105 /gi=23618828 /ug=Hs.344379 /len=1067	NM_016105	Hs.344379	NP_851939

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13280	0.022033	cDNA FLJ13792 fis, clone THYRO1000072, weakly similar to MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117). /cds=(9,1337) /gb=AK023854 /gi=10435918 /ug=Hs.154751 /len=2184	AK023854	Hs.154751	
13282	0.022033	LIS1-interacting protein NUDEL; endooligopeptidase A (NUDEL), mRNA /cds=(134,1171) /gb=NM_030808 /gi=13540599 /ug=Hs.3850 /len=2329	NM_030808	Hs.3850	NP_110435
13308	0.04789	ligand of numb-protein X (LNK), mRNA /cds=(236,2134) /gb=NM_032622 /gi=14249127 /ug=Hs.66295 /len=3737	NM_032622	Hs.66295	NP_116011
13315	0.035601	partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene	AJ295844		
13419	0.01081	EST(0a56h11.r1 NCI_CGAP_GCB1 clone IMAGE:1309029 5' contains MER10.b3 MER10 MER10 repeat)	AA746385		
13423	0.015602	mRNA; cDNA DKFZp686E1027 (from clone DKFZp686E1027) /gb=AL832759 /gi=21733340 /ug=Hs.269418 /len=5327	AL832759	Hs.269418	
13513	0.013024	EST(PM3-SN0020-270300-001-h08 SN0020)	AW865025		NP_115668
13515	0.013024	EST(hh87d03.x1 NCI_CGAP_GU1 clone IMAGE:2969765 3' contains Alu repeat)	AW627545		
13524	0.015602	hypothetical protein DKFZp586C1924 (DKFZp586C1924), mRNA /cds=(106,693) /gb=NM_032273 /gi=14150016 /ug=Hs.108338 /len=782	NM_032273	Hs.108338	NP_115649
13526	0.041383	non-SMC (structural maintenance of chromosomes) element 1 protein (NSE1), mRNA /cds=(24,794) /gb=NM_145080 /gi=21489972 /ug=Hs.284295 /len=992	NM_145080	Hs.284295	NP_659547
13565	0.01859	EST ni39e06.s1 NCI_CGAP_Lu1 cDNA clone IMAGE:979234 3' similar to contains Alu repetitive element; contains MER10.t2 MER10 repetitive element;	AA522708		
13569	0.030485	EST (tu41c10.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:2253618 3' similar to contains Alu repetitive element;)	AI686385		
13595	0.035601	zinc finger protein 274 (ZNF274), transcript variant ZNF274c, mRNA /cds=(460,2421) /gb=NM_133502 /gi=19743800 /ug=Hs.83761 /len=2839	NM_133502	Hs.83761	NP_598009

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Prot in Accession No.
13644	0.025981	AGENCOURT_6497573 NIH_MGC_125 cDNA clone IMAGE:5588748 5', mRNA sequence /clone=IMAGE:5588748 /clone_end=5' /gb=BM544964 /gi=18776658 /ug=Hs.406354 /len=1184	BM544964	Hs.406354	
13677	0.025981	KIAA1377 protein, partial cds /cds=UNKNOWN /gb=AB037798 /gi=7243134 /ug=Hs.188790 /len=3916	AB037798	Hs.188790	
13713	0.025981	heterogeneous nuclear ribonucleoprotein H2 (H') (HNRPH2), mRNA /cds=(79,1428) /gb=NM_019597 /gi=14141155 /ug=Hs.278857 /len=2220	NM_019597	Hs.278857	NP_062543
13748	0.041383	Similar to likely ortholog of yeast ARV1, clone IMAGE:4106796, mRNA /gb=BC018945 /gi=17511970 /ug=Hs.290444 /len=3219	BC018945	Hs.290444	
13792	0.019692	hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506 /ug=Hs.143692 /len=2260	NM_144721	Hs.143692	NP_653322
13811	0.04789	hypothetical protein FLJ20360 (FLJ20360), mRNA /cds=(80,2305) /gb=NM_017782 /gi=8923334 /ug=Hs.26434 /len=3041	NM_017782	Hs.26434	NP_060252
13828	0.030485	core-binding factor, beta subunit (CBFB), transcript variant 2, mRNA /cds=(11,559) /gb=NM_001755 /gi=13124872 /ug=Hs.179881 /len=2883	NM_001755	Hs.179881	NP_074036
13829	0.013024	FLJ11463 fis, clone HEMBA1001608 /cds=UNKNOWN /gb=AK021525 /gi=10432722 /ug=Hs.288888 /len=1898	AK021525	Hs.288888	
13835	0.04789	mRNA for KIAA1078 protein, partial cds. /cds=(1,4098) /gb=AB029001 /gi=20521755 /ug=Hs.23585 /len=6740	AB029001	Hs.23585	
13891	0.013024	cDNA FLJ38641 fis, clone HHDPC2003983 /gb=AK095960 /gi=21755328 /ug=Hs.24831 /len=2685	AK095960	Hs.24831	
13913	0.008919	EST(zx56f11.r1 Soares fetal liver spleen 1NFLS S1 cDNA clone 446541 5')	AA203529		
13922	0.005961	cDNA FLJ36579 fis, clone TRACH2012647 /gb=AK093898 /gi=21752852 /ug=Hs.48653 /len=2318	AK093898	Hs.48653	
13945	0.035601	EST(tx88e11.x1 NCI_CGAP_Ut4 clone IMAGE:2276684 3' contains Alu repeat)	AI690725		
13956	0.04789	zh79h09.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:418337 3', mRNA sequence /clone=IMAGE:418337 /clone_end=3' /gb=W92715 /gi=1421867 /ug=Hs.59358 /len=397	W92715	Hs.59358	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13959	0.022033	wi63d02.x1 NCI_CGAP_Kid12 cDNA clone IMAGE:2397987 3', mRNA sequence /clone=IMAGE:2397987 /clone_end=3' /gb=AI762877 /gi=5178544 /ug=Hs.369625 /len=467	AI762877	Hs.369625	
13969	0.041383	EST(te50g08.x1 Soares_NFL_T_GBC_S1 clone IMAGE:2090174 3')	AI539295		
13982	0.032841	EST(nv54h12.r1 NCI_CGAP_Ew1 cDNA clone IMAGE:1233671)	AA721522		
13992	0.003097	EST oi10c01.s1 NCI_CGAP_GC4 IMAGE:1476096 3'	AA872487		NP_055862
13996	0.04789	nuclear pore complex protein (NUP107), mRNA /cds=(116,2893) /gb=NM_020401 /gi=9966880 /ug=Hs.236204 /len=3131	NM_020401	Hs.236204	NP_065134
14060	0.04789	beta-amyloid binding protein precursor (BBP), mRNA /cds=(304,927) /gb=NM_032027 /gi=17738309 /ug=Hs.333541 /len=1250	NM_032027	Hs.333541	NP_114416
14069	0.035601	EST np77c06.s1 NCI_CGAP_Pr2 cDNA clone IMAGE:1132330 similar to contains Alu repetitive element;	AA622809		
14074	0.030485	EST tf62g05.x1 NCI_CGAP_Brn23 cDNA clone IMAGE:2103896 3' similar to gb:L21934 STEROL O-ACYLTRANSFERASE (HUMAN);contains L1.t1 L1 repetitive element ;	AI423779		
14080	0.04789	EST(af08g07.s1 Soares_testis_NHT cDNA clone IMAGE:1031100 3')	AA610081		
14085	0.015602	EST (np87f03.s1 NCI_CGAP_Thy1 IMAGE:1133309)	AA632677		
14094	0.022033	EST (wh67d04.x1 NCI_CGAP_Kid11 IMAGE:2385799 3')	AI766049		
14105	0.030485	Kruppel-like factor 12 (KLF12), transcript variant 1, mRNA /cds=(199,1407) /gb=NM_007249 /gi=21071073 /ug=Hs.23510 /len=10891	NM_007249	Hs.23510	NP_057369
14163	0.013024	EST(AV657608 GLC cDNA clone GLCFDF10 3')	AV657608		
14169	0.025981	UI-H-EI0-ayg-o-16-0-UI.s1 NCI_CGAP_EI0 cDNA clone UI-H-EI0-ayg-o-16-0-UI 3', mRNA sequence /clone=UI-H-EI0-ayg-o-16-0-UI /clone_end=3' /gb=CA449027 /gi=24813447 /ug=Hs.44888 /len=573	CA449027	Hs.44888	
14199	0.01859	EST(HS-1029-A1-B05-MF.abi CIT Genomic Sperm Library C genomic clone)	B35426		
14208	0.004826	EST (qh03a05.x1 Soares_NFL_T_GBC_S1 IMAGE:1843568 3')	AI222189		NP_002547

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14247	0.04789	clone IMAGE:4836898, mRNA /gb=BC042527 /gi=27502923 /ug=Hs.434231 /len=2935	BC042527	Hs.434231	
14250	0.025981	ferritin, light polypeptide (FTL), mRNA /cds=(189,716) /gb=NM_000146 /gi=20149497 /ug=Hs.430150 /len=878	NM_000146	Hs.430150	NP_000137
14295	0.013024	cDNA: FLJ22765 fis, clone KAIA1180. /gb=AK026418 /gi=10439279 /ug=Hs.163986 /len=1994	AK026418	Hs.163986	
14300	0.041383	twisted gastrulation 1 (Drosophila) (TWSG1), mRNA /cds=(106,777) /gb=NM_020648 /gi=21314788 /ug=Hs.247302 /len=3693	NM_020648	Hs.247302	NP_065699
14307	0.00388	EST(cDNA clone IMAGE:6104513 5')	BQ429184		
14322	0.041383	clone IMAGE:4297077, mRNA /gb=BC017920 /gi=17389820 /ug=Hs.375771 /len=1247	BC017920	Hs.375771	
14324	0.001162	EST, cDNA, 3' end /clone=IMAGE:1692758 /clone_end=3' /gb=AI092853 /gi=3431829 /ug=Hs.134911 /len=486	AI092853	Hs.134911	
14339	0.030485	7a19b02.x1 NCI_CGAP_GC6 cDNA clone IMAGE:3219147 3' similar to contains element MER36 repetitive element ;, mRNA sequence /clone=IMAGE:3219147 /clone_end=3' /gb=BE503478 /gi=9705875 /ug=Hs.281956 /len=356	BE503478	Hs.281956	
14345	0.025981	mRNA; cDNA DKFZp586E1624 (from clone DKFZp586E1624) /gb=AL110152 /gi=5817054 /ug=Hs.94030 /len=1341	AL110152	Hs.94030	
14353	0.035601	cDNA FLJ31303 fis, clone LIVER1000082. /gb=AK055865 /gi=16550700 /ug=Hs.350200 /len=2801	AK055865	Hs.350200	
14390	0.008919	BX097880 NCI_CGAP_Thy1 cDNA clone IMAGp998F242841, mRNA sequence /clone=IMAGp998F242841; IMAGE:11332 07 /gb=BX097880 /gi=27829041 /ug=Hs.208961 /len=354	BX097880	Hs.208961	
14415	0.004826	ESTs, cDNA, 5' end /clone=IMAGE:4515481 /clone_end=5' /gb=BG292389 /gi=13051140 /ug=Hs.374490 /len=887	BG292389	Hs.374490	
14417	0.035601	proteasome (prosome, macropain) subunit, alpha type, 4 (PSMA4), mRNA /cds=(137,922) /gb=NM_002789 /gi=23110940 /ug=Hs.251531 /len=1189	NM_002789	Hs.251531	NP_002780

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14419	0.025981	UI-H-ED0-awz-e-06-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5825645 3', mRNA sequence /clone=IMAGE:5825645 /clone_end=3' /gb=BM995013 /gi=19719914 /ug=Hs.23871 /len=1235	BM995013	Hs.23871	
14430	0.005961	ib38b12.y1 HR85 islet cDNA 5', mRNA sequence /clone_end=5' /gb=BG656191 /gi=13793600 /ug=Hs.409469 /len=574	BG656191	Hs.409469	
14439	0.023482	cDNA FLJ13571 fis, clone PLACE1008405. /gb=AK023633 /gi=10435617 /ug=Hs.116278 /len=2484	AK023633	Hs.116278	
14442	0.01859	cDNA FLJ12924 fis, clone NT2RP2004709. /gb=AK022986 /gi=10434694 /ug=Hs.38034 /len=2667	AK022986	Hs.38034	
14443	0.025981	nc77d11.s1 NCI_CGAP_Pr2 cDNA clone IMAGE:783381, mRNA sequence /clone=IMAGE:783381 /gb=AA468352 /gi=2194886 /ug=Hs.324201 /len=362	AA468352	Hs.324201	
14475	0.025981	EST, cDNA: FLJ23266 fis, clone COL06676, highly similar to HUMFRCC Homo sapiens clone s153 mRNA	AK026919		
14494	0.008919	No significant match	SEQ.ID.No.70		
14495	0.035601	No significant match	SEQ.ID.No.74		
14504	0.032841	No significant match (ORF:none)	SEQ.ID.No.22		
14533	0.01859	cDNA FLJ33669 fis, clone BRAMY2028740. /cds=(1,456) /gb=AK090988 /gi=21749257 /ug=Hs.396949 /len=2106	AK090988	Hs.396949	
14537	0.030485	EST (zv14e11.r1 Soares_NhHMPu_S1 cDNA clone IMAGE:753644 5')	AA479436		
14552	0.011207	hypothetical protein MGC18257 (MGC18257), mRNA /cds=(39,1415) /gb=NM_138569 /gi=20070373 /ug=Hs.350860 /len=1740	NM_138569	Hs.350860	NP_612636
14554	0.038534	clone 24707 mRNA sequence /gb=AF055007 /gi=3005728 /ug=Hs.124969 /len=1729	AF055007	Hs.124969	
14564	0.041383	mRNA for KIAA2019 protein. /cds=(15,8408) /gb=AB095939 /gi=24899201 /ug=Hs.57548 /len=9217	AB095939	Hs.57548	
14565	0.025981	oq98a10.x1 NCI_CGAP_Co12 cDNA clone IMAGE:1594362 3' similar to contains Alu repetitive element; mRNA sequence /clone=IMAGE:1594362 /clone_end=3' /gb=AI074369 /gi=3401013 /ug=Hs.386367 /len=478	AI074369	Hs.386367	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14567	0.04789	UI-H-FH1-bfp-m-06-0-UI.s1 NCI_CGAP_FH1 cDNA clone UI-H-FH1-bfp-m-06-0-UI 3', mRNA sequence /clone=UI-H-FH1-bfp-m-06-0-UI /clone_end=3' /gb=BU619573 /gi=23285788 /ug=Hs.312629 /len=1168	BU619573	Hs.312629	
14579	0.016419	EST(yv47g01.s1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:245904 3')	N55367		NP_004388
14612	0.04789	EST (AL536815 LTI_FL013_FBrn1 clone CS0DF020YK05 5')	AL536815		
14633	0.035601	EST(no86d01.s1 NCI_CGAP_AA1 cDNA clone IMAGE:1113697 3')	AA614000		
14637	0.002454	hypothetical protein PRO1331 (PRO1331), mRNA /cds=(423,617) /gb=NM_030778 /gi=13562115 /ug=Hs.301824 /len=1634	NM_030778	Hs.301824	NP_110405
14666	0.030485	EST(QV4-DT0021-281299-070-a12 DT0021)	AW936306		
14672	0.01081	EST (xq76f01.x1 NCI_CGAP_HN11 cDNA clone IMAGE:2756569 3')	AW265747		
14675	0.035601	EST (wi81d01.x1 NCI_CGAP_Kid12 cDNA clone IMAGE:2399713 3')	AI765544		
14717	0.035601	cDNA FLJ32589 fis, clone SPLEN2000443. /gb=AK057151 /gi=16552741 /ug=Hs.21342 /len=2178	AK057151	Hs.21342	
14722	0.032841	cDNA FLJ11439 fis, clone HEMBA1001299. /gb=AK021501 /gi=10432697 /ug=Hs.287416 /len=1500	AK021501	Hs.287416	
14741	0.025981	FLJ13882 fis, clone THYRO1001480 /cds=UNKNOWN /gb=AK023944 /gi=10436040 /ug=Hs.301435 /len=2446	AK023944	Hs.301435	
14760	0.00302	control			
14763	0.004826	EST(cDNA clone IMAGE:2224205 3'.)	AI589443		
14766	0.035601	cDNA FLJ30301 fis, clone BRACE2003217. /gb=AK054863 /gi=16549482 /ug=Hs.285728 /len=2186	AK054863	Hs.285728	
14770	0.041383	EST48277 Fetal spleen cDNA 3' end similar to EST containing Alu repeat, mRNA sequence /clone_end=3' /gb=AA342474 /gi=1994946 /ug=Hs.291585 /len=430	AA342474	Hs.291585	
14774	0.013024	clone IMAGE:5274897, mRNA /gb=BC037888 /gi=23138738 /ug=Hs.351680 /len=4246	BC037888	Hs.351680	
14775	0.01081	ESTs, cDNA /gb=AW963042 /gi=8152878 /ug=Hs.53455 /len=769	AW963042	Hs.53455	NP_003401
14777	0.015602	UI-E-EJ0-ahn-c-06-0-UI.s1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahn-c-06-0-UI 3', mRNA sequence /clone=UI-E-EJ0-ahn-c-06-0-UI /clone_end=3' /gb=BM674956 /gi=18984854 /ug=Hs.131705 /len=1017	BM674956	Hs.131705	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Prot in Accession No.
14830	0.04789	EST(MR1-MT0282-151200-003-e12 MT0282 cDNA, mRNA sequence)	BF903180		
14835	0.022033	BX115107 Soares fetal liver spleen 1NFLS cDNA clone IMAGp998G12373, mRNA sequence /clone=IMAGp998G12373 _IMAGE:19587 5 /gb=BX115107 /gi=27839238 /ug=Hs.431087 /len=758	BX115107	Hs.431087	
14847	0.01859	EST(UI-CF-DU1-aae-h-20-0-UI.s1 UI-CF-DU1 cDNA clone UI-CF-DU1-aae-h-20-0-UI 3')	BU674998		
14871	0.022033	EST, cDNA, 3' end /clone=IMAGE:2488402 /clone_end=3' /gb=AI970954 /gi=5767780 /ug=Hs.311478 /len=509	AI970954	Hs.311478	
14874	0.022033	yp52f01.s1 Soares retina N2b4HR cDNA clone IMAGE:191065 3', mRNA sequence /clone=IMAGE:191065 /clone_end=3' /gb=H40700 /gi=916752 /ug=Hs.33792 /len=504	H40700	Hs.33792	
14884	0.022033	602043661F1 NCI_CGAP_Brn67 cDNA clone IMAGE:4181462 5', mRNA sequence /clone=IMAGE:4181462 /clone_end=5' /gb=BF528488 /gi=11615851 /ug=Hs.433462 /len=885	BF528488	Hs.433462	
14893	0.013024	EST375707 MAGE resequences, MAGH cDNA, mRNA sequence /gb=AW963634 /gi=8153470 /ug=Hs.429581 /len=750	AW963634	Hs.429581	
14902	0.041383	poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA /cds=(89,1189) /gb=NM_005016 /gi=14141167 /ug=Hs.63525 /len=1362	NM_005016	Hs.63525	NP_114366
14903	0.030485	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence	NC_001144		
14924	0.001929	No significant match, ORF-3(1~195)	SEQ.ID.No.57		
14951	0.025981	clone IMAGE:4820928, mRNA /gb=BC033530 /gi=23272327 /ug=Hs.324359 /len=2018	BC033530	Hs.324359	
14971	0.007315	No significant match (ORF:+3: 3~180[179])	SEQ.ID.No.20		

TABLE 3D					
Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
21	0.011824	telomeric repeat binding factor (NIMA-interacting) 1 (TERF1), transcript variant 1, mRNA /cds=(16,1335) /gb=NM_017489 /gi=9257245 /ug=Hs.194562 /len=2686	NM_017489	Hs.194562	NP_059523
75	0.044639	GC20 protein (=AF077052 protein translation factor sui1 homologue)	AF064607		NP_005866
201	0.026896	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence	NC_001144		
233	0.034264	mitochondrion, complete genome	NC_001807		
328	0.020878	EST(yj40f11.r1 clone 151245 5')	H02533		NP_705833
358	0.043185	hypothetical protein FLJ35613 (FLJ35613), mRNA /cds=(126,2063) /gb=NM_173653 /gi=27734934 /ug=Hs.30022 /len=3568	NM_173653	Hs.30022	NP_775924
368	0.043185	mitochondrion, complete genome	NC_001807		
467	0.026896	small nuclear ribonucleoprotein polypeptide G (SNRPG), mRNA /cds=(89,319) /gb=NM_003096 /gi=21359839 /ug=Hs.77496 /len=606	NM_003096	Hs.77496	NP_003087
662	0.048295	insulin-like growth factor binding protein 5 (IGFBP5), mRNA /cds=(752,1570) /gb=NM_000599 /gi=10834981 /ug=Hs.380833 /len=1722	NM_000599	Hs.380833	NP_000590
674	0.011207	SMART/HDAC1 associated repressor protein (SHARP), mRNA /cds=(205,11199) /gb=NM_015001 /gi=14790189 /ug=Hs.184245 /len=12227	NM_015001	Hs.184245	NP_055816
678	0.038517	clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992	AF001542	Hs.356442	
690	0.043185	mRNA for KIAA0518 protein, partial cds. /cds=(1,1953) /gb=AB011090 /gi=3043559 /ug=Hs.23763 /len=4617	AB011090	Hs.23763	
700	0.038517	major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA /cds=(65,829) /gb=NM_019111 /gi=18641378 /ug=Hs.409805 /len=1237	NM_019111	Hs.409805	NP_061984
721	0.002459	mitochondrion, complete genome	NC_001807		
726	0.002051	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747	NM_012479	Hs.25001	NP_036611

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession N	Protein Accession No.
736	0.034264	myosin, heavy polypeptide 11, smooth muscle (MYH11), transcript variant SM2, mRNA /cds=(89,5905) /gb=NM_022844 /gi=13124874 /ug=Hs.78344 /len=6900	NM_022844	Hs.78344	NP_074035
806	0.043185	ring finger protein 19 (RNF19), mRNA /cds=(318,2834) /gb=NM_015435 /gi=19923421 /ug=Hs.48320 /len=4357	NM_015435	Hs.48320	NP_056250
807	0.007812	KIAA0102 gene product (KIAA0102), mRNA /cds=(308,679) /gb=NM_014752 /gi=7661907 /ug=Hs.77665 /len=1370	NM_014752	Hs.77665	NP_055567
808	0.043185	PIX1 mRNA (ORF)	AF037219		NP_570854
829	0.026896	zinc finger protein 103 (mouse) (ZFP103), mRNA /cds=(923,2980) /gb=NM_005667 /gi=5031824 /ug=Hs.155968 /len=3423	NM_005667	Hs.155968	NP_005658
834	0.048295	tetraspan 3 (TSPAN-3), mRNA /cds=(218,979) /gb=NM_005724 /gi=21264581 /ug=Hs.100090 /len=1842	NM_005724	Hs.100090	NP_005715
837	0.034264	serine/arginine repetitive matrix 2 (SRRM2), mRNA /cds=(226,8484) /gb=NM_016333 /gi=19923465 /ug=Hs.197114 /len=9027	NM_016333	Hs.197114	NP_057417
846	0.048295	LAG1 longevity assurance 2 (S. cerevisiae) (LASS2), mRNA /cds=(50,742) /gb=NM_013384 /gi=9937997 /ug=Hs.285976 /len=1646	NM_013384	Hs.285976	NP_071358
923	0.001703	eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa (EIF3S3), mRNA /cds=(6,1064) /gb=NM_003756 /gi=4503514 /ug=Hs.58189 /len=1280	NM_003756	Hs.58189	NP_003747
980	0.038517	cleavage and polyadenylation specific factor 6, 68kDa (CPSF6), mRNA /cds=(35,1690) /gb=NM_007007 /gi=5901927 /ug=Hs.64542 /len=3426	NM_007007	Hs.64542	NP_008938
1008	0.038517	Alg5, S. cerevisiae, of (ALG5), mRNA /cds=(28,1002) /gb=NM_013338 /gi=9665250 /ug=Hs.227933 /len=1125	NM_013338	Hs.227933	NP_037470
1058	0.006699	Williams-Beuren syndrome chromosome region 1 (WBSCR1), transcript variant 1, mRNA /cds=(9,755) /gb=NM_022170 /gi=11559922 /ug=Hs.180900 /len=2546	NM_022170	Hs.180900	NP_114381
1122	0.043185	RAB1B, member RAS oncogene family (RAB1B), mRNA /cds=(48,653) /gb=NM_030981 /gi=13569961 /ug=Hs.300816 /len=1985	NM_030981	Hs.300816	NP_112243

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	UniGene Accession No.	Protein Accession No.
1168	0.048295	thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556	NM_021109	Hs.75968	NP_066932
1196	0.012137	FK506 binding protein 14, 22 kDa (FKBP14), mRNA /cds=(146,781) /gb=NM_017946 /gi=8923658 /ug=Hs.264636 /len=2248	NM_017946	Hs.264636	NP_060416
1236	0.018314	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) (MMP9), mRNA /cds=(20,2143) /gb=NM_004994 /gi=4826835 /ug=Hs.151738 /len=2334	NM_004994	Hs.151738	NP_004985
1301	0.001408	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
1313	0.046968	Similar to LYRIC, clone MGC.41931 IMAGE:5298467, mRNA, complete cds /cds=(329,2077) /gb=BC045642 /gi=28277146 /ug=Hs.243901 /len=3729	BC045642	Hs.243901	
1375	0.020878	similar to embryonic seven-span transmembrane protein-like protein (H. sapiens) (LOC135428), mRNA	XM_059770		
1419	0.012137	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) (CD74), mRNA /cds=(8,706) /gb=NM_004355 /gi=10835070 /ug=Hs.84298 /len=1304	NM_004355	Hs.84298	NP_004346
1455	0.026896	CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA /cds=(260,2668) /gb=NM_001253 /gi=16357499 /ug=Hs.155174 /len=3012	NM_001253	Hs.155174	NP_001244
1456	0.012137	CGI-74 protein (CGI-59), mRNA /cds=(1,1209) /gb=NM_016019 /gi=7706309 /ug=Hs.7194 /len=2296	NM_016019	Hs.7194	NP_057103
1497	0.030399	hypothetical protein MGC45474 (MGC45474), mRNA /cds=(218,2035) /gb=NM_152369 /gi=22748794 /ug=Hs.234101 /len=2384	NM_152369	Hs.234101	
1520	0.034264	mRNA; cDNA DKFZp686G1167 (from clone DKFZp686G1167) /gb=AL833600 /gi=21734246 /ug=Hs.7720 /len=8355	AL833600	Hs.7720	NP_001367
1565	0.016017	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa (NDUFV3), mRNA /cds=(575,1945) /gb=NM_021075 /gi=21361323 /ug=Hs.59745 /len=2023	NM_021075	Hs.59745	NP_066553
1599	0.048295	protein XP_037672 (aa, 58%)	XP_037672		

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1647	0.038517	asporin (LRR class 1) (ASPN), mRNA /cds=(228,1373) /gb=NM_017680 /gi=16596677 /ug=Hs.10760 /len=2466	NM_017680	Hs.10760	NP_060150
1673	0.026896	endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 (HERPUD1), mRNA /cds=(96,1271) /gb=NM_014685 /gi=7661869 /ug=Hs.146393 /len=1884	NM_014685	Hs.146393	NP_055500
1682	0.030399	mRNA; cDNA DKFZp586A061 (from clone DKFZp586A061) /gb=AL080232 /gi=5262725 /ug=Hs.220696 /len=3052	AL080232	Hs.220696	
1683	0.038517	mitochondrion, complete genome	NC_001807		
1722	0.004872	S100 calcium binding protein A11 (calgizzarin) (S100A11), mRNA /cds=(121,438) /gb=NM_005620 /gi=5032056 /ug=Hs.417004 /len=595	NM_005620	Hs.417004	NP_005611
1741	0.048295	mRNA; cDNA DKFZp586F1822 (from clone DKFZp586F1822) /gb=AL117461 /gi=5911922 /ug=Hs.82719 /len=3943	AL117461	Hs.82719	
1763	0.009079	zinc finger protein 36, C3H type-like 1 (ZFP36L1), mRNA /cds=(131,1147) /gb=NM_004926 /gi=15812179 /ug=Hs.85155 /len=3022	NM_004926	Hs.85155	NP_004917
1787	0.043185	ras gene family, member E (ARHE), mRNA /cds=(141,875) /gb=NM_005168 /gi=21361257 /ug=Hs.6838 /len=2685	NM_005168	Hs.6838	NP_005159
1954	0.043185	glycolipid transfer protein (GLTP), mRNA /cds=(115,744) /gb=NM_016433 /gi=20357594 /ug=Hs.381256 /len=1449	NM_016433	Hs.381256	NP_057517
1999	0.005723	chromosome 20 open reading frame 40 (C20orf40), mRNA /cds=(208,396) /gb=NM_014054 /gi=7661709 /ug=Hs.105379 /len=417	NM_014054	Hs.105379	NP_054773
2032	0.024701	histone acetyltransferase (HBOA), mRNA /cds=(43,1878) /gb=NM_007067 /gi=5901961 /ug=Hs.21907 /len=3504	NM_007067	Hs.21907	NP_008998
2062	0.048295	ovarian carcinoma immunoreactive antigen (OCIA), mRNA /cds=(168,905) /gb=NM_017830 /gi=8923426 /ug=Hs.132071 /len=1434	NM_017830	Hs.132071	NP_060300
2064	0.010515	FK506 binding protein 5 (FKBP5), mRNA /cds=(154,1527) /gb=NM_004117 /gi=17149847 /ug=Hs.7557 /len=3781	NM_004117	Hs.7557	NP_004108
2103	0.004131	SRY (sex determining region Y)-box 12 (SOX12), mRNA /cds=(331,1278) /gb=NM_006943 /gi=21264338 /ug=Hs.43627 /len=4645	NM_006943	Hs.43627	NP_008874

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2104	0.010245	hPMS3 mRNA, partial cds. /cds=(1,773) /gb=D38435 /gi=600590 /ug=Hs.334451 /len=846	D38435	Hs.334451	
2112	0.026896	NRH:quinone oxidoreductase 2 gene (NQO2)	AB050248		
2150	0.043185	ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794 /ug=Hs.418650 /len=801	NM_002032	Hs.418650	NP_002023
2171	0.043185	zinc finger protein 202 (ZNF202), mRNA /cds=(11,1957) /gb=NM_003455 /gi=10835040 /ug=Hs.9443 /len=4053	NM_003455	Hs.9443	NP_003446
2190	0.043185	Deleted in split-hand/split-foot 1 region (DSS1), mRNA /cds=(129,341) /gb=NM_006304 /gi=5453639 /ug=Hs.333495 /len=509	NM_006304	Hs.333495	NP_006295
2212	0.018314	chromosome 21 open reading frame 4 (C21orf4), mRNA /cds=(159,635) /gb=NM_006134 /gi=8659558 /ug=Hs.284142 /len=750	NM_006134	Hs.284142	NP_006125
2213	0.005723	CGI-99 protein (CGI-99), mRNA /cds=(162,896) /gb=NM_016039 /gi=7706321 /ug=Hs.110803 /len=1105	NM_016039	Hs.110803	NP_057123
2237	0.043185	mRNA; cDNA DKFZp667F074 (from clone DKFZp667F074) /cds=(1,2388) /gb=AL834362 /gi=21740016 /ug=Hs.378933 /len=4245	AL834362	Hs.378933	
2242	0.030399	uncharacterized hypothalamus protein HT010 (HT010), mRNA /cds=(227,1420) /gb=NM_018471 /gi=8923807 /ug=Hs.6375 /len=2140	NM_018471	Hs.6375	NP_060941
2313	0.034264	Putative prostate cancer tumor suppressor (N33), mRNA /cds=(149,1195) /gb=NM_006765 /gi=6996933 /ug=Hs.71119 /len=1521	NM_006765	Hs.71119	NP_839952
2319	0.002459	retinol dehydrogenase 11 (all-trans and 9-cis) (RDH11), mRNA /cds=(41,997) /gb=NM_016026 /gi=20070271 /ug=Hs.179817 /len=2538	NM_016026	Hs.179817	NP_057110
2399	0.009079	mitochondrion, complete genome	NC_001807		
2404	0.048295	keratan sulfate proteoglycan	AF063301		NP_008966
2498	0.034264	ORF2 [Canis familiaris](60%)	AB012223		
2499	0.026896	dynein, cytoplasmic, light intermediate polypeptide 1 (DNCL1), mRNA /cds=(81,1652) /gb=NM_016141 /gi=7705852 /ug=Hs.266483 /len=2487	NM_016141	Hs.266483	NP_057225
2501	0.048295	replication protein A2, 32kDa (RPA2), mRNA /cds=(292,1104) /gb=NM_002946 /gi=21314636 /ug=Hs.79411 /len=1750	NM_002946	Hs.79411	NP_002937

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2507	0.007812	cDNA FLJ13552 fis, clone PLACE1007218. /gb=AK023614 /gi=10435594 /ug=Hs.204945 /len=1850	AK023614	Hs.204945	
2534	0.016017	dendritic cell protein (GA17), mRNA /cds=(53,1177) /gb=NM_006360 /gi=23397428 /ug=Hs.406648 /len=1268	NM_006360	Hs.406648	NP_006351
2549	0.030399	Tax1 T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA /cds=(89,2458) /gb=NM_006024 /gi=21361681 /ug=Hs.5437 /len=3028	NM_006024	Hs.5437	NP_006015
2557	0.016017	leucine-rich PPR-motif containing (LRPPRC), mRNA /cds=(46,3867) /gb=NM_133259 /gi=18959201 /ug=Hs.182490 /len=4782	NM_133259	Hs.182490	NP_573566
2578	0.034264	G protein Golf alpha gene	U55184		
2617	0.026896	collagen, type I, alpha 1 (COL1A1), mRNA /cds=(120,4514) /gb=NM_000088 /gi=14719826 /ug=Hs.172928 /len=5921	NM_000088	Hs.172928	NP_000079
2624	0.012137	RAB27A, member RAS oncogene family (RAB27A), mRNA /cds=(246,911) /gb=NM_004580 /gi=19923263 /ug=Hs.50477 /len=2496	NM_004580	Hs.50477	NP_004571
2681	0.038517	HBS1-like (S. cerevisiae) (HBS1L), mRNA /cds=(194,2248) /gb=NM_006620 /gi=24431963 /ug=Hs.221040 /len=7163	NM_006620	Hs.221040	NP_006611
2703	0.010515	clone IMAGE:5259179, mRNA /gb=BC035034 /gi=23958339 /ug=Hs.174905 /len=3863	BC035034	Hs.174905	
2747	0.048295	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 (STAM)	NM_003473		NP_003464
2790	0.023731	choroideremia (Rab escort protein 1) (CHM), transcript variant 2950156, mRNA /cds=(31,1992) /gb=NM_000390 /gi=9966760 /ug=Hs.2010 /len=2115	NM_000390	Hs.2010	NP_000381
2801	0.034264	Rattus norvegicus mitochondrial genome	NC_001665		
2824	0.034264	xeroderma pigmentosum, complementation group C (XPC), mRNA /cds=(16,2838) /gb=NM_004628 /gi=20127459 /ug=Hs.320 /len=3658	NM_004628	Hs.320	NP_004619
2830	0.004131	stem-loop (histone) binding protein (SLBP), mRNA /cds=(116,928) /gb=NM_006527 /gi=19913344 /ug=Hs.75257 /len=1743	NM_006527	Hs.75257	NP_006518

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2839	0.043185	synovial sarcoma translocation gene on chromosome 18-like 1 (SS18L1), mRNA /cds=(61,1251) /gb=NM_015558 /gi=27754185 /ug=Hs.154429 /len=3723	NM_015558	Hs.154429	NP_056373
2843	0.020878	UI-E-EJ0-ahj-n-19-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahj-n-19-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahj-n-19-0-UI /clone_end=5' /gb=BM701108 /gi=19014366 /ug=Hs.401941 /len=1923	BM701108	Hs.401941	
2855	0.043185	likely ortholog of mouse dynactin 6 (DCTN6), mRNA /cds=(88,660) /gb=NM_006571 /gi=18426895 /ug=Hs.39913 /len=1044	NM_006571	Hs.39913	NP_006562
2859	0.020878	lysyl-tRNA synthetase (KARS), mRNA /cds=(41,1834) /gb=NM_005548 /gi=5031814 /ug=Hs.3100 /len=1997	NM_005548	Hs.3100	NP_005539
2870	0.043185	threonyl-tRNA synthetase (TARS), mRNA /cds=(135,2270) /gb=NM_152295 /gi=25054078 /ug=Hs.84131 /len=2662	NM_152295	Hs.84131	NP_689508
2926	0.030399	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 24 (DDX24), mRNA /cds=(100,2679) /gb=NM_020414 /gi=14251213 /ug=Hs.155986 /len=2967	NM_020414	Hs.155986	NP_065147
2932	0.018314	cyclin D binding myb-like transcription factor 1 (DMTF1), mRNA /cds=(276,2558) /gb=NM_021145 /gi=10863946 /ug=Hs.5671 /len=3767	NM_021145	Hs.5671	NP_066968
2946	0.003489	CD164 antigen, sialomucin (CD164), mRNA /cds=(94,687) /gb=NM_006016 /gi=21361273 /ug=Hs.43910 /len=3038	NM_006016	Hs.43910	NP_006007
2976	0.043185	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_079425	Hs.77385	NP_524149
2980	0.009079	mRNA for KIAA0121 protein, partial cds. /cds=(411,1301) /gb=D50911 /gi=6633996 /ug=Hs.155584 /len=3787	D50911	Hs.155584	
3013	0.012137	uncharacterized hematopoietic stem/progenitor cells protein MDS031 (MDS031), mRNA /cds=(35,532) /gb=NM_018466 /gi=20070304 /ug=Hs.110853 /len=1358	NM_018466	Hs.110853	NP_060936
3024	0.043185	mRNA; cDNA DKFZp434J214 (from clone DKFZp434J214); partial cds /cds=(1,1082) /gb=AL080156 /gi=5262614 /ug=Hs.12813 /len=2749	AL080156	Hs.12813	NP_056323

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3050	0.043185	DnaJ (Hsp40) subfamily B, member 9 (DNAJB9), mRNA /cds=(203,874) /gb=NM_012328 /gi=9558754 /ug=Hs.6790 /len=2371	NM_012328	Hs.6790	NP_036460
3051	0.038517	clone MGC:45564 IMAGE:4384472, mRNA, complete cds /cds=(188,1123) /gb=BC036746 /gi=22477830 /ug=Hs.132230 /len=3767	BC036746	Hs.132230	
3052	0.034264	NADH dehydrogenase (ubiquinone) 1, beta subcomplex, 6, 17kDa (NDUFB6), mRNA /cds=(104,490) /gb=NM_002493 /gi=20149518 /ug=Hs.109646 /len=733	NM_002493	Hs.109646	NP_002484
3062	0.010515	myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), mRNA /cds=(115,630) /gb=NM_006471 /gi=5453739 /ug=Hs.180224 /len=944	NM_006471	Hs.180224	NP_006462
3067	0.043185	mitochondrion, complete genome	NC_001807		
3088	0.034264	sulfotransferase family, cytosolic, 1C, member 2 (SULT1C2), mRNA /cds=(330,1238) /gb=NM_006588 /gi=5730070 /ug=Hs.312644 /len=2143	NM_006588	Hs.312644	NP_006579
3098	0.030399	malate dehydrogenase 1, NAD (soluble) (MDH1), mRNA /cds=(57,1061) /gb=NM_005917 /gi=21735619 /ug=Hs.75375 /len=1268	NM_005917	Hs.75375	NP_005908
3100	0.013965	polymerase (DNA-directed) kappa (POLK), mRNA /cds=(173,2785) /gb=NM_016218 /gi=7705343 /ug=Hs.135756 /len=4074	NM_016218	Hs.135756	NP_057302
3116	0.034264	Hypothetical protein(cDNA FLJ11299 fis, clone PLACE1009845, highly similar to KIAA0905 protein)	AK002161		NP_057295
3140	0.034264	DKFZp451H2115_r1 451 (synonym: hlcc1) spinal cord cDNA clone DKFZp451H2115 5', mRNA sequence /clone=DKFZp451H2115 /clone_end=5' /gb=AL589315 /gi=13243087 /ug=Hs.332004 /len=517	AL589315	Hs.332004	
3144	0.016017	solute carrier family 20 (phosphate transporter), member 1 (SLC20A1), mRNA /cds=(371,2410) /gb=NM_005415 /gi=7382462 /ug=Hs.78452 /len=3220	NM_005415	Hs.78452	NP_005406
3147	0.005723	PRO0659 protein (PRO0659), mRNA /cds=(60,584) /gb=NM_014138 /gi=7662583 /ug=Hs.6451 /len=1416	NM_014138	Hs.6451	NP_054857
3187	0.034264	clone IMAGE:5229459, mRNA /gb=BC044229 /gi=28277403 /ug=Hs.266263 /len=2044	BC044229	Hs.266263	

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3207	0.038517	hypothetical protein LOC51240 (LOC51240), mRNA /cds=(59,520) /gb=NM_016467 /gi=24475967 /ug=Hs.7870 /len=1017	NM_016467	Hs.7870	NP_057551
3228	0.006699	cDNA FLJ13234 fis, clone OVARC1000302. /gb=AK023296 /gi=10435170 /ug=Hs.240075 /len=1713	AK023296	Hs.240075	
3291	0.018314	clathrin, light polypeptide (Lca) (CLTA), transcript variant brain-specific, mRNA /cds=(75,821) /gb=NM_007096 /gi=6005992 /ug=Hs.104143 /len=1105	NM_007096	Hs.104143	NP_009027
3318	0.026896	endothelial protein C receptor	AB026584		
3334	0.016017	cDNA: FLJ23307 fis, clone HEP11549, highly similar to AF041037 novel antagonist of FGF signaling (sprouty-1) mRNA. /gb=AK026960 /gi=10439945 /ug=Hs.88044 /len=2520	AK026960	Hs.88044	
3354	0.006699	ribosomal protein L23 (RPL23), mRNA /cds=(27,449) /gb=NM_000978 /gi=14591907 /ug=Hs.234518 /len=493	NM_000978	Hs.234518	NP_000969
3390	0.023731	phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2), mRNA /cds=(212,1321) /gb=NM_002767 /gi=22538484 /ug=Hs.13339 /len=1890	NM_002767	Hs.13339	NP_002758
3420	0.026896	heat shock 70kDa protein 8 (HSPA8), transcript variant 1, mRNA /cds=(79,2019) /gb=NM_006597 /gi=24234684 /ug=Hs.180414 /len=2276	NM_006597	Hs.180414	NP_694881
3426	0.038517	Escherichia coli K-12 MG1655 section 343 of 400 of the complete genome	AE000453		
3433	0.048295	interferon induced transmembrane protein 3 (1-8U) (IFITM3), mRNA /cds=(238,639) /gb=NM_021034 /gi=11995467 /ug=Hs.381234 /len=808	NM_021034	Hs.381234	NP_066362
3471	0.018314	RAN, member RAS oncogene family (RAN), mRNA /cds=(115,765) /gb=NM_006325 /gi=6042206 /ug=Hs.10842 /len=1656	NM_006325	Hs.10842	NP_006316
3521	0.048295	ubiquitin-like, containing PHD and RING finger domains 2 (URF2), transcript variant 1, mRNA /cds=(341,1852) /gb=NM_152306 /gi=23312361 /ug=Hs.348602 /len=3720	NM_152306	Hs.348602	NP_690856
3535	0.004131	mRNA; cDNA DKFZp761C169 (from clone DKFZp761C169); partial cds /cds=(997,2475) /gb=AL161991 /gi=7328122 /ug=Hs.71252 /len=3324	AL161991	Hs.71252	NP_075064
3564	0.018314	SOX6 (SOX6) gene	AF309471		

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3607	0.016017	mitochondrion, complete genome	NC_001807		
3650	0.023731	hypothetical protein FLJ10326 (FLJ10326), mRNA /cds=(3,2297) /gb=NM_018060 /gi=8922355 /ug=Hs.262823 /len=3016	NM_018060	Hs.262823	NP_060530
3751	0.018314	S100 calcium binding protein A11 (calgizzarin) (S100A11), mRNA /cds=(121,438) /gb=NM_005620 /gi=5032056 /ug=Hs.417004 /len=595	NM_005620	Hs.417004	NP_005611
3755	0.010515	zinc finger protein 84 (HPF2) (ZNF84), mRNA /cds=(352,2568) /gb=NM_003428 /gi=4508036 /ug=Hs.9450 /len=3257	NM_003428	Hs.9450	NP_003419
3793	0.043185	myosin, light polypeptide 5, regulatory (MYL5), mRNA /cds=(106,627) /gb=NM_002477 /gi=4505304 /ug=Hs.170482 /len=661	NM_002477	Hs.170482	NP_002468
3840	0.009079	sorcin (SRI), mRNA /cds=(13,609) /gb=NM_003130 /gi=4507206 /ug=Hs.422340 /len=952	NM_003130	Hs.422340	NP_003121
3852	0.048295	matrilin 3 (MATN3) precursor, mRNA /cds=(64,1524) /gb=NM_002381 /gi=13518040 /ug=Hs.278461 /len=2599	NM_002381	Hs.278461	NP_002372
3861	0.007812	basigin (BSG), mRNA /cds=(58,867) /gb=NM_001728 /gi=4502458 /ug=Hs.74631 /len=1638	NM_001728	Hs.74631	NP_001719
3888	0.030399	SAC2 suppressor of actin mutations 2-like (yeast) (SACM2L), transcript variant 1, mRNA /cds=(245,2416) /gb=NM_080564 /gi=18379336 /ug=Hs.169407 /len=2985	NM_080564	Hs.169407	NP_542131
3911	0.012137	mitochondrion, complete genome	NC_001807		
3938	0.023731	mitochondrion, complete genome	NC_001807		
3944	0.013965	mitochondrion, complete genome	NC_001807		
3951	0.034264	ATP synthase, H transporting, mitochondrial F1 complex, gamma polypeptide 1 (ATP5C1), mRNA /cds=(32,925) /gb=NM_005174 /gi=4885078 /ug=Hs.155433 /len=1078	NM_005174	Hs.155433	NP_005165
3991	0.001703	LGMD2B	AJ007973		
4004	0.043185	bromodomain containing 2 (BRD2), mRNA /cds=(1702,4107) /gb=NM_005104 /gi=12408641 /ug=Hs.75243 /len=4693	NM_005104	Hs.75243	NP_005095
4046	0.030399	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa (POLR2C), transcript variant gamma, mRNA /cds=(58,885) /gb=NM_032940 /gi=14702170 /ug=Hs.79402 /len=1782	NM_032940	Hs.79402	NP_116558

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4051	0.020878	methyl CpG binding protein 2 (Rett syndrome) (MECP2), mRNA /cds=(168,1628) /gb=NM_004992 /gi=7710148 /ug=Hs.3239 /len=10182	NM_004992	Hs.3239	NP_004983
4054	0.010515	histamine N-methyltransferase (HNMT), mRNA /cds=(253,1131) /gb=NM_006895 /gi=5901969 /ug=Hs.81182 /len=1667	NM_006895	Hs.81182	NP_008826
4090	0.048295	AGENCOURT_6413683 NIH_MGC_85 cDNA clone IMAGE:5497620 5', mRNA sequence /clone=IMAGE:5497620 /clone_end=5' /gb=BM458572 /gi=18507612 /ug=Hs.194215 /len=1106	BM458572	Hs.194215	
4092	0.003489	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) (NDUFS3), mRNA /cds=(13,807) /gb=NM_004551 /gi=4758787 /ug=Hs.429506 /len=899	NM_004551	Hs.429506	NP_004542
4159	0.043185	suppressor of Ty 3 (S. cerevisiae) (SUPT3H), mRNA /cds=(72,1025) /gb=NM_003599 /gi=4507308 /ug=Hs.304173 /len=1165	NM_003599	Hs.304173	NP_003590
4191	0.009079	signal sequence receptor, alpha (translocon-associated protein alpha) (SSR1), mRNA /cds=(112,972) /gb=NM_003144 /gi=6552340 /ug=Hs.250773 /len=3285	NM_003144	Hs.250773	NP_003135
4202	0.013965	serum/glucocorticoid regulated kinase-like (SGKL), transcript variant 1, mRNA /cds=(416,1705) /gb=NM_013257 /gi=25168264 /ug=Hs.380877 /len=4155	NM_013257	Hs.380877	NP_733827
4223	0.006699	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 (SLC25A20), mitochondrial protein encoded by nuclear gene, mRNA /cds=(37,942) /gb=NM_000387 /gi=6006040 /ug=Hs.13845 /len=1219	NM_000387	Hs.13845	NP_000378
4256	0.043185	retinoic acid receptor, alpha (RARA), mRNA /cds=(103,1491) /gb=NM_000964 /gi=4506418 /ug=Hs.361071 /len=2907	NM_000964	Hs.361071	NP_000955
4301	0.016017	mRNA for KIAA1404 protein, partial cds. /cds=(65,5842) /gb=AB037825 /gi=7243188 /ug=Hs.200317 /len=7204	AB037825	Hs.200317	NP_066363
4376	0.016017	KIAA0089 protein (KIAA0089), mRNA /cds=(66,1121) /gb=NM_015141 /gi=24307998 /ug=Hs.82432 /len=3959	NM_015141	Hs.82432	NP_055956

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4390	0.026896	ataxia telangiectasia and Rad3 related (ATR), mRNA /cds=(106,8040) /gb=NM_001184 /gi=20143978 /ug=Hs.77613 /len=8265	NM_001184	Hs.77613	NP_001175
4406	0.038517	mitochondrion, complete genome	NC_001807		
4425	0.018314	gene amplified in squamous cell carcinoma 1 (GASC1), mRNA /cds=(151,3321) /gb=NM_015061 /gi=24307986 /ug=Hs.149918 /len=4239	NM_015061	Hs.149918	NP_055876
4442	0.030399	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae) (SUGT1), mRNA /cds=(56,1057) /gb=NM_006704 /gi=14165471 /ug=Hs.421239 /len=1535	NM_006704	Hs.421239	NP_006695
4465	0.005723	HIV-1 rev binding protein 2 (HRB2), mRNA /cds=(30,1175) /gb=NM_007043 /gi=21359979 /ug=Hs.154762 /len=1527	NM_007043	Hs.154762	NP_008974
4498	0.048295	mRNA for KIAA0265 gene, partial cds. /cds=(1,1206) /gb=D87454 /gi=1665796 /ug=Hs.192966 /len=5551	D87454	Hs.192966	
4511	0.030399	syndecan binding protein (syntenin) (SDCBP), mRNA /cds=(149,1045) /gb=NM_005625 /gi=5032082 /ug=Hs.8180 /len=2193	NM_005625	Hs.8180	NP_005616
4513	0.020878	hepatitis B virus x interacting protein (HBXIP), mRNA /cds=(56,331) /gb=NM_006402 /gi=5454169 /ug=Hs.433355 /len=605	NM_006402	Hs.433355	NP_006393
4530	0.043185	I factor (complement) (IF), mRNA /cds=(15,1766) /gb=NM_000204 /gi=4504578 /ug=Hs.36602 /len=1963	NM_000204	Hs.36602	NP_000195
4538	0.048295	CGI-49 protein (CGI-49), mRNA /cds=(1,1287) /gb=NM_016002 /gi=7705766 /ug=Hs.238126 /len=2127	NM_016002	Hs.238126	NP_057086
4540	0.016017	decay accelerating factor for complement (CD55, Cromer blood group system) (DAF), mRNA /cds=(66,1211) /gb=NM_000574 /gi=10835142 /ug=Hs.1369 /len=2102	NM_000574	Hs.1369	NP_000565
4592	0.030399	CC chemokine gene cluster	AF088219		
4641	0.009079	major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA /cds=(63,863) /gb=NM_002124 /gi=4504410 /ug=Hs.375570 /len=1182	NM_002124	Hs.375570	NP_002115
4651	0.009079	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophysin) (DDX9), transcript variant 1, mRNA /cds=(81,3920) /gb=NM_001357 /gi=13514819 /ug=Hs.74578 /len=4199	NM_001357	Hs.74578	NP_085077

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4655	0.013965	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), mRNA /cds=(252,1457) /gb=NM_002546 /gi=22547122 /ug=Hs.81791 /len=2291	NM_002546	Hs.81791	NP_002537
4670	0.001158	UI-E-DW0-agg-j-14-0-UI.r1 UI-E-DW0 cDNA clone UI-E-DW0-agg-j-14-0-UI 5', mRNA sequence /clone=UI-E-DW0-agg-j-14-0-UI /clone_end=5' /gb=BM706185 /gi=19019443 /ug=Hs.433563 /len=949	BM706185	Hs.433563	
4672	0.002935	coronin, actin binding protein, 1C (CORO1C), mRNA /cds=(97,1521) /gb=NM_014325 /gi=27477119 /ug=Hs.17377 /len=3828	NM_014325	Hs.17377	NP_055140
4681	0.023731	RNA binding motif protein 8A (RBM8A), mRNA /cds=(30,554) /gb=NM_005105 /gi=15812217 /ug=Hs.10283 /len=2787	NM_005105	Hs.10283	NP_005096
4694	0.004131	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) (HIF1A), mRNA /cds=(265,2745) /gb=NM_001530 /gi=4504384 /ug=Hs.197540 /len=3933	NM_001530	Hs.197540	NP_851397
4701	0.023731	ubiquitin-like 5 (UBL5), mRNA /cds=(66,287) /gb=NM_024292 /gi=13236509 /ug=Hs.13836 /len=413	NM_024292	Hs.13836	NP_077268
4726	0.018314	fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), mRNA /cds=(717,2444) /gb=NM_004480 /gi=4758407 /ug=Hs.118722 /len=3280	NM_004480	Hs.118722	NP_835370
4747	0.030399	leucine zipper transcription factor-like 1 (LZTFL1), mRNA /cds=(125,1024) /gb=NM_020347 /gi=9966792 /ug=Hs.30824 /len=3384	NM_020347	Hs.30824	NP_065080
4758	0.026896	inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA /cds=(86,1366) /gb=NM_002192 /gi=4504698 /ug=Hs.727 /len=1840	NM_002192	Hs.727	NP_002183
4794	0.018314	mitochondrion, complete genome	NC_001807		
4797	0.026896	tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), mRNA /cds=(141,1358) /gb=NM_016000 /gi=20070270 /ug=Hs.102897 /len=1865	NM_016000	Hs.102897	NP_057084
4880	0.048295	cDNA FLJ12776 fis, clone NT2RP2001678. /gb=AK022838 /gi=10434465 /ug=Hs.372558 /len=2629	AK022838	Hs.372558	
4885	0.006699	clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992	AF001542	Hs.356442	

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4916	0.001408	collagen, type X, alpha 1 (Schmid metaphyseal chondrodysplasia) (COL10A1), mRNA /cds=(97,2139) /gb=NM_000493 /gi=18105031 /ug=Hs.179729 /len=3285	NM_000493	Hs.179729	NP_000484
4919	0.001158	KIAA0436 mRNA, partial cds. /cds=(1,2070) /gb=AB007896 /gi=2662152 /ug=Hs.110 /len=4661	AB007896	Hs.110	
4925	0.001158	tm68a09.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2163256 3', mRNA sequence /clone=IMAGE:2163256 /clone_end=3' /gb=AI498805 /gi=4390787 /ug=Hs.436349 /len=460	AI498805	Hs.436349	
4941	0.002051	mRNA; cDNA DKFZp451P176 (from clone DKFZp451P176) /gb=AL832365 /gi=21732928 /ug=Hs.159471 /len=5559	AL832365	Hs.159471	
4963	0.048295	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,327) /gb=NM_001865 /gi=18105035 /ug=Hs.70312 /len=470	NM_001865	Hs.70312	NP_001856
4968	0.004131	thioredoxin (TXN), mRNA /cds=(64,381) /gb=NM_003329 /gi=4507744 /ug=Hs.432922 /len=501	NM_003329	Hs.432922	NP_003320
5000	0.038517	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) (DTR), mRNA /cds=(262,888) /gb=NM_001945 /gi=4503412 /ug=Hs.799 /len=2360	NM_001945	Hs.799	NP_001936
5002	0.016017	mitochondrion, complete genome	NC_001807		
5004	0.048295	cytochrome P450, family 1, subfamily B, polypeptide 1 (CYP1B1), mRNA /cds=(373,2004) /gb=NM_000104 /gi=13325059 /ug=Hs.154654 /len=5128	NM_000104	Hs.154654	NP_000095
5018	0.018314	mRNA; cDNA DKFZp762B195 (from clone DKFZp762B195) /gb=AL359585 /gi=8655645 /ug=Hs.356766 /len=2183	AL359585	Hs.356766	
5026	0.023731	hect domain and RLD 2 (HERC2), mRNA /cds=(62,14566) /gb=NM_004667 /gi=5729867 /ug=Hs.266933 /len=15304	NM_004667	Hs.266933	NP_004658
5027	0.034264	nucleobindin 1 (NUCB1), mRNA /cds=(27,1412) /gb=NM_006184 /gi=20070227 /ug=Hs.172609 /len=2311	NM_006184	Hs.172609	NP_006175
5074	0.026896	mRNA; cDNA DKFZp762B195 (from clone DKFZp762B195) /gb=AL359585 /gi=8655645 /ug=Hs.356766 /len=2183	AL359585	Hs.356766	

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5102	0.007812	cofilin 1 (non-muscle) (CFL1), mRNA /cds=(52,552) /gb=NM_005507 /gi=5031634 /ug=Hs.180370 /len=1059	NM_005507	Hs.180370	NP_005498
5104	0.026896	T-cell activation leucine repeat-rich protein (TA-LRRP), mRNA /cds=(565,2976) /gb=NM_015350 /gi=21245133 /ug=Hs.199243 /len=3588	NM_015350	Hs.199243	NP_056165
5111	0.043185	chromosome 14 open reading frame 94 (C14orf94), mRNA /cds=(211,1302) /gb=NM_017815 /gi=8923395 /ug=Hs.8886 /len=1618	NM_017815	Hs.8886	NP_060285
5139	0.034264	nuclear receptor coactivator 4 (NCOA4), mRNA /cds=(141,1985) /gb=NM_005437 /gi=14149616 /ug=Hs.99908 /len=3506	NM_005437	Hs.99908	NP_005428
5192	0.020878	mRNA for KIAA0232 protein, partial cds. /cds=(435,4643) /gb=D86985 /gi=20521849 /ug=Hs.79276 /len=7840	D86985	Hs.79276	
5230	0.016017	CDC28 protein kinase regulatory subunit 2 (CKS2), mRNA /cds=(96,335) /gb=NM_001827 /gi=4502858 /ug=Hs.83758 /len=627	NM_001827	Hs.83758	NP_001818
5250	0.002459	SFRS protein kinase 1 (SRPK1), mRNA /cds=(10,1974) /gb=NM_003137 /gi=15834623 /ug=Hs.75761 /len=4244	NM_003137	Hs.75761	NP_003128
5257	0.026896	likely ortholog of mouse hypoxia induced gene 1 (HIG1), mRNA /cds=(93,374) /gb=NM_014056 /gi=7661619 /ug=Hs.7917 /len=1362	NM_014056	Hs.7917	NP_054775
5261	0.043185	replication factor C (activator 1) 4, 37kDa (RFC4), mRNA /cds=(284,1375) /gb=NM_002916 /gi=4506490 /ug=Hs.35120 /len=1446	NM_002916	Hs.35120	NP_002907
5262	0.018314	ALL1-fused gene from chromosome 1q (AF1Q), mRNA /cds=(353,625) /gb=NM_006818 /gi=21626459 /ug=Hs.75823 /len=1653	NM_006818	Hs.75823	NP_006809
5283	0.009079	transforming, acidic coiled-coil containing protein 2 (TACC2), mRNA /cds=(87,3167) /gb=NM_006997 /gi=11119413 /ug=Hs.272023 /len=3686	NM_006997	Hs.272023	NP_008928
5327	0.043185	zinc finger, DHHC domain containing 14 (ZDHHC14), mRNA /cds=(498,1964) /gb=NM_024630 /gi=24371240 /ug=Hs.38270 /len=2821	NM_024630	Hs.38270	NP_714968
5342	0.013965	KIAA0308 gene, partial cds /cds=UNKNOWN /gb=AB002306 /gi=2224556 /ug=Hs.10351 /len=6452	AB002306	Hs.10351	NP_525127

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5370	0.014664	laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=NM_002295 /gi=9845501 /ug=Hs.181357 /len=1039	NM_002295	Hs.181357	NP_002286
5392	0.001703	clone IMAGE:5398100, mRNA /gb=BC035584 /gi=23273438 /ug=Hs.407477 /len=1570	BC035584	Hs.407477	
5394	0.004872	hypothetical protein FLJ11294 (FLJ11294), mRNA /cds=(160,4170) /gb=NM_018383 /gi=19923528 /ug=Hs.107000 /len=4602	NM_018383	Hs.107000	NP_060853
5438	0.007812	mitochondrion, complete genome	NC_001807		
5445	0.030399	hypothetical protein FLJ20312 (FLJ20312), mRNA /cds=(384,803) /gb=NM_017761 /gi=20127576 /ug=Hs.7862 /len=2382	NM_017761	Hs.7862	NP_060231
5503	0.038517	HSPC142 protein (HSPC142), mRNA /cds=(127,1230) /gb=NM_014173 /gi=7661801 /ug=Hs.190722 /len=1432	NM_014173	Hs.190722	NP_054892
5504	0.030399	hypothetical protein FLJ22329 (FLJ22329), mRNA /cds=(36,767) /gb=NM_024656 /gi=13375904 /ug=Hs.367653 /len=2501	NM_024656	Hs.367653	NP_078932
5580	0.048295	PTK9L protein tyrosine kinase 9-like (A6-related protein) (PTK9L), mRNA /cds=(105,1154) /gb=NM_007284 /gi=6005845 /ug=Hs.6780 /len=1574	NM_007284	Hs.6780	NP_009215
5629	0.018314	folliculin (FST), transcript variant FST317, mRNA /cds=(28,981) /gb=NM_006350 /gi=7242223 /ug=Hs.9914 /len=1386	NM_006350	Hs.9914	NP_037541
5666	9.48E-04	KNP-1a (=U53007 GT335)	D86061		NP_004640
5671	0.002051	EPC-1 (=M76979 PEDF;U29953;M90493)	U57446		
5672	0.026896	clone IMAGE:5265581, mRNA /gb=BC035165 /gi=23272508 /ug=Hs.400548 /len=2237	BC035165	Hs.400548	
5723	0.003489	cytoskeleton-associated protein 4 (CKAP4), mRNA /cds=(85,1893) /gb=NM_006825 /gi=19920316 /ug=Hs.74368 /len=2913	NM_006825	Hs.74368	NP_006816
5744	0.023731	DNA segment on chromosome X (unique) 9928 expressed sequence (DXS9928E), mRNA /cds=(76,1095) /gb=NM_004699 /gi=4758219 /ug=Hs.54277 /len=1311	NM_004699	Hs.54277	NP_004690

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5748	0.030399	vasoactive intestinal peptide receptor 1 (VIPR1), mRNA /cds=(111,1484) /gb=NM_004624 /gi=15619005 /ug=Hs.348500 /len=2771	NM_004624	Hs.348500	NP_004615
5780	0.030399	chondroitin 4-O-sulfotransferase 2 (C4S-2), mRNA /cds=(145,1389) /gb=NM_018641 /gi=20070291 /ug=Hs.25204 /len=2117	NM_018641	Hs.25204	NP_061111
5787	0.034264	ADP-ribosylation factor guanine nucleotide factor 6 (EFA6R), mRNA /cds=(53,1657) /gb=NM_015310 /gi=7662395 /ug=Hs.6763 /len=6722	NM_015310	Hs.6763	NP_056125
5793	0.016017	zinc finger protein 265 (ZNF265), mRNA /gb=NM_005455 /gi=19923317 /ug=Hs.194718 /len=2837	NM_005455	Hs.194718	NP_005446
5812	0.038517	hypothetical protein FLJ12439 (FLJ12439), mRNA /cds=(41,736) /gb=NM_023077 /gi=12751490 /ug=Hs.349905 /len=1614	NM_023077	Hs.349905	NP_075565
5815	0.043185	at74h07.x1 Barstead colon HPLRB7 cDNA clone IMAGE:2377789 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;, mRNA sequence /clone=IMAGE:2377789 /clone_end=3' /gb=AI833064 /gi=5455044 /ug=Hs.369949 /len=553	AI833064	Hs.369949	
5822	0.023731	enhancer of zeste 1 (Drosophila) (EZH1), mRNA /cds=(123,2366) /gb=NM_001991 /gi=19923201 /ug=Hs.194669 /len=4640	NM_001991	Hs.194669	NP_001982
5863	0.020878	polypyrimidine tract binding protein 2 (PTBP2), mRNA /cds=(53,1648) /gb=NM_021190 /gi=10863996 /ug=Hs.34956 /len=3054	NM_021190	Hs.34956	NP_067013
5873	0.004872	blood-stage membrane protein Ag-1 [Plasmodium yoelii]	AF103869		
5919	0.012137	chromosome 4 open reading frame 1 (C4orf1), mRNA /cds=(121,1827) /gb=NM_006345 /gi=7656945 /ug=Hs.270956 /len=3250	NM_006345	Hs.270956	NP_006336
5997	0.038517	NTT gene (L1 Alu and MER 38 repeat regions)	U54776		
6009	0.034264	methylmalonyl Coenzyme A mutase (MUT), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,2329) /gb=NM_000255 /gi=4557766 /ug=Hs.155212 /len=2798	NM_000255	Hs.155212	NP_000246

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6013	0.016017	Similar to hect domain and RLD 2, clone IMAGE:4830978, mRNA /gb=BC033888 /gi=21706785 /ug=Hs.429904 /len=4297	BC033888	Hs.429904	
6028	0.034264	protein-tyrosine kinase, trkB	X75958		NP_006171
6063	0.018314	eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA /cds=(16,1239) /gb=NM_001967 /gi=9945313 /ug=Hs.173912 /len=1864	NM_001967	Hs.173912	NP_001958
6068	0.013965	mitochondrial ribosomal protein L27 (MRPL27), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA /cds=(32,316) /gb=NM_148571 /gi=22547130 /ug=Hs.7736 /len=2472	NM_148571	Hs.7736	NP_683412
6081	0.020878	mitochondrial ribosomal protein L33 (MRPL33), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA /cds=(60,257) /gb=NM_004891 /gi=21735607 /ug=Hs.14454 /len=541	NM_004891	Hs.14454	NP_663303
6082	0.016017	proteasome (prosome, macropain) subunit, alpha type, 4 (PSMA4), mRNA /cds=(137,922) /gb=NM_002789 /gi=23110940 /ug=Hs.251531 /len=1189	NM_002789	Hs.251531	NP_002780
6083	0.006699	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA /cds=(9,536) /gb=NM_002495 /gi=4505368 /ug=Hs.10758 /len=668	NM_002495	Hs.10758	NP_002486
6129	0.012137	myosin, light polypeptide 3, alkali; ventricular, skeletal, slow (MYL3), mRNA /cds=(51,638) /gb=NM_000258 /gi=4557776 /ug=Hs.1815 /len=872	NM_000258	Hs.1815	NP_000249
6139	0.048295	cofilin 1 (non-muscle) (CFL1), mRNA /cds=(52,552) /gb=NM_005507 /gi=5031634 /ug=Hs.180370 /len=1059	NM_005507	Hs.180370	NP_005498
6191	0.004872	calsyntenin 3 (CLSTN3), mRNA /cds=(539,3445) /gb=NM_014718 /gi=7662267 /ug=Hs.107809 /len=4300	NM_014718	Hs.107809	NP_055533
6237	0.012137	cDNA FLJ12807 fis, clone NT2RP2002316. /gb=AK022869 /gi=10434511 /ug=Hs.188361 /len=2697	AK022869	Hs.188361	
6244	0.020674	lumican (LUM), mRNA /cds=(142,1158) /gb=NM_002345 /gi=21359858 /ug=Hs.79914 /len=1804	NM_002345	Hs.79914	NP_002336
6248	0.046968	tumor differentially expressed 1 (TDE1), mRNA /cds=(78,1499) /gb=NM_006811 /gi=5803192 /ug=Hs.272168 /len=1892	NM_006811	Hs.272168	NP_006802

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6258	0.004872	deleted in liver cancer 1 (DLC1), mRNA /cds=(296,3571) /gb=NM_006094 /gi=6633799 /ug=Hs.8700 /len=3821	NM_006094	Hs.8700	NP_006085
6267	0.012678	mRNA for KIAA1965 protein. /cds=(1,1699) /gb=AB075845 /gi=18916817 /ug=Hs.71730 /len=4299	AB075845	Hs.71730	
6295	0.016017	Notch 2 (Drosophila) (NOTCH2), mRNA /cds=(257,7672) /gb=NM_024408 /gi=24041034 /ug=Hs.8121 /len=11433	NM_024408	Hs.8121	NP_077719
6297	0.009079	5'-nucleotidase, cytosolic II (NT5C2), mRNA /cds=(145,1830) /gb=NM_012229 /gi=20149601 /ug=Hs.138593 /len=3364	NM_012229	Hs.138593	NP_036361
6302	0.041767	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) (DTR), mRNA /cds=(262,888) /gb=NM_001945 /gi=4503412 /ug=Hs.799 /len=2360	NM_001945	Hs.799	NP_001936
6307	0.032747	cDNA FLJ37296 fis, clone BRAMY2015420. /gb=AK094615 /gi=21753707 /ug=Hs.4983 /len=3181	AK094615	Hs.4983	
6365	0.010515	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene avian) (EGFR), mRNA /cds=(187,3819) /gb=NM_005228 /gi=4885198 /ug=Hs.77432 /len=5532	NM_005228	Hs.77432	NP_005219
6382	0.026896	hypothetical protein HSPC210 (HSPC210), mRNA /cds=(138,605) /gb=NM_016472 /gi=24475986 /ug=Hs.4104 /len=1152	NM_016472	Hs.4104	NP_057556
6385	0.013965	RAB32, member RAS oncogene family (RAB32), mRNA /cds=(183,860) /gb=NM_006834 /gi=20127508 /ug=Hs.32217 /len=1236	NM_006834	Hs.32217	NP_006825
6386	0.002935	mitochondrion, complete genome	NC_001807		
6395	0.038517	SOCS box-containing WD protein SWIP-1 (WSB1), transcript variant 3, mRNA /cds=(317,1051) /gb=NM_134264 /gi=20143909 /ug=Hs.187991 /len=4243	NM_134264	Hs.187991	NP_599027
6402	0.026896	actin, gamma 1 (ACTG1), mRNA /cds=(75,1202) /gb=NM_001614 /gi=11038618 /ug=Hs.14376 /len=1919	NM_001614	Hs.14376	NP_001605
6405	0.043185	cyclic AMP-regulated phosphoprotein (90% match)	AF112220		NP_057384
6442	0.007812	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), mRNA /cds=(115,1677) /gb=NM_004566 /gi=4758899 /ug=Hs.195471 /len=4322	NM_004566	Hs.195471	NP_004557

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6464	0.038517	KIAA0250 gene	NM_014837		NP_055652
6469	0.034264	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA /cds=(407,1972) /gb=NM_000944 /gi=19923130 /ug=Hs.272458 /len=4425	NM_000944	Hs.272458	NP_000935
6522	0.030399	Rattus norvegicus mitochondrial genome	NC_001665		
6530	0.034264	pleckstrin domain containing, family A (phosphoinositide binding specific) member 4 (PLEKHA4), mRNA /cds=(526,2865) /gb=NM_020904 /gi=10190743 /ug=Hs.9469 /len=3056	NM_020904	Hs.9469	NP_065955
6543	0.020878	general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), mRNA /cds=(161,1807) /gb=NM_005316 /gi=19923304 /ug=Hs.89578 /len=2989	NM_005316	Hs.89578	NP_005307
6550	0.023731	t-complex-associated-testis-expressed 1-like 1 (TCTEL1), mRNA /cds=(1,342) /gb=NM_006519 /gi=5730084 /ug=Hs.266940 /len=713	NM_006519	Hs.266940	NP_006510
6574	0.012137	RCC1	D00591		
6577	0.048295	ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=NM_004152 /gi=9845504 /ug=Hs.281960 /len=986	NM_004152	Hs.281960	NP_004143
6581	0.007812	mitogen inducible gene mig-2, complete CDS. /cds=(1,2165) /gb=Z24725 /gi=505032 /ug=Hs.75260 /len=3270	Z24725	Hs.75260	NP_006823
6584	0.012137	likely ortholog of mouse monocyte macrophage 19 (MMRP19), mRNA /cds=(78,806) /gb=NM_015957 /gi=7705723 /ug=Hs.104058 /len=1226	NM_015957	Hs.104058	NP_057041
6590	0.020878	mRNA for KIAA0981 protein, partial cds. /cds=(1,1738) /gb=AB023198 /gi=4589605 /ug=Hs.158135 /len=5182	AB023198	Hs.158135	
6598	0.026896	phosphomannomutase 2 (PMM2) gene (5e-10 match)	AF157794		
6603	0.026896	tm68a09.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2163256 3', mRNA sequence /clone=IMAGE:2163256 /clone_end=3' /gb=AI498805 /gi=4390787 /ug=Hs.436349 /len=460	AI498805	Hs.436349	
6619	0.001703	phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA	NM_005019		NP_005010

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6630	9.48E-04	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase) (NDUFS6), mRNA /cds=(11,385) /gb=NM_004553 /gi=4758791 /ug=Hs.49767 /len=547	NM_004553	Hs.49767	NP_004544
6661	0.043185	stromal antigen 1 (STAG1), mRNA /cds=(401,4177) /gb=NM_005862 /gi=5032062 /ug=Hs.286148 /len=4337	NM_005862	Hs.286148	NP_005853
6666	0.016017	tigger transposable element derived 1 (TIGD1), mRNA /cds=(635,2410) /gb=NM_145702 /gi=22209000 /ug=Hs.351348 /len=2448	NM_145702	Hs.351348	NP_663748
6687	0.020878	qe80a05.x1 Soares_fetal_lung_NbHL19W cDNA clone IMAGE:1745264 3' similar to Q04323 HYPOTHETICAL 33.4 KD PROTEIN.;, mRNA sequence /clone=IMAGE:1745264 /clone_end=3' /gb=AI193849 /gi=3745058 /ug=Hs.386662 /len=586	AI193849	Hs.386662	
6722	0.034264	syndecan 1 (SDC1), mRNA /cds=(253,1185) /gb=NM_002997 /gi=21359855 /ug=Hs.82109 /len=2484	NM_002997	Hs.82109	NP_002988
6732	0.005723	dermatan-4-sulfotransferase-1 (D4ST-1), mRNA /cds=(1,1131) /gb=NM_130468 /gi=18497303 /ug=Hs.24947 /len=1960	NM_130468	Hs.24947	NP_569735
6738	6.26E-04	ankyrin repeat and SOCS box-containing 3 (ASB3), transcript variant 1, mRNA /cds=(136,1692) /gb=NM_016115 /gi=22208952 /ug=Hs.9893 /len=2214	NM_016115	Hs.9893	NP_665862
6745	0.001408	mRNA; cDNA DKFZp434A163 (from clone DKFZp434A163); partial cds /cds=(1,4964) /gb=AL110218 /gi=5817150 /ug=Hs.127401 /len=5084	AL110218	Hs.127401	
6754	0.002935	TSC-22 related protein (TSC-22R) (=AF228339 glucocorticoid-induced GILZ)	AF153603		NP_004080
6795	0.003489	KIAA0438 gene product (KIAA0438), mRNA /cds=(118,2244) /gb=NM_014819 /gi=7662123 /ug=Hs.279849 /len=4765	NM_014819	Hs.279849	NP_055634
6825	0.034264	hypothetical protein MGC4400 (MGC4400), mRNA /cds=(381,1817) /gb=NM_032679 /gi=14249251 /ug=Hs.130891 /len=3067	NM_032679	Hs.130891	NP_116068

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6836	0.038517	UI-E-DW1-ahd-d-13-0-UI.s1 UI-E-DW1 cDNA clone UI-E-DW1-ahd-d-13-0-UI 3', mRNA sequence /clone=UI-E-DW1-ahd-d-13-0-UI /clone_end=3' /gb=BU737702 /gi=23673914 /ug=Hs.405983 /len=1215	BU737702	Hs.405983	
6883	0.001408	platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA /cds=(395,3664) /gb=NM_006206 /gi=15451787 /ug=Hs.74615 /len=6633	NM_006206	Hs.74615	NP_006197
6891	0.034264	protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA /cds=(167,1423) /gb=NM_002736 /gi=4506064 /ug=Hs.77439 /len=3259	NM_002736	Hs.77439	NP_002727
6914	0.038517	gene trap ankyrin repeat (GTAR), mRNA /cds=(118,7926) /gb=NM_032217 /gi=27477106 /ug=Hs.12329 /len=9016	NM_032217	Hs.12329	NP_115593
6950	0.038517	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) (SFPQ), mRNA /cds=(86,2209) /gb=NM_005066 /gi=4826997 /ug=Hs.180610 /len=3071	NM_005066	Hs.180610	NP_005057
6972	0.023731	similar to zinc finger protein (LOC91172), mRNA (=FLJ12859,=FLJ11645)	XM_036627		
7035	0.002935	hypothetical protein (KIAA0238)	D87075		NP_005107
7077	0.048295	mitochondrion, complete genome	NC_001807		
7087	0.038517	mitochondrion, complete genome	NC_001807		
7098	0.012137	inactive progesterone receptor, 23 kD (TEBP), mRNA /cds=(107,589) /gb=NM_006601 /gi=23308578 /ug=Hs.278270 /len=1490	NM_006601	Hs.278270	NP_006592
7102	0.003489	survival of motor neuron protein interacting protein 1 (SIP1), mRNA /cds=(84,926) /gb=NM_003616 /gi=4506960 /ug=Hs.102456 /len=1285	NM_003616	Hs.102456	NP_003607
7116	0.010515	7i76f10.y1 NCI_CGAP_Brn20 cDNA clone IMAGE:3340651.5', mRNA sequence /clone=IMAGE:3340651 /clone_end=5' /gb=BF057907 /gi=10811803 /ug=Hs.439614 /len=133	BF057907	Hs.439614	
7178	0.013965	supervillin (SVIL), transcript variant 2, mRNA /cds=(754,7398) /gb=NM_021738 /gi=11496981 /ug=Hs.154567 /len=8300	NM_021738	Hs.154567	NP_068506

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7217	0.004872	ATPase, Na /K transporting, beta 3 polypeptide (ATP1B3), mRNA /cds=(1,840) /gb=NM_001679 /gi=4502280 /ug=Hs.76941 /len=1679	NM_001679	Hs.76941	NP_001670
7221	0.043185	602410168F1 NIH_MGC_92 cDNA clone IMAGE:4538560 5', mRNA sequence /clone=IMAGE:4538560 /clone_end=5' /gb=BG394022 /gi=13287470 /ug=Hs.421597 /len=1059	BG394022	Hs.421597	
7222	0.013965	REV3-like, catalytic subunit of DNA polymerase zeta (yeast) (REV3L), mRNA /cds=(823,9981) /gb=NM_002912 /gi=4506482 /ug=Hs.115521 /len=10919	NM_002912	Hs.115521	NP_002903
7265	0.018314	thioredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) /gb=NM_006472 /gi=5454161 /ug=Hs.179526 /len=2704	NM_006472	Hs.179526	NP_006463
7310	0.007812	UI-H-BI2-agp-f-12-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2725031 3', mRNA sequence /clone=IMAGE:2725031 /clone_end=3' /gb=AW292456 /gi=6699092 /ug=Hs.437793 /len=745	AW292456	Hs.437793	
7331	0.034264	AGENCOURT_8856629 Lupski_sciatic_nerve cDNA clone IMAGE:6200636 5', mRNA sequence /clone=IMAGE:6200636 /clone_end=5' /gb=BQ947179 /gi=22362657 /ug=Hs.356605 /len=1277	BQ947179	Hs.356605	
7339	0.005723	major histocompatibility complex, class II, DR beta 3 (HLA-DRB3), mRNA /cds=(41,841) /gb=NM_022555 /gi=18641371 /ug=Hs.308026 /len=1158	NM_022555	Hs.308026	NP_072049
7341	0.048295	peroxiredoxin 5 (PRDX5), mRNA /cds=(37,681) /gb=NM_012094 /gi=6912237 /ug=Hs.31731 /len=805	NM_012094	Hs.31731	NP_036226
7382	0.018314	cortactin binding protein 2 (CORTBP2), mRNA /cds=(93,5084) /gb=NM_033427 /gi=16975495 /ug=Hs.293539 /len=5975	NM_033427	Hs.293539	NP_219499
7399	0.030399	Similar to alpha-methylacyl-CoA racemase, clone MGC:3743 IMAGE:2958112, mRNA, complete cds	BC009471		NP_055139
7414	0.010515	tetraspanin similar to TM4SF9 (DC-TM4F2), mRNA /cds=(79,891) /gb=NM_030927 /gi=13569888 /ug=Hs.101395 /len=2556	NM_030927	Hs.101395	NP_112189

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7439	0.030399	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA /cds=(396,902) /gb=NM_002825 /gi=27552761 /ug=Hs.44 /len=1029	NM_002825	Hs.44	NP_002816
7450	0.030399	KIAA0097 gene product (KIAA0097), mRNA /cds=(27,5945) /gb=NM_014756 /gi=24307972 /ug=Hs.76989 /len=6449	NM_014756	Hs.76989	NP_055571
7581	0.043185	FK506 binding protein 5 (FKBP5), mRNA /cds=(154,1527) /gb=NM_004117 /gi=17149847 /ug=Hs.7557 /len=3781	NM_004117	Hs.7557	NP_004108
7611	0.038517	RAB14, member RAS oncogene family (RAB14), mRNA /cds=(184,831) /gb=NM_016322 /gi=19923482 /ug=Hs.5807 /len=4106	NM_016322	Hs.5807	NP_057406
7623	0.046968	growth factor receptor-bound protein 10 (GRB10), mRNA /cds=(782,2548) /gb=NM_005311 /gi=19923302 /ug=Hs.81875 /len=5431	NM_005311	Hs.81875	NP_005302
7632	0.030399	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA /cds=(95,1048) /gb=NM_020529 /gi=10092618 /ug=Hs.81328 /len=1550	NM_020529	Hs.81328	NP_065390
7642	0.034264	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
7651	0.013965	DZIP3 mRNA, partial cds	AF279370		NP_055463
7660	3.22E-04	bladder cancer overexpressed protein (BLOV1), mRNA /cds=(72,1136) /gb=NM_018656 /gi=8922084 /ug=Hs.125830 /len=2324	NM_018656	Hs.125830	NP_061126
7672	0.030399	solute carrier family 25 (mitochondrial carrier, brain), member 14 (SLC25A14), transcript variant long, nuclear gene encoding mitochondrial protein, mRNA /cds=(207,1184) /gb=NM_003951 /gi=6006039 /ug=Hs.194686 /len=1601	NM_003951	Hs.194686	NP_073721
7694	0.004131	cDNA FLJ25013 fis, clone CBL01365. /gb=AK057742 /gi=16553667 /ug=Hs.380091 /len=2200	AK057742	Hs.380091	
7723	0.001623	yp24c06.s1 Soares breast 3NbHBst cDNA clone IMAGE:188362 3' similar to gb:M10942_cds1 metallothionein-1e gene mRNA sequence /clone=IMAGE:188362 /clone_end=3' /gb=H43642 /gi=919694 /ug=Hs.418241 /len=452	H43642	Hs.418241	

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7727	0.038517	hypothetical protein FLJ13081 (FLJ13081), mRNA /cds=(171,2099) /gb=NM_024834 /gi=13376242 /ug=Hs.180638 /len=4113	NM_024834	Hs.180638	NP_079110
7728	0.038517	Down syndrome critical region gene 5 (DSCR5), transcript variant 3, mRNA /cds=(342,668) /gb=NM_016430 /gi=24497594 /ug=Hs.408790 /len=875	NM_016430	Hs.408790	NP_710149
7741	0.026896	major histocompatibility complex, class II, DR beta 3 (HLA-DRB3), mRNA /cds=(41,841) /gb=NM_022555 /gi=18641371 /ug=Hs.308026 /len=1158	NM_022555	Hs.308026	NP_072049
7927	0.004414	UI-H-EZ1-bca-n-05-0-UI.s1 NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-bca-n-05-0-UI 3', mRNA sequence /clone=UI-H-EZ1-bca-n-05-0-UI /clone_end=3' /gb=BQ774356 /gi=21982825 /ug=Hs.43227 /len=1083	BQ774356	Hs.43227	
7946	0.038517	EST (AV746410 NPA H.sapiens cDNA clone NPABDD10 5')	AV746410		NP_006463
8054	0.043185	pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence /cds=UNKNOWN/gb=AF334710 /gi=12658438 /ug=Hs.8364 /len=1819	AF334710	Hs.8364	NP_002603
8097	0.048295	mRNA for KIAA1915 protein, partial cds. /cds=(356,2536) /gb=AB067502 /gi=15620888 /ug=Hs.12915 /len=7801	AB067502	Hs.12915	
8128	0.026896	mRNA for KIAA1545 protein, partial cds. /cds=(1,2909) /gb=AB046765 /gi=20521935 /ug=Hs.127270 /len=4307	AB046765	Hs.127270	
8198	0.043185	PHD zinc finger protein XAP135 (XAP135), transcript variant 2, mRNA /cds=(222,1448) /gb=NM_133325 /gi=19747275 /ug=Hs.7759 /len=1583	NM_133325	Hs.7759	NP_579866
8201	0.048295	KIAA1892 protein (KIAA1892), mRNA /cds=(308,1669) /gb=NM_015397 /gi=22218618 /ug=Hs.102669 /len=3636	NM_015397	Hs.102669	NP_056212
8208	0.030399	SPT3-associated factor 42 (STAF42), mRNA /cds=(22,1029) /gb=NM_053053 /gi=16596695 /ug=Hs.107968 /len=2122	NM_053053	Hs.107968	NP_444281
8209	0.023731	UI-E-EJ0-ahj-n-19-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahj-n-19-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahj-n-19-0-UI /clone_end=5' /gb=BM701108 /gi=19014366 /ug=Hs.401941 /len=1923	BM701108	Hs.401941	

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8244	0.048295	peptidylprolyl isomerase (cyclophilin)-like 4 (PPIL4), mRNA /cds=(31,1509) /gb=NM_139126 /gi=22538483 /ug=Hs.11065 /len=2481	NM_139126	Hs.11065	NP_624311
8260	0.013965	EST(zd17f12.r1 Soares fetal heart NbHH19W cDNA clone 340943 5')	W57908		
8269	0.013965	clone IMAGE:5243705, mRNA /gb=BC043383 /gi=27695948 /ug=Hs.439631 /len=2177	BC043383	Hs.439631	
8341	0.016017	EST(we27d09.x1 NCI_CGAP_Lu24 clone IMAGE:2342321 3')	AI797144		NP_002877
8359	0.048295	UI-H-BW1-amn-b-05-0-UI.s1 NCI_CGAP_Sub7 cDNA clone IMAGE:3070401 3', mRNA sequence /clone=IMAGE:3070401 /clone_end=3' /gb=BF513064 /gi=11598243 /ug=Hs.446233 /len=777	BF513064	Hs.446233	
8368	0.013965	EST(qq29d09.x1 Soares_NhHMPu_S1 clone IMAGE:1933937 3')	AI338976		NP_001101
8376	0.009079	EST(zk54c05.r1 Soares_pregnant_uterus_NbHPU cDNA clone IMAGE:486632 5')	AA044356		NP_001767
8381	0.023731	Tho2 mRNA, complete cds /cds=(1,4437) /gb=AF441770 /gi=20799317 /ug=Hs.16411 /len=4452	AF441770	Hs.16411	
8399	0.038517	EST(nc26d02.r1 NCI_CGAP_Pr1 cDNA clone IMAGE:1009251 similar to contains Alu repetitive element)	AA226526		
8437	0.002459	EST(yi83h07.r1 Soares infant brain 1NIB IMAGE:44845 5')	H06795		
8454	0.043185	EST ae93d05.s1 Stratagene schizo brain S11'H.sapiens cDNA clone IMAGE:1020489 3'	AA780434		
8505	0.020878	EST(hv67h07.x1 NCI_CGAP_Lu24 IMAGE:3178525 3')	BE220163		
8518	0.032747	clone IMAGE:5311197, mRNA /gb=BC042002 /gi=27469533 /ug=Hs.260395 /len=1498	BC042002	Hs.260395	
8529	0.018314	EST(602645742F1 NIH_MGC_76 clone IMAGE:4767299 5')	BG618375		
8571	0.002459	AGENCOURT_6758988 NIH_MGC_115 cDNA clone IMAGE:5755234 5', mRNA sequence /clone=IMAGE:5755234 /clone_end=5' /gb=BQ067651 /gi=19896697 /ug=Hs.204354 /len=1385	BQ067651	Hs.204354	
8581	0.048295	EST(AV718982 GLC cDNA clone GLCACH01 5')	AV718982		
8590	0.048295	EST(601509721F1 NIH_MGC_71 cDNA clone IMAGE:3911140 5')	BE886324		NP_777581

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8607	0.018314	AGENCOURT_6796992 NIH_MGC_85 cDNA clone IMAGE:5787783 5', mRNA sequence /clone=IMAGE:5787783 /clone_end=5' /gb=BQ049841 /gi=19809181 /ug=Hs.292457 /len=1391	BQ049841	Hs.292457	
8621	0.023731	ah42f05.s1 Soares_testis_NHT cDNA clone 1292193 3' similar to P54687 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, CYTOSOLIC ; mRNA sequence /clone=1292193 /clone_end=3' /gb=AA705851 /gi=2715769 /ug=Hs.443872 /len=412	AA705851	Hs.443872	
8657	0.010515	UI-E-EJ1-ajj-p-12-0-UI.s1 UI-E-EJ1 cDNA clone UI-E-EJ1-ajj-p-12-0-UI 3', mRNA sequence /clone=UI-E-EJ1-ajj-p-12-0-UI /clone_end=3' /gb=BM684924 /gi=18994820 /ug=Hs.18514 /len=1033	BM684924	Hs.18514	
8675	0.006699	UI-H-EI0-ayo-a-20-0-UI.s1 NCI_CGAP_EI0 cDNA clone IMAGE:5841307 3', mRNA sequence /clone=IMAGE:5841307 /clone_end=3' /gb=BQ004581 /gi=19729481 /ug=Hs.412459 /len=1095	BQ004581	Hs.412459	
8709	0.004131	clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992	AF001542	Hs.356442	
8746	0.023731	tg02e02.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2107610 3', mRNA sequence /clone=IMAGE:2107610 /clone_end=3' /gb=AI380429 /gi=4190282 /ug=Hs.172445 /len=478	AI380429	Hs.172445	
8782	0.001703	mitochondrion, complete genome	NC_001807		
8796	0.043185	ESTs, cDNA, 3' end /clone=UI-E-EJ0-aii-l-19-0-UI /clone_end=3' /gb=BM681301 /gi=18991197 /ug=Hs.355029 /len=591	BM681301	Hs.355029	
8801	0.006699	cDNA, 5' end /clone=IMAGE:5185850 /clone_end=5' /gb=BI759660 /gi=15751238 /ug=Hs.250691 /len=866	BI759660	Hs.250691	
8803	0.018314	clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992	AF001542	Hs.356442	
8808	0.012137	EST(cDNA clone CS0DF021YG07 5 prime)	AL535948		NP_006612
8828	0.043185	cDNA FLJ13443 fis, clone PLACE1002853	AK023505		NP_078968
8840	0.038517	No significant match	SEQ.ID.No.54		
8856	0.020878	control			

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8954	0.005723	nj20a07.s1 NCI_CGAP_AA1 cDNA clone IMAGE:993012 3', mRNA sequence /clone=IMAGE:993012 /clone_end=3' /gb=AA570674 /gi=2344654 /ug=Hs.162392 /len=435	AA570674	Hs.162392	
8972	0.038517	EST (ym20a08.r1 Soares infant brain 1NIB IMAGE:48353 5')	H15948		
8990	0.016017	hypothetical protein FLJ39514 (FLJ39514), mRNA /cds=(121,2040) /gb=NM_152540 /gi=22749126 /ug=Hs.48565 /len=2221	NM_152540	Hs.48565	NP_689753
9088	0.030399	clone IMAGE:3875308, mRNA, partial cds /cds=UNKNOWN /gb=BC013784 /gi=15489380 /ug=Hs.351379 /len=2872	BC013784	Hs.351379	
9162	0.012137	ah98a04.s1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:1327086 3', mRNA sequence /clone=IMAGE:1327086 /clone_end=3' /gb=AA757363 /gi=2805226 /ug=Hs.105224 /len=444	AA757363	Hs.105224	
9192	0.043185	mRNA full length insert cDNA clone EUROIMAGE 1271944 /cds=UNKNOWN /gb=AJ420453 /gi=17066317 /ug=Hs.351834 /len=1186	AJ420453	Hs.351834	NP_006435
9217	0.030399	EST (clone IMAGE:4719448 5')	BG570753		
9222	0.010515	EST(cDNA clone CS0DI054YF18 5 prime)	AL549795		NP_003109
9225	0.048295	UI-H-DT0-atx-c-08-0-UI.s1 NCI_CGAP_DT0 cDNA clone IMAGE:5865535 3', mRNA sequence /clone=IMAGE:5865535 /clone_end=3' /gb=BM992885 /gi=19712274 /ug=Hs.436581 /len=1301	BM992885	Hs.436581	
9266	0.026896	clone FLB2932 mRNA sequence /gb=AF138859 /gi=7340965 /ug=Hs.274405 /len=2990	AF138859	Hs.274405	
9274	0.002459	mRNA; cDNA DKFZp586G2120 (from clone DKFZp586G2120); complete cds /cds=(19,2604) /gb=AL136924 /gi=12053342 /ug=Hs.62349 /len=4137	AL136924	Hs.62349	NP_061866
9275	0.003489	ESTs, cDNA, 5' end /clone=IMAGE:3857750 /clone_end=5' /gb=BF035134 /gi=10742846 /ug=Hs.195789 /len=847	BF035134	Hs.195789	

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9289	0.048295	UI-CF-EC1-abq-b-24-0-UI.s1 UI-CF-EC1 cDNA clone UI-CF-EC1-abq-b-24-0-UI 3', mRNA sequence /clone=UI-CF-EC1-abq-b-24-0-UI /clone_end=3' /gb=BM972502 /gi=19590088 /ug=Hs.366185 /len=718	BM972502	Hs.366185	
9310	0.038517	No significant match	SEQ.ID.No.71		
9319	9.48E-04	No significant match (ORF:+2:2~226[225]), low complexity	SEQ.ID.No.17		
9326	0.034264	UI-1-BB1p-akc-h-10-0-UI.s1 NCI_CGAP_PI6 cDNA clone UI-1-BB1p-akc-h-10-0-UI 3', mRNA sequence /clone=UI-1-BB1p-akc-h-10-0-UI /clone_end=3' /gb=BQ026175 /gi=19761454 /ug=Hs.127786 /len=1398	BQ026175	Hs.127786	
9447	0.030399	hypothetical protein PNAS-131 (PNAS-131), mRNA /cds=(288,686) /gb=NM_031446 /gi=21361962 /ug=Hs.37883 /len=1124	NM_031446	Hs.37883	NP_113634
9468	0.013965	hypothetical protein MGC13159 (MGC13159), mRNA /cds=(592,1017) /gb=NM_032927 /gi=14249719 /ug=Hs.12845 /len=1759	NM_032927	Hs.12845	NP_116316
9489	0.002935	similar to putative (H. sapiens) (LOC129641), mRNA	XM_059369		
9498	0.005723	PFTAIRE protein kinase 1 (PFTK1), mRNA /cds=(145,1500) /gb=NM_012395 /gi=6912583 /ug=Hs.57856 /len=4957	NM_012395	Hs.57856	NP_036527
9511	0.034264	emopamil binding related protein, delta8-delta7 sterol isomerase related protein (EBRP), mRNA /cds=(53,673) /gb=NM_032565 /gi=14211872 /ug=Hs.433278 /len=931	NM_032565	Hs.433278	NP_115954
9516	0.007812	ras gene family, member E (ARHE), mRNA /cds=(141,875) /gb=NM_005168 /gi=21361257 /ug=Hs.6838 /len=2685	NM_005168	Hs.6838	NP_005159
9530	0.030399	hypothetical protein FLJ10856 (FLJ10856), mRNA /cds=(148,1233) /gb=NM_018247 /gi=8922719 /ug=Hs.108530 /len=3720	NM_018247	Hs.108530	NP_060717
9533	0.023731	hypothetical protein FLJ20303 (FLJ20303), mRNA /cds=(86,1681) /gb=NM_017755 /gi=8923284 /ug=Hs.17138 /len=2427	NM_017755	Hs.17138	NP_060225
9570	0.034264	ERO1-like (S. cerevisiae) (ERO1L), mRNA /cds=(227,1633) /gb=NM_014584 /gi=7657068 /ug=Hs.25740 /len=3334	NM_014584	Hs.25740	NP_055399

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	D scription	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9581	0.007812	partial steerin-1 gene	AJ251973		
9722	0.043185	EST(nk66b07.s1 NCI_CGAP_Sch1 clone IMAGE:1018453)	AA578852		
9745	0.020878	hypothetical protein MGC32104 (MGC32104), mRNA /cds=(101,1651) /gb=NM_144684 /gi=21389584 /ug=Hs.147025 /len=4732	NM_144684	Hs.147025	NP_653285
9762	0.004131	poly(A) binding protein, cytoplasmic 5 (PABPC5), mRNA /cds=(441,1589) /gb=NM_080832 /gi=18201887 /ug=Hs.190614 /len=3521	NM_080832	Hs.190614	NP_543022
9817	0.016017	EST (nh05d12.s1 NCI_CGAP_Thy1 IMAGE:943415)	AA493662		
9820	0.034264	EST (nk75h03.s1 NCI_CGAP_Sch1 cDNA clone IMAGE:1019381 3')	AA551135		
9835	0.043185	armadillo repeat protein ALEX2 (ALEX2), mRNA /cds=(458,2356) /gb=NM_014782 /gi=21361239 /ug=Hs.48924 /len=2788	NM_014782	Hs.48924	NP_808818
9886	0.013965	mRNA, cDNA DKFZp451F1910 (from clone DKFZp451F1910) /gb=AL833265 /gi=21733898 /ug=Hs.332030 /len=5254	AL833265	Hs.332030	
9913	0.048295	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 (SERPINE1), mRNA /cds=(76,1284) /gb=NM_000602 /gi=10835158 /ug=Hs.82085 /len=2876	NM_000602	Hs.82085	NP_000593
9965	0.004872	hypothetical protein DKFZp434K1421 (DKFZP434K1421), mRNA /cds=(29,1705) /gb=NM_032141 /gi=14149806 /ug=Hs.374609 /len=2547	NM_032141	Hs.374609	NP_115517
9977	0.030399	mitochondrial carrier 2 (MTCH2), nuclear gene encoding mitochondrial protein, mRNA /cds=(49,960) /gb=NM_014342 /gi=7657346 /ug=Hs.279609 /len=1104	NM_014342	Hs.279609	NP_055157
9978	0.005723	cerebral cavernous malformations 1 (CCM1), mRNA /cds=(26,1615) /gb=NM_004912 /gi=4758657 /ug=Hs.93810 /len=2004	NM_004912	Hs.93810	NP_004903
9990	0.034264	hypothetical protein FLJ23467 (FLJ23467), mRNA /cds=(103,657) /gb=NM_024575 /gi=13375749 /ug=Hs.16179 /len=1196	NM_024575	Hs.16179	NP_078851
10026	0.002935	dishevelled associated activator of morphogenesis 1 (DAAM1), mRNA /cds=(126,3362) /gb=NM_014992 /gi=21071076 /ug=Hs.197751 /len=4256	NM_014992	Hs.197751	NP_055807

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Prot in Accession No.
10051	0.012137	DNA segment on chromosome X and Y (unique) 155 expressed sequence (DXYS155E), mRNA /cds=(167,1324) /gb=NM_005088 /gi=10835221 /ug=Hs.21595 /len=3233	NM_005088	Hs.21595	NP_005079
10052	0.048295	casein kinase (LOC149420), mRNA /cds=(290,1315) /gb=NM_152835 /gi=22779869 /ug=Hs.29911 /len=4299	NM_152835	Hs.29911	NP_690048
10053	0.048295	inorganic pyrophosphatase (SID6-306), mRNA /cds=(108,932) /gb=NM_006903 /gi=13491177 /ug=Hs.5123 /len=1115	NM_006903	Hs.5123	NP_789845
10077	0.018314	ATPase, H transporting, lysosomal 70kDa; V1 subunit A, isoform 1 (ATP6V1A1), mRNA /cds=(67,1920) /gb=NM_001690 /gi=19913423 /ug=Hs.281866 /len=4567	NM_001690	Hs.281866	NP_001681
10080	4.04E-04	hypothetical protein DKFZp761N0624 (DKFZp761N0624), mRNA /cds=(113,1444) /gb=NM_032295 /gi=14150046 /ug=Hs.21893 /len=2973	NM_032295	Hs.21893	NP_115671
10134	0.020878	xl59d02.x1 NCI_CGAP_Pan1 cDNA clone IMAGE:2678979 3', mRNA sequence /clone=IMAGE:2678979 /clone_end=3' /gb=AW190111 /gi=6464591 /ug=Hs.377837 /len=248	AW190111	Hs.377837	
10151	0.023731	cDNA FLJ36605 fis, clone TRACH2015316, highly similar to VIMENTIN. /cds=(631,1317) /gb=AK093924 /gi=21752883 /ug=Hs.379100 /len=2665	AK093924	Hs.379100	
10181	0.016017	UI-1-BB1p-aut-a-09-0-UI.s1 NCI_CGAP_PI6 cDNA clone UI-1-BB1p-aut-a-09-0-UI 3', mRNA sequence /clone=UI-1-BB1p-aut-a-09-0-UI /clone_end=3' /gb=BQ024447 /gi=19759726 /ug=Hs.150289 /len=1021	BQ024447	Hs.150289	
10183	0.026896	cDNA: FLJ20924 fis, clone ADSE00928. /gb=AK024577 /gi=10436889 /ug=Hs.306692 /len=1516	AK024577	Hs.306692	
10189	0.038517	EST(ag56f05.s1 Gessler Wilms tumor clone 1126977 3')	AA665893		
10205	0.001703	EST (ol74f05.s1 NCI_CGAP_Kid3 cDNA clone IMAGE:1535361 3')	AA919165		
10235	0.043185	UI-H-ED0-awz-e-06-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5825645 3', mRNA sequence /clone=IMAGE:5825645 /clone_end=3' /gb=BM995013 /gi=19719914 /ug=Hs.23871 /len=1235	BM995013	Hs.23871	

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10240	0.030399	hypothetical protein DKFZp586C1924 (DKFZp586C1924), mRNA /cds=(106,693) /gb=NM_032273 /gi=14150016 /ug=Hs.108338 /len=782	NM_032273	Hs.108338	NP_115649
10247	0.023731	vimentin (VIM) gene	M18895		
10274	0.007812	EST (EST97907 Thyroid cDNA 5')	AA384394		
10323	0.030399	mRNA; cDNA DKFZp434K1115 (from clone DKFZp434K1115); complete cds /cds=(97,2877) /gb=AL136764 /gi=12053044 /ug=Hs.42676 /len=4868	AL136764	Hs.42676	
10328	0.030399	EST (CM0-UM0033-010300-257-c04 UM0033)	AW796764		
10350	0.007812	hypothetical protein FLJ90013 (FLJ90013), mRNA /cds=(15,1703) /gb=NM_153365 /gi=23503310 /ug=Hs.25119 /len=3382	NM_153365	Hs.25119	NP_699196
10382	0.026896	hypothetical protein DKFZp761N0624 (DKFZp761N0624), mRNA /cds=(113,1444) /gb=NM_032295 /gi=14150046 /ug=Hs.21893 /len=2973	NM_032295	Hs.21893	NP_115671
10385	0.038517	chondroitin sulfate GalNAcT-2 (GALNAcT-2), mRNA /cds=(336,1964) /gb=NM_018590 /gi=24429591 /ug=Hs.180758 /len=3745	NM_018590	Hs.180758	NP_061060
10388	0.016017	UI-CF-FN0-aes-e-05-0-UI.s1 UI-CF-FN0 cDNA clone UI-CF-FN0-aes-e-05-0-UI 3', mRNA sequence /clone=UI-CF-FN0-aes-e-05-0-UI /clone_end=3' /gb=BU607793 /gi=23272751 /ug=Hs.188375 /len=1090	BU607793	Hs.188375	
10443	0.032747	EST(xw02a10.x1 NCI_CGAP_Brn53 cDNA clone IMAGE:2826810 3' similar to TR:Q12791 Q12791 CALCIUM-ACTIVATED POTASSIUM CHANNEL)	AW305218		NP_002238
10474	0.048295	EST(cDNA clone IMAGE:2505486 3')	AW004819		NP_612487
10505	0.013965	mRNA; cDNA DKFZp451B134 (from clone DKFZp451B134) /gb=AL832009 /gi=21732549 /ug=Hs.102796 /len=4843	AL832009	Hs.102796	
10566	0.034264	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
10596	0.038517	602584296F1 NIH_MGC_76 cDNA clone IMAGE:4712302 5', mRNA sequence /clone=IMAGE:4712302 /clone_end=5' /gb=BG564611 /gi=13572263 /ug=Hs.136470 /len=896	BG564611	Hs.136470	

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigen Accession No.	Protein Accession No.
10627	0.016017	602584221F1 NIH_MGC_76 cDNA clone IMAGE:4712140 5', mRNA sequence /clone=IMAGE:4712140 /clone_end=5' /gb=BG564543 /gi=13572195 /ug=Hs.105449 /len=981	BG564543	Hs.105449	
10633	0.018314	UI-E-CL1-afa-n-02-0-UI.r1 UI-E-CL1 cDNA clone UI-E-CL1-afa-n-02-0-UI 5', mRNA sequence /clone=UI-E-CL1-afa-n-02-0-UI /clone_end=5' /gb=BM696235 /gi=19009493 /ug=Hs.446332 /len=1366	BM696235	Hs.446332	
10675	0.006699	cDNA FLJ11309 fis, clone PLACE1010076. /gb=AK002171 /gi=7023887 /ug=Hs.28005 /len=3232	AK002171	Hs.28005	
10680	0.013965	cDNA, 5' end /clone=IMAGE:4513481 /clone_end=5' /gb=BG287554 /gi=13041502 /ug=Hs.374391 /len=988	BG287554	Hs.374391	NP_776158
10717	0.004131	No significant match	SEQ.ID.No.83		
10771	0.023731	HUM515D03B Clontech placenta polyA mRNA (#6518) cDNA clone GEN-515D03 5', mRNA sequence /clone=GEN-515D03 /clone_end=5' /gb=D58893 /gi=968527 /ug=Hs.335953 /len=365	D58893	Hs.335953	
10788	0.006699	yg45f12.s1 Soares infant brain 1NIB cDNA clone IMAGE:35625 3', mRNA sequence /clone=IMAGE:35625 /clone_end=3' /gb=R45691 /gi=822137 /ug=Hs.268774 /len=574	R45691	Hs.268774	
10804	0.038517	EST (yr74c11.s1 Soares fetal liver spleen 1NFLS IMAGE:211028 3')	H65780		
10847	0.038517	hypothetical protein MGC3200 (MGC3200), mRNA /cds=(108,764) /gb=NM_032305 /gi=14150063 /ug=Hs.9088 /len=1191	NM_032305	Hs.9088	NP_115681
10855	0.016017	EST 7h93e02.x1 NCI_CGAP_Co16 cDNA clone IMAGE:3323546 3'	BF064070		
10869	0.026896	EST DKFZp434D1916_r1 434 (synonym:htes3) cDNA clone DKFZp434D1916 5'	AL041117		
10898	0.016017	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) (HSPA5), mRNA /cds=(205,2169) /gb=NM_005347 /gi=21361242 /ug=Hs.75410 /len=3925	NM_005347	Hs.75410	NP_005338
10901	0.030399	CCR4-NOT transcription complex, subunit 7 (CNOT7), transcript variant 1, mRNA /cds=(340,1128) /gb=NM_013354 /gi=17978498 /ug=Hs.380963 /len=2653	NM_013354	Hs.380963	NP_473367

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10940	0.004872	mRNA, cDNA DKFZp686K192 (from clone DKFZp686K192) /gb=AL832209 /gi=21732754 /ug=Hs.259347 /len=6707	AL832209	Hs.259347	
10972	0.026896	fetal liver cDNA library Human cDNA	AI132941		
10976	0.034264	in56e04.x1 HR85 islet cDNA clone IMAGE:6126055 3', mRNA sequence /clone=IMAGE:6126055 /clone_end=3' /gb=BU784825 /gi=23830229 /ug=Hs.442971 /len=548	BU784825	Hs.442971	
10984	0.034264	ESTs, cDNA, 3' end /clone=IMAGE:2385007 /clone_end=3' /gb=AI796655 /gi=5362118 /ug=Hs.132315 /len=516	AI796655	Hs.132315	
10992	0.048295	mRNA, cDNA DKFZp586K1922 (from clone DKFZp586K1922) /gb=AL110204 /gi=5817123 /ug=Hs.193784 /len=3561	AL110204	Hs.193784	
11003	0.026896	cDNA FLJ14832 fis, clone OVARC1001169. /gb=AK027738 /gi=14042638 /ug=Hs.235860 /len=2350	AK027738	Hs.235860	
11009	0.034264	EST(adult retina cDNA Danio rerio cDNA clone 4201579 3' similar to TR:Q9YH14 Q9YH14 PROGESTERONE RECEPTOR BINDING PROTEIN.)	BI880587		
11032	0.009079	nj38c05.s1 NCI_CGAP_AA1 cDNA clone IMAGE:994760 3' similar to gb:M62424 THROMBIN RECEPTOR PRECURSOR mRNA sequence /clone=IMAGE:994760 /clone_end=3' /gb=AA548630 /gi=2318912 /ug=Hs.105848 /len=555	AA548630	Hs.105848	
11132	0.048295	UI-H-CO0-aqz-b-03-0-UI.s1 NCI_CGAP_Sub9 cDNA clone IMAGE:3105700 3', mRNA sequence /clone=IMAGE:3105700 /clone_end=3' /gb=BQ027621 /gi=19762900 /ug=Hs.442094 /len=922	BQ027621	Hs.442094	
11136	0.048295	clone IMAGE:3138608, mRNA /cds=UNKNOWN /gb=BC007266 /gi=13938277 /ug=Hs.334566 /len=1635	BC007266	Hs.334566	
11141	0.023731	cDNA FLJ38591 fis, clone HEART1000151. /gb=AK095910 /gi=21755261 /ug=Hs.63243 /len=2411	AK095910	Hs.63243	
11143	0.020878	EST(NIH_MGC_75 cDNA clone IMAGE:4614964 5')	BG427835		
11146	0.038517	EST380541 MAGE resequences, MAGJ cDNA, mRNA sequence /gb=AW968465 /gi=8158306 /ug=Hs.351848 /len=658	AW968465	Hs.351848	

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11161	0.043185	ESTs, cDNA /gb=AW975851 /gi=8167072 /ug=Hs.361171 /len=684	AW975851	Hs.361171	
11164	0.026896	UI-H-CO0-arf-f-05-0-UI.s1 NCI_CGAP_Sub9 cDNA clone IMAGE:3106304 3', mRNA sequence /clone=IMAGE:3106304 /clone_end=3' /gb=BQ027925 /gi=19763204 /ug=Hs.162459 /len=968	BQ027925	Hs.162459	
11165	0.026896	mRNA full length insert cDNA clone EUROIMAGE 73337. /gb=AL109705 /gi=5689834 /ug=Hs.9997 /len=1227	AL109705	Hs.9997	
11203	4.04E-04	cDNA FLJ38383 fis, clone FEBRA2003726. /gb=AK095702 /gi=21755022 /ug=Hs.433517 /len=3240	AK095702	Hs.433517	
11243	0.009079	apoA polymorphism Kringle IV gene, exons 1 and 2	L14005		
11321	0.026896	transient receptor potential cation channel, subfamily C, member 1 (TRPC1), mRNA /cds=(138,2417) /gb=NM_003304 /gi=27545448 /ug=Hs.250687 /len=4085	NM_003304	Hs.250687	NP_003295
11365	0.028869	Rho-specific guanine-nucleotide exchange factor 164 kDa (P164RHOGF), mRNA /cds=(16,6207) /gb=NM_014786 /gi=21361457 /ug=Hs.45180 /len=7540	NM_014786	Hs.45180	NP_055601
11376	0.020878	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), mRNA /cds=(38,3655) /gb=NM_014243 /gi=21265036 /ug=Hs.27916 /len=5821	NM_014243	Hs.27916	NP_055058
11380	0.009079	clone IMAGE:4837455, mRNA /gb=BC045818 /gi=28279091 /ug=Hs.406481 /len=2600	BC045818	Hs.406481	
11402	0.043185	cytochrome c, somatic (CYCS), mRNA /cds=(61,378) /gb=NM_018947 /gi=21361707 /ug=Hs.169248 /len=3990	NM_018947	Hs.169248	NP_061820
11427	0.034264	DKFZP586A0522 protein (DKFZP586A0522), mRNA /cds=(21,755) /gb=NM_014033 /gi=13378140 /ug=Hs.288771 /len=1705	NM_014033	Hs.288771	NP_054752
11438	0.013965	hypothetical protein FLJ20360 (FLJ20360), mRNA /cds=(80,2305) /gb=NM_017782 /gi=8923334 /ug=Hs.26434 /len=3041	NM_017782	Hs.26434	NP_060252
11467	0.030399	SMT3 suppressor of mif two 3 1 (yeast) (SMT3H1), mRNA /cds=(95,406) /gb=NM_006936 /gi=5902095 /ug=Hs.85119 /len=1733	NM_006936	Hs.85119	NP_008867

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11482	0.043185	clone IMAGE:5271722, mRNA /gb=BC038786 /gi=24270905 /ug=Hs.190456 /len=1535	BC038786	Hs.190456	
11502	0.023731	mRNA for KIAA1229 protein, partial cds /cds=UNKNOWN /gb=AB033055 /gi=6330699 /ug=Hs.71109/len=5654	AB033055	Hs.71109	
11546	0.020878	EST(PM3-NT0011-120400-001-b03 NT0011)	AW888715		
11584	0.043185	clone IMAGE:4769230, mRNA /gb=BC022409 /gi=18490247 /ug=Hs.346398 /len=1667	BC022409	Hs.346398	
11593	0.006699	602634689F1 NCI_CGAP_Skn3 cDNA clone IMAGE:4779575 5', mRNA sequence /clone=IMAGE:4779575 /clone_end=5' /gb=BG743384 /gi=14054037 /ug=Hs.32345 /len=805	BG743384	Hs.32345	
11597	0.048295	EST HUM517A08B Clontech human placenta polyA mRNA (#6572) Human sapiens cDNA clone GEN-517A08 5'	D63277		
11615	0.016017	mRNA for KIAA0261 gene, partial cds. /cds=(1,3866) /gb=D87450 /gi=1665788 /ug=Hs.154978 /len=6155	D87450	Hs.154978	
11617	0.013965	UI-H-EI1-azc-f-09-0-UI.s1 NCI_CGAP_EI1 cDNA clone IMAGE:5846792 3', mRNA sequence /clone=IMAGE:5846792 /clone_end=3' /gb=BQ026855 /gi=19762134 /ug=Hs.446663 /len=875	BQ026855	Hs.446663	
11634	0.010515	hypothetical protein FLJ12118 (FLJ12118), mRNA /cds=(24,1718) /gb=NM_024537 /gi=13375694 /ug=Hs.381043 /len=1843	NM_024537	Hs.381043	NP_078813
11636	0.018314	hypothetical protein FLJ20719 (FLJ20719), mRNA /cds=(402,2213) /gb=NM_017940 /gi=24308174 /ug=Hs.446473 /len=3745	NM_017940	Hs.446473	NP_060410
11654	0.038517	clone IMAGE:5260918, mRNA /gb=BC035085 /gi=23958865 /ug=Hs.250448 /len=3052	BC035085	Hs.250448	
11733	0.030399	hypothetical protein FLJ14360 (FLJ14360), mRNA /cds=(110,2014) /gb=NM_032775 /gi=24432025 /ug=Hs.347964 /len=2602	NM_032775	Hs.347964	NP_116164
11770	0.048295	FLJ33160 fis, clone UTERU2000485 /cds=UNKNOWN /gb=AK057722 /gi=16553641 /ug=Hs.124733 /len=2328	AK057722	Hs.124733	
11851	0.026896	mitochondrion, complete genome	NC_001807		

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11855	0.013965	vacuolar protein sorting 41 (yeast) (VPS41), transcript variant 1, mRNA /cds=(27,2591) /gb=NM_014396 /gi=18105059 /ug=Hs.180941 /len=4914	NM_014396	Hs.180941	NP_542198
11870	0.043185	clone 114 tumor rejection antigen mRNA, complete cds /cds=(3482,3544) /gb=AF445027 /gi=17386079 /ug=Hs.24723 /len=3648	AF445027	Hs.24723	
11883	0.048295	nuclear receptor co-repressor 2 (NCOR2), mRNA /cds=(2,7555) /gb=NM_006312 /gi=5454073 /ug=Hs.287994 /len=8561	NM_006312	Hs.287994	NP_006303
11897	0.016017	hypothetical protein FLJ20701 (FLJ20701), mRNA /cds=(39,938) /gb=NM_017933 /gi=8923631 /ug=Hs.424598 /len=2284	NM_017933	Hs.424598	NP_060403
11901	0.048295	chromosome 14 open reading frame 103 (C14orf103), mRNA /cds=(354,2342) /gb=NM_018036 /gi=21361677 /ug=Hs.168241 /len=3361	NM_018036	Hs.168241	NP_060506
11907	0.026896	hypothetical gene supported by AL117650 (LOC123223), mRNA	XM_071824		
11913	0.048295	mRNA; cDNA DKFZp434H2019 (from clone DKFZp434H2019) /gb=AL137535 /gi=6808211 /ug=Hs.15806 /len=1974	AL137535	Hs.15806	
11946	0.013965	hypothetical protein FLJ20432 (FLJ20432), mRNA /cds=(603,1361) /gb=NM_017819 /gi=8923404 /ug=Hs.57898 /len=1654	NM_017819	Hs.57898	NP_060289
11947	0.032747	polymerase (RNA) II (DNA directed) polypeptide H (POLR2H), mRNA /cds=(88,540) /gb=NM_006232 /gi=14589952 /ug=Hs.432574 /len=821	NM_006232	Hs.432574	NP_006223
11967	0.020878	TNF receptor-associated factor 5 (TRAF5), transcript variant 1, mRNA /cds=(194,1867) /gb=NM_004619 /gi=22027625 /ug=Hs.29736 /len=4132	NM_004619	Hs.29736	NP_665702
11974	0.034264	cDNA FLJ12280 fis, clone MAMMA1001744. /gb=AK022342 /gi=10433719 /ug=Hs.288467 /len=3189	AK022342	Hs.288467	
11979	0.046968	chromosome 20 open reading frame 6 (C20orf6), mRNA /cds=(109,2664) /gb=NM_016649 /gi=22507381 /ug=Hs.88820 /len=3216	NM_016649	Hs.88820	NP_057733
11985	0.030399	protocadherin beta 16 (PCDHB16), mRNA /cds=(1156,3486) /gb=NM_020957 /gi=14195604 /ug=Hs.147674 /len=4827	NM_020957	Hs.147674	NP_066008

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigen Accession No.	Protein Accession No.
12080	0.030399	AGENCOURT_8899857 NIH_MGC_142 cDNA clone IMAGE:6451082 5', mRNA sequence /clone=IMAGE:6451082 /clone_end=5' /gb=BU595281 /gi=23247040 /ug=Hs.5250 /len=1163	BU595281	Hs.5250	
12085	0.016017	retinoic acid induced 14 (RAI14), mRNA /cds=(112,3054) /gb=NM_015577 /gi=13470085 /ug=Hs.15165 /len=4925	NM_015577	Hs.15165	NP_056392
12087	0.043185	hypothetical protein FLJ21313 (FLJ21313), mRNA /cds=(199,1497) /gb=NM_023927 /gi=12965196 /ug=Hs.235445 /len=2912	NM_023927	Hs.235445	NP_076416
12099	0.019416	nuclear cap binding protein subunit 2, 20kDa (NCBP2), mRNA /cds=(27,497) /gb=NM_007362 /gi=19923386 /ug=Hs.240770 /len=2120	NM_007362	Hs.240770	NP_031388
12103	0.032747	UI-H-FH0-bce-d-09-0-UI.s1 NCI_CGAP_FH0 cDNA clone UI-H-FH0-bce-d-09-0-UI 3', mRNA sequence /clone=UI-H-FH0-bce-d-09-0-UI /clone_end=3' /gb=BQ774102 /gi=21982578 /ug=Hs.380398 /len=1094	BQ774102	Hs.380398	
12161	0.012137	EST(hh76d05.y1 NCI_CGAP_GU1 cDNA clone IMAGE:2968713 5' similar to contains L1.t1 L1 repetitive element ;	AW663260		
12224	0.030399	gp25L2 protein (HSGP25L2G), mRNA /cds=(76,720) /gb=NM_017510 /gi=24475637 /ug=Hs.279929 /len=1420	NM_017510	Hs.279929	NP_059980
12229	0.034264	clone IMAGE:3924941, mRNA /gb=BC029341 /gi=20379505 /ug=Hs.391380 /len=1657	BC029341	Hs.391380	
12233	0.026896	chemokine-like factor super family 3 (CKLF3), mRNA /cds=(527,1075) /gb=NM_144601 /gi=21389400 /ug=Hs.7773 /len=2318	NM_144601	Hs.7773	NP_653202
12243	0.038517	mRNA; cDNA DKFZp313P0434 (from clone DKFZp313P0434) /gb=AL832702 /gi=21733281 /ug=Hs.125019 /len=2995	AL832702	Hs.125019	
12248	0.021523	EST(yd28g06.r1 Soares fetal liver spleen 1NFLS IMAGE:109594 5')	T82238		
12257	0.048295	EST390958 MAGE resequences, MAGP cDNA, mRNA sequence /gb=AW978849 /gi=8170126 /ug=Hs.124977 /len=678	AW978849	Hs.124977	
12267	0.018314	EST (op46b10.s1 Soares_NFL_T_GBC_S1 IMAGE:1579867 3')	AA978266		

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	D scription	Gene Accession N .	Unigene Accession No.	Protein Accession No.
12355	0.043185	cDNA FLJ36238 fis, clone THYMU2001422. /gb=AK093557 /gi=21752458 /ug=Hs.345588 /len=2269	AK093557	Hs.345588	
12389	0.030399	UI-HF-BN0-afr-f-07-0-UI.r1 NIH_MGC_50 cDNA clone IMAGE:3067908 5', mRNA sequence /clone=IMAGE:3067908 /clone_end=5' /gb=BU431616 /gi=22770103 /ug=Hs.202538 /len=551	BU431616	Hs.202538	
12426	0.010515	602590145F1 NIH_MGC_76 cDNA clone IMAGE:4724074 5', mRNA sequence /clone=IMAGE:4724074 /clone_end=5' /gb=BG564169 /gi=13571821 /ug=Hs.444093 /len=792	BG564169	Hs.444093	
12429	0.006699	EST(cDNA clone IMAGE:3913767 5')	BE890088		
12440	0.034264	clone IMAGE:5286019, mRNA /gb=BC042960 /gi=27693187 /ug=Hs.5724 /len=3174	BC042960	Hs.5724	
12470	0.038517	cDNA: FLJ22930 fis, clone KAT07255. /gb=AK026583 /gi=10439467 /ug=Hs.90790 /len=1600	AK026583	Hs.90790	
12484	0.041767	qa50a08.x1 Soares_NhHMPu_S1 cDNA clone IMAGE:1690166 3', mRNA sequence /clone=IMAGE:1690166 /clone_end=3' /gb=AI123569 /gi=3539335 /ug=Hs.117060 /len=773	AI123569	Hs.117060	
12540	0.023731	UI-H-FE0-bbv-m-15-0-UI.s1 NCI_CGAP_FE0 cDNA clone UI-H-FE0-bbv-m-15-0-UI 3', mRNA sequence /clone=UI-H-FE0-bbv-m-15-0-UI /clone_end=3' /gb=CA416757 /gi=24779408 /ug=Hs.399730 /len=759	CA416757	Hs.399730	
12541	9.48E-04	yb61c11.s1 Stratagene ovary (#937217) cDNA clone IMAGE:75668 3', mRNA sequence /clone=IMAGE:75668 /clone_end=3' /gb=T58438 /gi=660275 /ug=Hs.189678 /len=506	T58438	Hs.189678	
12562	0.023731	C14379 Clontech aorta polyA mRNA (#6572) cDNA clone GEN-051F07 3', mRNA sequence /clone=GEN-051F07 /clone_end=3' /gb=C14379 /gi=1569086 /ug=Hs.439346 /len=417	C14379	Hs.439346	
12574	0.043185	UI-H-ED0-awx-b-15-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5824814 3', mRNA sequence /clone=IMAGE:5824814 /clone_end=3' /gb=BQ020068 /gi=19755345 /ug=Hs.396278 /len=1351	BQ020068	Hs.396278	
12604	0.001703	EST(IL3-HT0618-120500-138-D11 HT0618 cDNA, MRNA sequence)	BE179957		

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12664	0.016017	hypothetical protein FLJ12888 (FLJ12888), mRNA /cds=(333,2210) /gb=NM_024945 /gi=13376426 /ug=Hs.284137 /len=3413	NM_024945	Hs.284137	NP_079221
12685	0.013965	EST (th94c08.x1Soares_NSF_F8_9W_OT_P A_P_S1 cDNA clone IMAGE:2126318 3'	AI435422		
12695	0.038517	mitochondrion, complete genome	NC_001807		
12725	0.043185	EST(CM3-BN0151-130400-146-f01_1 BN0151)	BE008220		
12732	0.006699	mitochondrion, complete genome	NC_001807		
12734	1.21E-05	mRNA for FLJ00201 protein. /cds=(1,2119) /gb=AK074129 /gi=18676605 /ug=Hs.353001 /len=4443	AK074129	Hs.353001	
12739	0.043185	xn86b03.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2701325 3', mRNA sequence /clone=IMAGE:2701325 /clone_end=3' /gb=AW195867 /gi=6475097 /ug=Hs.370978 /len=571	AW195867	Hs.370978	
12836	0.002935	BX090814 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGp998J084249 ; IMAGE:1673959, mRNA sequence /clone=IMAGp998J084249_ IMAGE:1673959 /gb=BX090814 /gi=27824521 /ug=Hs.125457 /len=471	BX090814	Hs.125457	
12850	0.043185	mitogen-activated protein kinase kinase 2 (MAP3K2), mRNA /cds=(102,1964) /gb=NM_006609 /gi=21735555 /ug=Hs.28827 /len=3336	NM_006609	Hs.28827	NP_006600
12851	0.012137	FLJ11311 fis, clone PLACE1010102/cds=UNKNOWN /gb=AK002173 /gi=7023889 /ug=Hs.5518 /len=1839	AK002173	Hs.5518	NP_689971
12892	0.012137	ESTs, cDNA, 5' end /clone=IMAGE:1554245 /clone_end=5' /gb=AI792925 /gi=5340641 /ug=Hs.137097 /len=585	AI792925	Hs.137097	
12944	0.043162	QV0-CT0181-041199-048-h11 CT0181 cDNA, mRNA sequence /gb=AW752027 /gi=7667063 /ug=Hs.293346 /len=634	AW752027	Hs.293346	
12970	0.038517	EST(yy21h08.s1 Soares melanocyte 2NbHM H.sapiens cDNA clone IMAGE:271935 3')	N35259		NP_079229
12983	0.048295	EST(cDNA clone IMAGE:2771386 3')	AW269219		NP_689632

Genes Corrsponding To Differentially Expr ssed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13006	0.043185	BX109725 Soares retina N2b4HR cDNA clone IMAGp998H04439, mRNA sequence /clone=IMAGp998H04439 ;_IMAGE:221235 /gb=BX109725 /gi=27877852 /ug=Hs.16886 /len=720	BX109725	Hs.16886	
13007	0.009079	EST(cDNA clone GKCAHD03 5')	AV696986		NP_072179
13015	0.00412	hypothetical protein FLJ31131 (FLJ31131), mRNA /cds=(20,421) /gb=NM_152535 /gi=22749108 /ug=Hs.23853 /len=1970	NM_152535	Hs.23853	
13021	0.00412	EST(cDNA clone GLCAOE01 3')	AV646538		
13065	0.026896	control			
13073	0.025373	UI-H-BI4-aqa-c-02-0-UI.s1 NCI_CGAP_Sub8 cDNA clone IMAGE:3089258 3', mRNA sequence /clone=IMAGE:3089258 /clone_end=3' /gb=BF508251 /gi=11591549 /ug=Hs.197875 /len=1237	BF508251	Hs.197875	
13106	0.013965	growth arrest and DNA-damage-inducible, beta (GADD45B), mRNA /cds=(101,586) /gb=NM_015675 /gi=9945331 /ug=Hs.110571 /len=1121	NM_015675	Hs.110571	NP_056490
13140	0.012137	epithelial V-like antigen 1 (EVA1), transcript variant 1, mRNA /cds=(142,789) /gb=NM_005797 /gi=21536270 /ug=Hs.116651 /len=2634	NM_005797	Hs.116651	NP_658911
13148	0.030399	likely ortholog of mouse nervous system polycomb 1 (NSPC1), mRNA /cds=(28,771) /gb=NM_032673 /gi=14249239 /ug=Hs.316750 /len=904	NM_032673	Hs.316750	NP_116062
13161	0.023731	hypothetical protein FLJ10035 (FLJ10035), mRNA /cds=(251,1132) /gb=NM_030803 /gi=24475809 /ug=Hs.16390 /len=2404	NM_030803	Hs.16390	NP_110430
13202	0.023731	hypothetical protein FLJ12806 (FLJ12806), mRNA /cds=(158,1078) /gb=NM_022831 /gi=12383075 /ug=Hs.107637 /len=2485	NM_022831	Hs.107637	NP_073742
13210	0.048295	hypothetical protein FLJ13188 (FLJ13188), mRNA /cds=(247,948) /gb=NM_022063 /gi=11545770 /ug=Hs.11859 /len=2746	NM_022063	Hs.11859	NP_071346
13237	0.048295	KIAA0635 gene product (KIAA0635), mRNA /cds=(833,3373) /gb=NM_014645 /gi=7662215 /ug=Hs.185091 /len=5138	NM_014645	Hs.185091	NP_055460

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gen Accession No.	Unigene Accession No.	Protein Accession No.
13319	0.043185	cDNA FLJ33540 fis, clone BRAMY2007613. /gb=AK090859 /gi=21749098 /ug=Hs.21213 /len=2030	AK090859	Hs.21213	
13335	0.013965	hypothetical protein FLJ12118 (FLJ12118), mRNA /cds=(24,1718) /gb=NM_024537 /gi=13375694 /ug=Hs.381043 /len=1843	NM_024537	Hs.381043	NP_078813
13339	0.013965	mRNA for KIAA1133 protein, partial cds. /cds=(1,2676) /gb=AB051436 /gi=13195720 /ug=Hs.318584 /len=6542	AB051436	Hs.318584	
13385	0.043185	membrane-bound transcription factor protease, site 1 (MBTPS1), mRNA /cds=(497,3655) /gb=NM_003791 /gi=4506774 /ug=Hs.75890 /len=4338	NM_003791	Hs.75890	NP_003782
13459	0.006699	N-ethylmaleimide-sensitive factor (NSF), mRNA /cds=(61,2295) /gb=NM_006178 /gi=11079227 /ug=Hs.108802 /len=3960	NM_006178	Hs.108802	NP_006169
13514	0.023731	cDNA FLJ39478 fis, clone PROST2013605. /gb=AK096797 /gi=21756367 /ug=Hs.372680 /len=2507	AK096797	Hs.372680	
13522	0.020878	mRNA; cDNA DKFZp451O1818 (from clone DKFZp451O1818) /gb=AL832650 /gi=21733226 /ug=Hs.12396 /len=4870	AL832650	Hs.12396	
13528	0.018314	AGENCOURT_6428635 NIH_MGC_85 cDNA clone IMAGE:5505112 5', mRNA sequence /clone=IMAGE:5505112 /clone_end=5' /gb=BM464974 /gi=18514016 /ug=Hs.446428 /len=1097	BM464974	Hs.446428	
13529	0.038517	mRNA; cDNA DKFZp313K2018 (from clone DKFZp313K2018) /gb=AL832067 /gi=21732608 /ug=Hs.194603 /len=7379	AL832067	Hs.194603	
13530	0.012137	synaptic nuclei expressed gene 1 (SYNE- 1), transcript variant beta, mRNA /cds=(121,10086) /gb=NM_015293 /gi=19526752 /ug=Hs.192102 /len=10742	NM_015293	Hs.192102	NP_598411
13559	7.73E-04	EST(7f95d03.x1 NCI_CGAP_Brn23 cDNA clone IMAGE:3304709 3')	BE858787		NP_115872
13581	0.048295	dishevelled 1 (homologous to Drosophila dsh) (DVL1), mRNA	XM_001589		
13601	0.013965	similar to rat myomegalin (LOC64182), mRNA /cds=(336,1268) /gb=NM_022359 /gi=21314705 /ug=Hs.333512 /len=1717	NM_022359	Hs.333512	NP_071754
13615	0.002051	mRNA full length insert cDNA clone EUROIMAGE 1476475 /gb=AJ420560 /gi=17066424 /ug=Hs.93231 /len=1346	AJ420560	Hs.93231	

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13664	0.005723	prothymosin, alpha (gene sequence 28) (PTMA), mRNA /cds=(182,514) /gb=NM_002823 /gi=21359859 /ug=Hs.250655 /len=1233	NM_002823	Hs.250655	NP_002814
13678	0.020878	toll-like receptor 3 (TLR3), mRNA /cds=(102,2816) /gb=NM_003265 /gi=19718735 /ug=Hs.29499 /len=3057	NM_003265	Hs.29499	NP_003256
13708	0.013965	CUG triplet repeat RNA-binding protein 1 (CUGBP1), mRNA /cds=(137,1585) /gb=NM_006560 /gi=5729793 /ug=Hs.81248 /len=2113	NM_006560	Hs.81248	NP_006551
13717	0.032747	HRAS-like suppressor 3 (HRASLS3), mRNA /cds=(408,896) /gb=NM_007069 /gi=5901975 /ug=Hs.37189 /len=1070	NM_007069	Hs.37189	NP_009000
13755	0.043185	cyclin H (CCNH), mRNA /cds=(233,1204) /gb=NM_001239 /gi=17738313 /ug=Hs.514 /len=1398	NM_001239	Hs.514	NP_001230
13766	0.005723	zinc finger protein 363 (ZNF363), mRNA /cds=(27,812) /gb=NM_015436 /gi=24308060 /ug=Hs.48297 /len=1543	NM_015436	Hs.48297	NP_056251
13786	0.038517	mitochondrion, complete genome	NC_001807		
13817	0.030399	MAD, mothers against decapentaplegic 7 (Drosophila) (MADH7), mRNA /cds=(296,1576) /gb=NM_005904 /gi=5174516 /ug=Hs.100602 /len=3111	NM_005904	Hs.100602	NP_005895
13830	0.041767	ATPase, H transporting, lysosomal 9kDa, V0 subunit e (ATP6V0E), mRNA /cds=(76,321) /gb=NM_003945 /gi=19913435 /ug=Hs.415629 /len=849	NM_003945	Hs.415629	NP_003936
13837	0.020878	mRNA; cDNA DKFZp434A0225 (from clone DKFZp434A0225) /cds=(1,1628) /gb=AL137349 /gi=6807861 /ug=Hs.83293 /len=4087	AL137349	Hs.83293	
13843	0.048295	ankyrin repeat domain 10 (ANKRD10), mRNA /cds=(136,1398) /gb=NM_017664 /gi=8923103 /ug=Hs.172572 /len=2509	NM_017664	Hs.172572	NP_060134
13891	0.023731	cDNA FLJ38641 fis, clone HHDPC2003983. /gb=AK095960 /gi=21755328 /ug=Hs.24831 /len=2685	AK095960	Hs.24831	
13896	0.032747	UI-H-FL1-bfx-j-06-0-UI.s1 NCI_CGAP_FL1 cDNA clone UI-H-FL1-bfx-j-06-0-UI 3', mRNA sequence /clone=UI-H-FL1-bfx-j-06-0-UI /clone_end=3' /gb=BU620821 /gi=23287036 /ug=Hs.12420 /len=1123	BU620821	Hs.12420	
13961	0.034264	Novel	SEQ.ID.No.90		

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13972	0.020878	zo15e02.s1 Stratagene colon (#937204) cDNA clone IMAGE:586970 3' similar to contains Alu repetitive element;contains element PTR5 repetitive element ;, mRNA sequence /clone=IMAGE:586970 /clone_end=3' /gb=AA130992 /gi=1692483 /ug=Hs.426360 /len=489	AA130992	Hs.426360	
13985	0.030399	EST (wd75h02.x1 NCI_CGAP_Lu24 cDNA clone IMAGE:2337459 3')	AI914259		
13995	0.048295	p10-binding protein (BITE), mRNA /cds=(149,1942) /gb=NM_024491 /gi=13346499 /ug=Hs.42315 /len=2628	NM_024491	Hs.42315	NP_077817
14059	0.043185	EST (cDNA clone IMAGE:2490676 3')	AI972954		NP_000996
14070	0.020878	EST wr69a08.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2492918 3' similar to contains Alu repetitive element;contains element MSR1 repetitive element ;	AI978999		
14111	0.010515	hypothetical protein MGC3121 (MGC3121), mRNA /cds=(179,1936) /gb=NM_024031 /gi=13128979 /ug=Hs.293629 /len=2063	NM_024031	Hs.293629	NP_076936
14122	0.006699	602152950F1 NIH_MGC_81 cDNA clone IMAGE:4293853 5', mRNA sequence /clone=IMAGE:4293853 /clone_end=5' /gb=BF673050 /gi=11946945 /ug=Hs.208558 /len=830	BF673050	Hs.208558	
14129	0.043185	zu07g05.s1 Soares_testis_NHT cDNA clone IMAGE:731192 3' similar to P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ;, mRNA sequence /clone=IMAGE:731192 /clone_end=3' /gb=AA417352 /gi=2077434 /ug=Hs.445851 /len=519	AA417352	Hs.445851	
14135	0.030399	mitochondrion, complete genome	NC_001807		
14163	0.043185	EST(AV657608 GLC cDNA clone GLCFDF10 3')	AV657608		
14185	0.026896	EST (CM0-UM0041-240200-241-h10 UM0041 cDNA)	AW797721		
14248	0.004872	UI-H-BI1-adn-h-11-0-UI.s1 NCI_CGAP_Sub3 cDNA clone IMAGE:2717445 3', mRNA sequence /clone=IMAGE:2717445 /clone_end=3' /gb=AW136054 /gi=6140187 /ug=Hs.437432 /len=820	AW136054	Hs.437432	
14286	0.012137	mRNA; cDNA DKFZp434J214 (from clone DKFZp434J214); partial cds /cds=(1,1082) /gb=AL080156 /gi=5262614 /ug=Hs.12813 /len=2749	AL080156	Hs.12813	NP_056323

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14289	0.012678	clone DJ0798C17, complete sequence	AC004889		
14375	5.04E-04	ESTs, cDNA, 3' end /clone=IMAGE:2402646 /clone_end=3' /gb=AI768858 /gi=5235367 /ug=Hs.157149 /len=562	AI768858	Hs.157149	NP_066012
14387	0.018314	likely ortholog of rat V-1 protein (V-1), mRNA /cds=(229,585) /gb=NM_145808 /gi=21956644 /ug=Hs.21321 /len=3770	NM_145808	Hs.21321	NP_665807
14415	0.002935	ESTs, cDNA, 5' end /clone=IMAGE:4515481 /clone_end=5' /gb=BG292389 /gi=13051140 /ug=Hs.374490 /len=887	BG292389	Hs.374490	
14418	0.048295	cDNA: FLJ22844 fis, clone KAIA5181. /gb=AK026497 /gi=10439371 /ug=Hs.296322 /len=2381	AK026497	Hs.296322	
14485	0.026896	No significant match, ORF-1(2~259), +3(120~344)	SEQ.ID.No.5		
14603	0.038517	cDNA, 5' end /clone=IMAGE:4475610 /clone_end=5' /gb=BG256145 /gi=12765961 /ug=Hs.5905 /len=949	BG256145	Hs.5905	NP_002031
14617	0.013965	hypothetical protein FLJ20719 (FLJ20719), mRNA /cds=(402,2213) /gb=NM_017940 /gi=24308174 /ug=Hs.446473 /len=3745	NM_017940	Hs.446473	NP_060410
14623	0.028869	hypothetical protein FLJ35779 (FLJ35779), mRNA /cds=(42,1694) /gb=NM_152408 /gi=22748864 /ug=Hs.432726 /len=1698	NM_152408	Hs.432726	NP_689621
14631	0.018314	EST(12h2 retina cDNA randomly primed sublibrary)	W26795		
14637	0.034264	hypothetical protein PRO1331 (PRO1331), mRNA /cds=(423,617) /gb=NM_030778 /gi=13562115 /ug=Hs.301824 /len=1634	NM_030778	Hs.301824	NP_110405
14671	0.016017	UI-H-EI0-aye-c-17-0-UI.s1 NCI_CGAP_EI0 cDNA clone UI-H-EI0-aye-c-17-0-UI 3', mRNA sequence /clone=UI-H-EI0-aye-c-17-0-UI /clone_end=3' /gb=CA447385 /gi=24811805 /ug=Hs.420740 /len=812	CA447385	Hs.420740	
14676	0.020878	EST(QV0-CT0225-101299-071-b01 CT0225)	AW377614		NP_842565
14766	0.038517	cDNA FLJ30301 fis, clone BRACE2003217. /gb=AK054863 /gi=16549482 /ug=Hs.285728 /len=2186	AK054863	Hs.285728	
14828	0.030399	ESTs, cDNA, 3' end /clone=IMAGE:2342469 /clone_end=3' /gb=AI871745 /gi=5545717 /ug=Hs.117777 /len=542	AI871745	Hs.117777	

Genes Corresponding To Differentially Expressed Genes in Figure 11 - Systemic Steroids					
Spot	p-value	Description	Gene Accession No.	Unig n Accession No.	Protein Accession No.
14831	0.026896	clone IMAGE:4183899, mRNA /cds=UNKNOWN /gb=BC008625 /gi=14250384 /ug=Hs.55336 /len=1413	BC008625	Hs.55336	
14871	0.048295	EST, cDNA, 3' end /clone=IMAGE:2488402 /clone_end=3' /gb=AI970954 /gi=5767780 /ug=Hs.311478 /len=509	AI970954	Hs.311478	
14896	0.012137	mitochondrion, complete genome	NC_001807		
14942	0.048295	EST, cDNA /gb=AW360966 /gi=6865616 /ug=Hs.6653 /len=661	AW360966	Hs.6653	NP_055942
14951	0.023731	clone IMAGE:4820928, mRNA /gb=BC033530 /gi=23272327 /ug=Hs.324359 /len=2018	BC033530	Hs.324359	

TABLE 3E					
Genes Corresponding T Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
22	0.039765	54TmP (54tm) (=S83365 RAB5-interaction protein)	AF004876		NP_065203
59	0.017681	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) (SPTAN1), mRNA /cds=(103,7521) /gb=NM_003127 /gi=4507190 /ug=Hs.77196 /len=7787	NM_003127	Hs.77196	NP_003118
115	0.018081	laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=NM_002295 /gi=9845501 /ug=Hs.181357 /len=1039	NM_002295	Hs.181357	NP_002286
144	0.018081	KIAA0961 protein	NM_014898		NP_055713
154	0.032959	hypothetical protein DJ328E19.C1.1 (DJ328E19.C1.1), mRNA /cds=(18,2783) /gb=NM_015383 /gi=7657016 /ug=Hs.218329 /len=3689	NM_015383	Hs.218329	NP_056198
169	0.031117	nuclear protein double minute 1 (MDM1), mRNA /cds=(93,2237) /gb=NM_017440 /gi=24586654 /ug=Hs.12871 /len=2942	NM_017440	Hs.12871	NP_064513
170	0.036914	Duffy blood group (FY), mRNA /cds=(495,1511) /gb=NM_002036 /gi=4503818 /ug=Hs.183 /len=1559	NM_002036	Hs.183	NP_002027
207	9.44E-04	putative p150	AAC51271		
214	0.008722	neuronal thread protein AD7c-NTP	NP_055301		
224	0.005674	ubiquitin specific protease 7 (herpes virus-associated) (USP7), mRNA /cds=(200,3508) /gb=NM_003470 /gi=4507856 /ug=Hs.78683 /len=4022	NM_003470	Hs.78683	NP_003461
288	0.01072	phosphodiesterase 8B (PDE8B), mRNA /cds=(46,2703) /gb=NM_003719 /gi=26006850 /ug=Hs.78106 /len=3567	NM_003719	Hs.78106	NP_003710
290	0.032959	Niemann-Pick disease, type C2 (NPC2), mRNA /cds=(116,571) /gb=NM_006432 /gi=20149580 /ug=Hs.433222 /len=929	NM_006432	Hs.433222	NP_006423
298	0.024584	KIAA0429 gene product (KIAA0429), mRNA /cds=(2374,3444) /gb=NM_014751 /gi=7662113 /ug=Hs.77694 /len=5645	NM_014751	Hs.77694	NP_055566
323	0.032959	associated molecule with the SH3 domain of STAM (AMSH), mRNA /cds=(188,1462) /gb=NM_006463 /gi=17738303 /ug=Hs.12479 /len=2107	NM_006463	Hs.12479	NP_006454
325	0.007886	thyroid autoantigen 70kDa (Ku antigen) (G22P1), mRNA /cds=(656,2485) /gb=NM_001469 /gi=20070134 /ug=Hs.197345 /len=2743	NM_001469	Hs.197345	NP_001460

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigen Accession No.	Protein Accession No.
326	0.024587	proteasome (prosome, macropain) 26S subunit, ATPase, 5 (PSMC5), mRNA /cds=(42,1262) /gb=NM_002805 /gi=24497434 /ug=Hs.79387 /len=1332	NM_002805	Hs.79387	NP_002796
332	0.041254	similar to rat nuclear ubiquitous casein kinase 2 (NUCKS), mRNA /cds=(67,558) /gb=NM_022731 /gi=12232386 /ug=Hs.118064 /len=1811	NM_022731	Hs.118064	NP_073568
342	0.013102	cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA /cds=(61,288) /gb=NM_004374 /gi=17999531 /ug=Hs.351875 /len=444	NM_004374	Hs.351875	NP_004365
344	0.03489	tumor necrosis factor, alpha-induced protein 6 (TNFAIP6), mRNA /cds=(77,910) /gb=NM_007115 /gi=26051242 /ug=Hs.29352 /len=1440	NM_007115	Hs.29352	NP_009046
357	0.016974	deleted in pancreatic carcinoma (DPC4) gene, exon 3	AF045440		
366	0.0261	voltage-dependent anion channel 1 (VDAC1), mRNA /cds=(100,951) /gb=NM_003374 /gi=4507878 /ug=Hs.149155 /len=1806	NM_003374	Hs.149155	NP_003365
367	0.048543	RNA (guanine-7-) methyltransferase (RNMT), mRNA /cds=(197,1627) /gb=NM_003799 /gi=4506566 /ug=Hs.8086 /len=6203	NM_003799	Hs.8086	NP_003790
371	0.011469	ecotropic viral integration site 2A (EVI2A), mRNA /cds=(220,918) /gb=NM_014210 /gi=7657074 /ug=Hs.70499 /len=1563	NM_014210	Hs.70499	NP_055025
378	0.023148	vanilloid receptor; CARKL and CTNS; TIP1; P2X5b and P2X5a; HUMINAE	AF168787		
383	0.001232	zinc finger protein 223 (ZNF223), mRNA /cds=(239,1687) /gb=NM_013361 /gi=7019588 /ug=Hs.279782 /len=2033	NM_013361	Hs.279782	NP_037493
384	0.009349	ADP-ribosylation factor-like 6 interacting protein (ARL6IP), mRNA /cds=(70,681) /gb=NM_015161 /gi=24308006 /ug=Hs.75249 /len=2280	NM_015161	Hs.75249	NP_055976
396	0.01072	hypothetical protein FLJ20445 (FLJ20445), mRNA /cds=(293,1129) /gb=NM_017824 /gi=19923500 /ug=Hs.343748 /len=3896	NM_017824	Hs.343748	NP_060294
430	0.048543	hypothetical protein MGC13061 (MGC13061), mRNA /cds=(52,684) /gb=NM_032322 /gi=14150095 /ug=Hs.29874 /len=1947	NM_032322	Hs.29874	NP_115698

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
434	0.00242	phosphoglycerate kinase 1 (PGK1), mRNA /cds=(70,1323) /gb=NM_000291 /gi=22095338 /ug=Hs.78771 /len=2338	NM_000291	Hs.78771	NP_000282
436	0.041254	golgi phosphoprotein 4 (GOLPH4), mRNA /cds=(14,2104) /gb=NM_014498 /gi=7657137 /ug=Hs.143600 /len=2506	NM_014498	Hs.143600	NP_055313
441	0.004203	ATP binding protein associated with cell differentiation (APACD), mRNA /cds=(130,810) /gb=NM_005783 /gi=18104958 /ug=Hs.153884 /len=1494	NM_005783	Hs.153884	NP_005774
444	0.024587	HSPC019 protein (HSPC019), mRNA /cds=(58,444) /gb=NM_014028 /gi=7661737 /ug=Hs.163724 /len=2411	NM_014028	Hs.163724	NP_054747
448	0.001232	laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=NM_002295 /gi=9845501 /ug=Hs.181357 /len=1039	NM_002295	Hs.181357	NP_002286
450	0.0261	nuclear factor NF-IL6	X52560		
453	0.007056	WD repeat domain 1 (WDR1), transcript variant 1, mRNA /cds=(203,2023) /gb=NM_017491 /gi=17105397 /ug=Hs.85100 /len=3079	NM_017491	Hs.85100	NP_059830
476	0.008722	KIAA1116 protein (KIAA1116), mRNA /cds=(186,4001) /gb=NM_014892 /gi=7662491 /ug=Hs.227602 /len=4664	NM_014892	Hs.227602	NP_055707
512	0.010015	myosin IXB (MYO9B), mRNA /cds=(1,6069) /gb=NM_004145 /gi=4758749 /ug=Hs.159629 /len=6069	NM_004145	Hs.159629	NP_004136
565	0.009763	topoisomerase (DNA) III alpha (TOP3A), mRNA /cds=(230,3235) /gb=NM_004618 /gi=20143947 /ug=Hs.91175 /len=3807	NM_004618	Hs.91175	NP_004609
575	0.007634	tenascin XB (TNXB), transcript variant XB, mRNA /cds=(205,13074) /gb=NM_019105 /gi=20544188 /ug=Hs.169886 /len=13268	NM_019105	Hs.169886	NP_115859
595	0.038337	NS1-associated protein 1 (NSAP1), mRNA /cds=(526,2397) /gb=NM_006372 /gi=23397426 /ug=Hs.373499 /len=2932	NM_006372	Hs.373499	NP_006363
598	0.025888	glutamyl-tRNA synthetase (QARS), mRNA /cds=(6,2333) /gb=NM_005051 /gi=4826959 /ug=Hs.79322 /len=2437	NM_005051	Hs.79322	NP_005042
599	0.01747	hypothetical protein similar to RNA-binding protein lark (MGC10871), mRNA /cds=(54,1133) /gb=NM_031492 /gi=13899353 /ug=Hs.49994 /len=1821	NM_031492	Hs.49994	NP_113680

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
607	0.043544	ribosomal protein S27a (RPS27A), mRNA /cds=(39,509) /gb=NM_002954 /gi=27436941 /ug=Hs.311640 /len=541	NM_002954	Hs.311640	NP_002945
634	0.039267	mitofusin 1 (MFN1), transcript variant 1, mRNA /cds=(84,2309) /gb=NM_033540 /gi=16117784 /ug=Hs.197877 /len=3275	NM_033540	Hs.197877	NP_284941
671	0.047349	KIAA0471 gene product (KIAA0471), mRNA /cds=(413,1525) /gb=NM_014857 /gi=7662143 /ug=Hs.242271 /len=6834	NM_014857	Hs.242271	NP_055672
678	0.048238	clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992	AF001542	Hs.356442	
679	0.014931	hypothetical protein LOC51255 (LOC51255), mRNA /cds=(31,492) /gb=NM_016494 /gi=24475978 /ug=Hs.11156 /len=601	NM_016494	Hs.11156	NP_057578
703	0.00223	cytochrome b-245, beta polypeptide (chronic granulomatous disease) (CYBB), mRNA /cds=(15,1727) /gb=NM_000397 /gi=6996020 /ug=Hs.88974 /len=4266	NM_000397	Hs.88974	NP_000388
726	0.041254	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747	NM_012479	Hs.25001	NP_036611
776	0.031156	GW128 protein (GW128), mRNA /cds=(699,890) /gb=NM_014052 /gi=7661715 /ug=Hs.182238 /len=2011	NM_014052	Hs.182238	
787	0.039034	cargo selection protein (mannose 6 phosphate receptor binding protein) (TIP47), mRNA /cds=(67,1371) /gb=NM_005817 /gi=20127485 /ug=Hs.140452 /len=2239	NM_005817	Hs.140452	NP_005808
794	0.005674	zn87g06.x5 Stratagene lung carcinoma 937218 cDNA clone IMAGE:565210 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ; mRNA sequence /clone=IMAGE:565210 /clone_end=3' /gb=AI732466 /gi=5053579 /ug=Hs.193133 /len=526	AI732466	Hs.193133	
802	0.011469	striated muscle contraction regulatory protein (Id2B) mRNA, complete cds. /cds=(110,220) /gb=M96843 /gi=397775 /ug=Hs.296811 /len=1167	M96843	Hs.296811	

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
805	0.048543	ribosomal protein S17 (RPS17), mRNA /cds=(26,433) /gb=NM_001021 /gi=14591913 /ug=Hs.5174 /len=515	NM_001021	Hs.5174	NP_001012
810	0.039034	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 /len=1705	NM_006855	Hs.250696	NP_057839
835	0.00489	likely ortholog of mouse tumor differentially expressed 1, like (TDE1L), mRNA /cds=(76,1437) /gb=NM_020755 /gi=24308212 /ug=Hs.146668 /len=3149	NM_020755	Hs.146668	NP_065806
844	0.021781	sorting nexin 2 (SNX2), mRNA /cds=(50,1609) /gb=NM_003100 /gi=23111037 /ug=Hs.11183 /len=2091	NM_003100	Hs.11183	NP_003091
851	0.005674	of89c05.s1 NCI_CGAP_Li5 cDNA clone IMAGE:1437512 3' similar to contains Alu repetitive element, mRNA sequence /clone=IMAGE:1437512 /clone_end=3' /gb=AA894384 /gi=3030785 /ug=Hs.432123 /len=296	AA894384	Hs.432123	
865	0.043576	mitochondrion, complete genome	NC_001807		
866	7.88E-04	polycystic kidney disease 2 (autosomal dominant) (PKD2), mRNA /cds=(67,2973) /gb=NM_000297 /gi=4505834 /ug=Hs.82001 /len=5057	NM_000297	Hs.82001	NP_000288
868	0.048543	hypothetical protein LOC123803 (LOC123803), mRNA /cds=(15,947) /gb=NM_173474 /gi=27735048 /ug=Hs.351573 /len=1146	NM_173474	Hs.351573	NP_775745
870	0.00527	KIAA0062 mRNA, partial cds /cds=(1,1598) /gb=D31887 /gi=505101 /ug=Hs.89868 /len=4573	D31887	Hs.89868	
882	0.015924	hypothetical protein H41 (H41), mRNA /cds=(324,1100) /gb=NM_017548 /gi=24475997 /ug=Hs.283690 /len=3346	NM_017548	Hs.283690	NP_060018
917	0.023148	mRNA for integrin, alpha subunit /gb=X68742 /gi=33949 /ug=Hs.116774 /len=3453	X68742	Hs.116774	
923	0.023148	eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa (EIF3S3), mRNA /cds=(6,1064) /gb=NM_003756 /gi=4503514 /ug=Hs.58189 /len=1280	NM_003756	Hs.58189	NP_003747
939	0.016974	protein phosphatase 1, regulatory (inhibitor) subunit 8 (PPP1R8), transcript variant 2, mRNA /cds=(836,1465) /gb=NM_138558 /gi=20336238 /ug=Hs.356590 /len=2691	NM_138558	Hs.356590	NP_612568

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	D scription	Gene Accession No.	Unigene Accession No.	Protein Accession No.
943	0.011469	XIST, coding sequence "a" mRNA (locus DXS399E). /gb=X56199 /gi=37987 /ug=Hs.352403 /len=1614	X56199	Hs.352403	
944	0.043576	neuronal protein	X79682		
953	2.73E-04	mRNA for KIAA0592 protein, partial cds. /cds=(1,4062) /gb=AB011164 /gi=3043707 /ug=Hs.439367 /len=4623	AB011164	Hs.439367	
954	0.015924	cell cycle progression 8 protein (CPR8), mRNA /cds=(13,1140) /gb=NM_004748 /gi=4758047 /ug=Hs.82506 /len=1856	NM_004748	Hs.82506	NP_004739
965	0.031117	testis enhanced gene transcript (TEGT), mRNA /cds=(41,754) /gb=NM_003217 /gi=4507432 /ug=Hs.74637 /len=2600	NM_003217	Hs.74637	NP_003208
976	0.020482	engulfment and cell motility 1 (ced-12 C. elegans) (ELMO1), transcript variant 1, mRNA /cds=(253,2436) /gb=NM_014800 /gi=18765699 /ug=Hs.31463 /len=3657	NM_014800	Hs.31463	NP_569709
978	0.031117	cyclin D binding myb-like transcription factor 1 (DMTF1), mRNA /cds=(276,2558) /gb=NM_021145 /gi=10863946 /ug=Hs.5671 /len=3767	NM_021145	Hs.5671	NP_066968
985	0.012262	PABP-interacting protein 2 (PAIP2), mRNA /cds=(150,533) /gb=NM_016480 /gi=19923458 /ug=Hs.396644 /len=1514	NM_016480	Hs.396644	NP_057564
986	0.031117	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein) (DBI), mRNA /cds=(20,334) /gb=NM_020548 /gi=24475624 /ug=Hs.78888 /len=556	NM_020548	Hs.78888	NP_065438
987	0.024587	brain protein 44-like (BRP44L), mRNA /cds=(123,452) /gb=NM_016098 /gi=7706368 /ug=Hs.108725 /len=988	NM_016098	Hs.108725	NP_057182
989	0.009349	5.8S ribosomal RNA	J01866		
992	0.01925	chemokine (C-X-C motif) ligand 3 (CXCL3), mRNA /cds=(78,398) /gb=NM_002090 /gi=4504156 /ug=Hs.89690 /len=1064	NM_002090	Hs.89690	NP_002081
998	0.024587	down-regulator of transcription 1, TBP-binding (negative cofactor 2) (DR1), mRNA /cds=(548,1078) /gb=NM_001938 /gi=4503380 /ug=Hs.16697 /len=1375	NM_001938	Hs.16697	NP_001929
1008	0.024587	Alg5, S. cerevisiae, of (ALG5), mRNA /cds=(28,1002) /gb=NM_013338 /gi=9665250 /ug=Hs.227933 /len=1125	NM_013338	Hs.227933	NP_037470

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1011	0.001737	v-raf-1 murine leukemia viral oncogene 1 (RAF1), mRNA /cds=(130,2076) /gb=NM_002880 /gi=4506400 /ug=Hs.349650 /len=2977	NM_002880	Hs.349650	NP_002871
1014	0.041254	likely ortholog of rat vacuole membrane protein 1 (VMP1), mRNA /cds=(114,1334) /gb=NM_030938 /gi=20070348 /ug=Hs.166254 /len=2530	NM_030938	Hs.166254	NP_112200
1015	0.013102	actinin, alpha 1 (ACTN1), mRNA /cds=(184,2862) /gb=NM_001102 /gi=12025669 /ug=Hs.119000 /len=3398	NM_001102	Hs.119000	NP_001093
1026	0.010015	methionine adenosyltransferase II, beta (MAT2B), mRNA /cds=(73,1077) /gb=NM_013283 /gi=20127525 /ug=Hs.54642 /len=2054	NM_013283	Hs.54642	NP_037415
1028	7.18E-04	ATP synthase, H transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=NM_006886 /gi=21327678 /ug=Hs.177530 /len=417	NM_006886	Hs.177530	NP_008817
1031	0.023148	decorin (DCN), transcript variant A1, mRNA /cds=(200,1279) /gb=NM_001920 /gi=19743844 /ug=Hs.433989 /len=1751	NM_001920	Hs.433989	NP_598014
1048	0.041254	tetraspan 2 (TSPAN-2), mRNA /cds=(33,698) /gb=NM_005725 /gi=21264579 /ug=Hs.234863 /len=3179	NM_005725	Hs.234863	NP_005716
1057	0.013102	mRNA for KIAA1609 protein, partial cds. /cds=(1,1423) /gb=AB046829 /gi=15425661 /ug=Hs.14449 /len=4683	AB046829	Hs.14449	
1060	0.009349	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa (NDUFB4), mRNA /cds=(9,398) /gb=NM_004547 /gi=6041668 /ug=Hs.227750 /len=464	NM_004547	Hs.227750	NP_004538
1063	0.015924	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult)) (SOD1), mRNA /cds=(1,465) /gb=NM_000454 /gi=4507148 /ug=Hs.75428 /len=560	NM_000454	Hs.75428	NP_000445
1080	0.015924	Similar to RIKEN cDNA 4833424O15 gene, clone IMAGE:4793707, mRNA /gb=BC040174 /gi=25777829 /ug=Hs.312481 /len=3745	BC040174	Hs.312481	
1082	0.012262	KIAA0349 gene	AB002347		NP_056070

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unig ne Accession No.	Protein Accession No.
1087	0.015924	heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, mRNA /cds=(94,2133) /gb=NM_004134 /gi=24234687 /ug=Hs.3069 /len=2852	NM_004134	Hs.3069	NP_004125
1099	0.004328	DKFZP586O0120 protein (DKFZP586O0120), mRNA /cds=(21,359) /gb=NM_014077 /gi=7661695 /ug=Hs.4766 /len=1465	NM_014077	Hs.4766	NP_054796
1102	0.027691	basic leucine zipper and W2 domains 1 (BZW1), mRNA /cds=(81,1340) /gb=NM_014670 /gi=7661849 /ug=Hs.155291 /len=2998	NM_014670	Hs.155291	NP_055485
1107	0.018081	similar to RIKEN cDNA 2610030J16 gene (MGC2541), mRNA /cds=(738,1712) /gb=NM_080670 /gi=18087848 /ug=Hs.173103 /len=2685	NM_080670	Hs.173103	NP_542401
1108	0.041254	frizzled 9 (Drosophila) (FZD9), mRNA /cds=(26,1801) /gb=NM_003508 /gi=4503834 /ug=Hs.158335 /len=2184	NM_003508	Hs.158335	NP_003499
1110	0.011469	ribosomal protein L41 (RPL41), mRNA /cds=(84,161) /gb=NM_021104 /gi=10863874 /ug=Hs.356795 /len=478	NM_021104	Hs.356795	NP_066927
1111	0.021781	hypothetical protein (HSPC016), mRNA /cds=(39,233) /gb=NM_015933 /gi=7705430 /ug=Hs.397853 /len=384	NM_015933	Hs.397853	NP_057017
1113	0.00527	nischarin (NISCH), mRNA /cds=(27,4541) /gb=NM_007184 /gi=6005787 /ug=Hs.26285 /len=5132	NM_007184	Hs.26285	NP_009115
1114	0.014931	stromal antigen 2 (STAG2), mRNA /cds=(405,3893) /gb=NM_006603 /gi=27552767 /ug=Hs.8217 /len=4197	NM_006603	Hs.8217	NP_006594
1118	0.007056	hypothetical protein FLJ12584 (FLJ12584), mRNA /cds=(97,1623) /gb=NM_025139 /gi=13376722 /ug=Hs.288897 /len=1744	NM_025139	Hs.288897	NP_079415
1119	0.013991	pp9974 mRNA, complete cds /cds=(2009,2350) /gb=AF318382 /gi=18027855 /ug=Hs.251664 /len=2630	AF318382	Hs.251664	
1120	0.001033	clone 25032 mRNA sequence /cds=UNKNOWN /gb=AF131764 /gi=4406586 /ug=Hs.13399 /len=1798	AF131764	Hs.13399	NP_071919
1121	0.007056	cDNA FLJ31399 fis, clone NT2NE1000181. /gb=AK055961 /gi=16550820 /ug=Hs.179833 /len=2159	AK055961	Hs.179833	
1122	0.032959	RAB1B, member RAS oncogene family (RAB1B), mRNA /cds=(48,653) /gb=NM_030981 /gi=13569961 /ug=Hs.300816 /len=1985	NM_030981	Hs.300816	NP_112243

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1125	0.015924	hypothetical protein BC006130 (LOC93622), mRNA /cds=(110,469) /gb=NM_138699 /gi=20162561 /ug=Hs.6815 /len=1961	NM_138699	Hs.6815	NP_619644
1138	0.043576	brain and nasopharyngeal carcinoma susceptibility protein (NSG-X), mRNA /cds=(186,518) /gb=NM_014411 /gi=14149650 /ug=Hs.26937 /len=1897	NM_014411	Hs.26937	NP_055226
1144	0.023148	mRNA; cDNA DKFZp761M0223 (from clone DKFZp761M0223) /gb=AL137938 /gi=6851002 /ug=Hs.77646 /len=3764	AL137938	Hs.77646	
1145	0.046005	hypothetical protein FLJ22843 (FLJ22843), mRNA /cds=(532,1287) /gb=NM_025184 /gi=13376775 /ug=Hs.301143 /len=2291	NM_025184	Hs.301143	NP_079460
1151	0.004203	RAD21 (S. pombe) (RAD21), mRNA /cds=(185,2080) /gb=NM_006265 /gi=5453993 /ug=Hs.81848 /len=3647	NM_006265	Hs.81848	NP_006256
1163	0.007578	reticulon 4 (RTN4), mRNA /cds=(245,3823) /gb=NM_020532 /gi=24638438 /ug=Hs.65450 /len=4166	NM_020532	Hs.65450	NP_722550
1170	0.015924	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_079425	Hs.77385	NP_524149
1172	0.009349	hypothetical protein FLJ23445 (FLJ23445), mRNA /cds=(44,658) /gb=NM_025075 /gi=13376622 /ug=Hs.288151 /len=963	NM_025075	Hs.288151	NP_079351
1179	0.032959	ribosomal protein, large, P0 (RPLP0), transcript variant 2, mRNA /cds=(111,1064) /gb=NM_053275 /gi=16933545 /ug=Hs.406511 /len=1148	NM_053275	Hs.406511	NP_444505
1187	0.015924	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), mRNA /cds=(233,1489) /gb=NM_000295 /gi=21361197 /ug=Hs.297681 /len=1584	NM_000295	Hs.297681	NP_000286
1198	0.003332	hypothetical protein FLJ20729 (FLJ20729), mRNA /cds=(135,1547) /gb=NM_017953 /gi=20149642 /ug=Hs.5111 /len=2821	NM_017953	Hs.5111	NP_060423
1199	0.029363	unnamed protein product	BAB15362		
1200	0.024587	hypothetical gene supported by XM_000590 (LOC59176)	XM_000590		
1208	0.023027	mitochondrion, complete genome	NC_001807		

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gen Accession No.	Unigene Accession No.	Protein Accession No.
1224	0.046005	CASP8 and FADD-like apoptosis regulator (CFLAR), mRNA /cds=(482,1924) /gb=NM_003879 /gi=21361768 /ug=Hs.195175 /len=2243	NM_003879	Hs.195175	NP_003870
1229	3.02E-04	mRNA for KIAA0642 protein, partial cds. /cds=(200,4189) /gb=AB014542 /gi=20521116 /ug=Hs.323317 /len=5937	AB014542	Hs.323317	
1231	0.01072	alpha-2 macroglobulin family protein VIP (VIP), mRNA /cds=(18,5675) /gb=NM_015692 /gi=23510326 /ug=Hs.375610 /len=5852	NM_015692	Hs.375610	NP_056507
1235	0.015924	mRNA, cDNA DKFZp564A026 (from clone DKFZp564A026) /gb=AL050367 /gi=4914600 /ug=Hs.66762 /len=3958	AL050367	Hs.66762	
1236	0.004536	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) (MMP9), mRNA /cds=(20,2143) /gb=NM_004994 /gi=4826835 /ug=Hs.151738 /len=2334	NM_004994	Hs.151738	NP_004985
1240	0.01925	HSPC273 (=KIAA1192)	AF161391		NP_060555
1242	0.024587	programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 2, mRNA /cds=(361,1737) /gb=NM_145341 /gi=21735597 /ug=Hs.326248 /len=2403	NM_145341	Hs.326248	NP_663314
1243	0.004677	MAD, mothers against decapentaplegic 7 (Drosophila) (MADH7), mRNA /cds=(296,1576) /gb=NM_005904 /gi=5174516 /ug=Hs.100602 /len=3111	NM_005904	Hs.100602	NP_005895
1247	0.016974	NICE-5 protein (HSA243666), mRNA /cds=(7,660) /gb=NM_017582 /gi=21361606 /ug=Hs.337078 /len=2523	NM_017582	Hs.337078	NP_060052
1253	0.003603	helicase with zinc finger domain (HELZ), mRNA /cds=(146,5974) /gb=NM_014877 /gi=7661883 /ug=Hs.3085 /len=6274	NM_014877	Hs.3085	NP_055692
1257	0.003603	isovaleryl-CoA dehydrogenase (IVD) gene, exon 12 and partial cds	AF038318		
1264	0.048543	mRNA for KIAA1143 protein, partial cds. /cds=(1,351) /gb=AB032969 /gi=6329965 /ug=Hs.173042 /len=4946	AB032969	Hs.173042	
1266	2.73E-04	ATP-binding cassette, sub-family A (ABC1), member 5 (ABCA5), transcript variant 1, mRNA /cds=(1219,6147) /gb=NM_018672 /gi=27262623 /ug=Hs.180513 /len=7044	NM_018672	Hs.180513	NP_758424

G n s Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gen Acc ssion No.	Unigene Accession No.	Prot in Acc ssion No.
1272	0.00527	collagen, type XII, alpha-1 (COL12A1), transcript variant long, mRNA /cds=(114,9305) /gb=NM_004370 /gi=18201922 /ug=Hs.101302 /len=11554	NM_004370	Hs.101302	NP_542376
1274	0.023148	HSJ1a (HSJ1) mRNA, complete cds; alternatively spliced. /cds=(26,859) /gb=S37375 /gi=250081 /ug=Hs.433237 /len=1760	S37375	Hs.433237	
1275	0.008722	gp25L2 protein (HSGP25L2G), mRNA /cds=(76,720) /gb=NM_017510 /gi=24475637 /ug=Hs.279929 /len=1420	NM_017510	Hs.279929	NP_059980
1282	0.037092	hypothetical protein MDS025 (MDS025), mRNA /cds=(363,1127) /gb=NM_021825 /gi=21361605 /ug=Hs.154938 /len=1585	NM_021825	Hs.154938	NP_068597
1286	0.003332	FLJ22781 fis, clone KAIA1958 /cds=UNKNOWN /gb=AK026434 /gi=10439298 /ug=Hs.213236 /len=2599	AK026434	Hs.213236	
1291	0.032959	Similar to adducin 1 (alpha), clone MGC:44427 IMAGE:5297337, mRNA, complete cds /cds=(869,2857) /gb=BC042998 /gi=28175763 /ug=Hs.183706 /len=4761	BC042998	Hs.183706	NP_789771
1297	0.031195	hypothetical protein MGC3232 (MGC3232), mRNA /cds=(85,2181) /gb=NM_032313 /gi=14150077 /ug=Hs.8715 /len=2316	NM_032313	Hs.8715	NP_115689
1300	0.046432	laminin, gamma 1 (formerly LAMB2) (LAMC1), mRNA /cds=(300,5129) /gb=NM_002293 /gi=9845497 /ug=Hs.432855 /len=7923	NM_002293	Hs.432855	NP_002284
1302	0.024587	hypothetical protein FLJ11286 (FLJ11286), mRNA /cds=(96,971) /gb=NM_018381 /gi=8922978 /ug=Hs.12151 /len=1911	NM_018381	Hs.12151	NP_060851
1304	0.002054	eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=NM_001959 /gi=16519564 /ug=Hs.421608 /len=961	NM_001959	Hs.421608	NP_066944
1305	1.63E-04	cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA /cds=(90,281) /gb=NM_001867 /gi=18105039 /ug=Hs.430075 /len=448	NM_001867	Hs.430075	NP_001858
1306	0.020748	poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA /cds=(503,2404) /gb=NM_002568 /gi=4505574 /ug=Hs.172182 /len=2848	NM_002568	Hs.172182	NP_002559

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1312	0.012262	endothelial zinc finger protein 2 (EZF-2), mRNA /cds=(234,1214) /gb=NM_018337 /gi=8922893 /ug=Hs.24545 /len=1907	NM_018337	Hs.24545	NP_060807
1313	0.041547	Similar to LYRIC, clone MGC:41931 IMAGE:5298467, mRNA, complete cds /cds=(329,2077) /gb=BC045642 /gi=28277146 /ug=Hs.243901 /len=3729	BC045642	Hs.243901	
1316	0.007886	ubiquitin-like 5 (UBL5), mRNA /cds=(66,287) /gb=NM_024292 /gi=13236509 /ug=Hs.13836 /len=413	NM_024292	Hs.13836	NP_077268
1318	0.003152	SH3-domain binding protein 5 (BTK-associated) (SH3BP5), mRNA /cds=(64,1341) /gb=NM_004844 /gi=4759057 /ug=Hs.109150 /len=2570	NM_004844	Hs.109150	NP_004835
1321	0.012262	general transcription factor IIIC, polypeptide 5, 63kDa (GTF3C5), mRNA /cds=(293,1852) /gb=NM_012087 /gi=6912401 /ug=Hs.286088 /len=2385	NM_012087	Hs.286088	NP_036219
1322	0.005674	high-mobility group 20B (HMG20B), mRNA /cds=(19,1044) /gb=NM_006339 /gi=5454079 /ug=Hs.32317 /len=1232	NM_006339	Hs.32317	NP_006330
1323	0.012262	KIAA1630 protein (KIAA1630), mRNA /cds=(72,2831) /gb=NM_018706 /gi=18375677 /ug=Hs.271586 /len=3180	NM_018706	Hs.271586	NP_061176
1343	0.036914	hypothetical protein FLJ12438 (FLJ12438), mRNA /cds=(174,1340) /gb=NM_021933 /gi=11345471 /ug=Hs.8595 /len=1575	NM_021933	Hs.8595	NP_068752
1349	0.01286	mRNA; cDNA DKFZp313D2314 (from clone DKFZp313D2314) /gb=AL832057 /gi=21732598 /ug=Hs.3685 /len=3141	AL832057	Hs.3685	
1369	2.05E-04	peroxiredoxin 2 (PRDX2), mRNA /cds=(90,686) /gb=NM_005809 /gi=5902725 /ug=Hs.432121 /len=937	NM_005809	Hs.432121	NP_005800
1370	0.010212	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6 (SLC25A6), nuclear gene encoding mitochondrial protein, mRNA /cds=(93,989) /gb=NM_001636 /gi=27764862 /ug=Hs.407372 /len=1455	NM_001636	Hs.407372	NP_001627
1374	0.00527	likely ortholog of rat p47 (p47), mRNA /cds=(86,1198) /gb=NM_016143 /gi=20149634 /ug=Hs.12865 /len=1450	NM_016143	Hs.12865	
1376	0.036914	chaperonin containing TCP1, subunit 5 (epsilon) (CCT5), mRNA /cds=(92,1717) /gb=NM_012073 /gi=24307938 /ug=Hs.1600 /len=1961	NM_012073	Hs.1600	NP_036205

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1377	0.006106	procollagen (type III) N-endopeptidase (PCOLN3), mRNA /cds=(41,997) /gb=NM_002768 /gi=4506138 /ug=Hs.183138 /len=2474	NM_002768	Hs.183138	NP_002759
1386	0.00633	AGENCOURT_6424254 NIH_MGC_67 cDNA clone IMAGE:5491531 5', mRNA sequence /clone=IMAGE:5491531 /clone_end=5' /gb=BM479954 /gi=18528996 /ug=Hs.381243 /len=1112	BM479954	Hs.381243	
1389	7.18E-04	heparan sulfate proteoglycan (HSPG2) mRNA, complete cds	M85289		NP_005520
1401	0.009763	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), mRNA /cds=(39,1613) /gb=NM_002778 /gi=11386146 /ug=Hs.406455 /len=2767	NM_002778	Hs.406455	NP_002769
1420	0.00527	ribosomal protein L36a-like (RPL36AL), mRNA /cds=(95,415) /gb=NM_001001 /gi=16306559 /ug=Hs.419465 /len=537	NM_001001	Hs.419465	NP_000992
1421	0.036914	mRNA; cDNA DKFZp434K052 (from clone DKFZp434K052) /gb=AL137398 /gi=6807944 /ug=Hs.169639 /len=1921	AL137398	Hs.169639	
1423	0.048543	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,327) /gb=NM_001865 /gi=18105035 /ug=Hs.70312 /len=470	NM_001865	Hs.70312	NP_001856
1424	0.003893	RAP1A, member of RAS oncogene family (RAP1A), mRNA /cds=(313,867) /gb=NM_002884 /gi=4506412 /ug=Hs.865 /len=1579	NM_002884	Hs.865	NP_002875
1433	0.043576	PAI-1 gene, PAI-1-HindIII-2 allele, 3' sequence	AF110527		
1447	0.027691	Hypothetical protein(KIAA0993)	AB023210		NP_848700
1454	0.015924	Dmx-like 1 (DMXL1), mRNA /cds=(81,9164) /gb=NM_005509 /gi=21536473 /ug=Hs.181042 /len=11072	NM_005509	Hs.181042	NP_005500
1477	0.041547	zinc finger protein 302 (ZNF302), mRNA /cds=(337,1773) /gb=NM_018675 /gi=11034834 /ug=Hs.125287 /len=2978	NM_018675	Hs.125287	NP_061145
1485	0.048543	SRY (sex determining region Y)-box 5 (SOX5), transcript variant B, mRNA /cds=(373,2625) /gb=NM_152989 /gi=23308714 /ug=Hs.87224 /len=4492	NM_152989	Hs.87224	NP_821078
1489	0.016974	mRNA for KIAA1432 protein, partial cds. /cds=(1,2391) /gb=AB037853 /gi=20521915 /ug=Hs.279556 /len=4961	AB037853	Hs.279556	

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1494	0.011469	basic leucine zipper and W2 domains 2 (BZW2), mRNA /cds=(163,1422) /gb=NM_014038 /gi=7661743 /ug=Hs.5216 /len=1869	NM_014038	Hs.5216	NP_054757
1501	0.003893	tropomyosin 4	Y00169		
1503	0.003079	retrovirus-related leucine zipper protein p40 - human retrotransposon L1.1	I38587		
1514	0.015924	defender against cell death 1 (DAD1), mRNA /cds=(67,408) /gb=NM_001344 /gi=4503252 /ug=Hs.82890 /len=699	NM_001344	Hs.82890	NP_001335
1518	0.009349	KIAA0466 protein	AB007935		NP_001533
1521	0.020482	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1), mRNA /cds=(289,2511) /gb=NM_004939 /gi=4826685 /ug=Hs.78580 /len=2706	NM_004939	Hs.78580	NP_004930
1522	0.001465	G protein-coupled receptor 64 (GPR64), mRNA /cds=(73,3117) /gb=NM_005756 /gi=5031732 /ug=Hs.184942 /len=4665	NM_005756	Hs.184942	NP_005747
1529	0.011469	ubiquinol-cytochrome c reductase binding protein (UQCRB), mRNA /cds=(54,389) /gb=NM_006294 /gi=20070231 /ug=Hs.131255 /len=965	NM_006294	Hs.131255	NP_006285
1535	0.014701	mRNA for KIAA0752 protein, partial cds. /cds=(1,1006) /gb=AB018295 /gi=3882224 /ug=Hs.126779 /len=4332	AB018295	Hs.126779	NP_775934
1543	0.023148	actin, alpha 2, smooth muscle, aorta (ACTA2), mRNA /cds=(48,1181) /gb=NM_001613 /gi=4501882 /ug=Hs.195851 /len=1330	NM_001613	Hs.195851	NP_001604
1549	0.001465	BRCA1, Rho7 and vat1 genes, complete cds, and ipf35 gene, partial cds	L78833		
1552	0.006566	RNA-binding region (RNP1, RRM) containing 2 (RNPC2), mRNA /cds=(150,1724) /gb=NM_004902 /gi=4757925 /ug=Hs.145696 /len=2595	NM_004902	Hs.145696	NP_004893
1553	0.039034	lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA /cds=(174,2057) /gb=NM_002298 /gi=7382490 /ug=Hs.381099 /len=3723	NM_002298	Hs.381099	NP_002289
1555	0.03489	KIAA1573 mRNA protein	AB046793		
1572	0.015924	ribosomal protein L27a (RPL27A), mRNA /cds=(23,469) /gb=NM_000990 /gi=14141189 /ug=Hs.76064 /len=514	NM_000990	Hs.76064	NP_000981
1577	0.021781	POM121 membrane glycoprotein (rat) (POM121), mRNA /cds=(978,3932) /gb=NM_172020 /gi=26051277 /ug=Hs.295112 /len=6014	NM_172020	Hs.295112	NP_742017

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1580	0.0261	profilin 1 (PFN1), mRNA /cds=(137,559) /gb=NM_005022 /gi=16753213 /ug=Hs.408943 /len=847	NM_005022	Hs.408943	NP_005013
1587	0.03489	PTD012 protein (PTD012), mRNA /cds=(200,997) /gb=NM_014039 /gi=21361494 /ug=Hs.8360 /len=2403	NM_014039	Hs.8360	NP_054758
1592	0.041547	KIAA0071 gene, partial cds /cds=UNKNOWN /gb=D31888 /gi=506340 /ug=Hs.78398 /len=5241	D31888	Hs.78398	NP_055971
1593	0.032959	hypothetical protein BC018068 (LOC221044), mRNA /cds=(231,695) /gb=NM_145314 /gi=21687122 /ug=Hs.112998 /len=840	NM_145314	Hs.112998	NP_660357
1598	0.029363	troponin I, skeletal, slow (TNNI1), mRNA /cds=(74,637) /gb=NM_003281 /gi=21361554 /ug=Hs.84673 /len=1108	NM_003281	Hs.84673	NP_003272
1607	0.0261	sulfatase SULF1 precursor, mRNA, complete cds /cds=(707,3322) /gb=AF545571 /gi=28191289 /ug=Hs.70823 /len=5699	AF545571	Hs.70823	NP_055985
1630	2.73E-04	calpain 2, (mII) large subunit (CAPN2), mRNA /cds=(143,2245) /gb=NM_001748 /gi=12408645 /ug=Hs.76288 /len=3419	NM_001748	Hs.76288	NP_001739
1652	0.031117	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD), mRNA /cds=(201,2384) /gb=NM_000302 /gi=4557836 /ug=Hs.75093 /len=3115	NM_000302	Hs.75093	NP_000293
1654	0.016974	DKFZp434M092 (from clone DKFZp434M092)	AL137412		NP_057479
1659	0.041254	likely ortholog of mouse elongation protein 3 (S. cerevisiae) (ELP3), mRNA /cds=(7,1650) /gb=NM_018091 /gi=23510282 /ug=Hs.267905 /len=3095	NM_018091	Hs.267905	NP_060561
1661	0.006106	cofactor required for Sp1 transcriptional activation, subunit 3, 130kDa (CRSP3), mRNA /cds=(120,4226) /gb=NM_004830 /gi=7019352 /ug=Hs.29679 /len=5176	NM_004830	Hs.29679	NP_057063
1662	0.020482	NS1-binding protein (NS1-BP), mRNA /cds=(556,2484) /gb=NM_006469 /gi=24475846 /ug=Hs.197298 /len=4137	NM_006469	Hs.197298	NP_006460
1663	0.015924	sarcolipin (SLN), mRNA /cds=(169,264) /gb=NM_003063 /gi=4507062 /ug=Hs.334629 /len=716	NM_003063	Hs.334629	NP_003054

Genes Corrsponding To Differentially Express d Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1665	0.008133	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
1666	0.003079	interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA /cds=(207,1919) /gb=NM_002182 /gi=24430220 /ug=Hs.173880 /len=4726	NM_002182	Hs.173880	NP_608273
1667	0.032959	interleukin 1 receptor, type I (IL1R1), mRNA /cds=(83,1792) /gb=NM_000877 /gi=27894331 /ug=Hs.82112 /len=4909	NM_000877	Hs.82112	NP_000868
1674	0.027691	calreticulin (CALR), mRNA /cds=(69,1322) /gb=NM_004343 /gi=5921996 /ug=Hs.353170 /len=1899	NM_004343	Hs.353170	NP_004334
1675	0.004536	coagulation factor XIII, A1 polypeptide (F13A1), mRNA /cds=(102,2300) /gb=NM_000129 /gi=9961355 /ug=Hs.80424 /len=3833	NM_000129	Hs.80424	NP_000120
1676	0.032959	muscle specific gene (M9), mRNA /cds=(172,828) /gb=NM_013234 /gi=10801344 /ug=Hs.283781 /len=911	NM_013234	Hs.283781	NP_037366
1682	0.007056	mRNA; cDNA DKFZp586A061 (from clone DKFZp586A061) /gb=AL080232 /gi=5262725 /ug=Hs.220696 /len=3052	AL080232	Hs.220696	
1687	0.002625	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein) (DBI), mRNA /cds=(20,334) /gb=NM_020548 /gi=24475624 /ug=Hs.78888 /len=556	NM_020548	Hs.78888	NP_065438
1703	7.88E-04	cDNA FLJ35517 fis, clone SPLEN2000698. /gb=AK092836 /gi=21751529 /ug=Hs.291804 /len=2536	AK092836	Hs.291804	
1710	0.016974	RNA binding motif, single stranded interacting protein (RBMS3), mRNA /cds=(175,1410) /gb=NM_014483 /gi=7657505 /ug=Hs.158446 /len=1461	NM_014483	Hs.158446	NP_055298
1712	0.013991	TNFAIP3 interacting protein 2 (TNIP2), mRNA /cds=(376,1344) /gb=NM_024309 /gi=13236543 /ug=Hs.288991 /len=1960	NM_024309	Hs.288991	NP_077285
1730	0.043576	mitochondrion, complete genome	NC_001807		
1731	0.027656	hypothetical protein dJ122O8.2 (DJ122O8.2), mRNA /cds=(34,300) /gb=NM_020466 /gi=20070310 /ug=Hs.268115 /len=902	NM_020466	Hs.268115	NP_065199
1742	0.01925	KIAA0998 protein (KIAA0998), mRNA /cds=(71,2524) /gb=NM_015072 /gi=19923419 /ug=Hs.131525 /len=3122	NM_015072	Hs.131525	NP_055887

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1759	0.00527	MEP50 protein (MEP50), mRNA /cds=(40,1068) /gb=NM_024102 /gi=20127622 /ug=Hs.11039 /len=2428	NM_024102	Hs.11039	NP_077007
1760	0.027691	FLJ32238 fis, clone PLACE6004993 /cds=UNKNOWN /gb=AK056800 /gi=16552307 /ug=Hs.183161 /len=2204	AK056800	Hs.183161	NP_036595
1769	0.003603	ribosomal protein L10 (RPL10), mRNA /cds=(42,686) /gb=NM_006013 /gi=15718685 /ug=Hs.412900 /len=2188	NM_006013	Hs.412900	NP_006004
1773	0.003893	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994
1795	0.01925	serine/threonine kinase 16 (STK16), mRNA /cds=(119,1051) /gb=NM_003691 /gi=4505836 /ug=Hs.153003 /len=1382	NM_003691	Hs.153003	NP_003682
1797	0.006566	cDNA FLJ14066 fis, clone HEMBB1001197. /gb=AK024128 /gi=10436433 /ug=Hs.306665 /len=2086	AK024128	Hs.306665	
1798	0.021781	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa (NDUFV1), mRNA /cds=(70,1464) /gb=NM_007103 /gi=20149567 /ug=Hs.7744 /len=1566	NM_007103	Hs.7744	NP_009034
1809	0.015924	clone IMAGE:3907313, mRNA /gb=BC041424 /gi=27370744 /ug=Hs.434753 /len=1700	BC041424	Hs.434753	
1832	0.032959	ubiquitin protein ligase (UBE3B), mRNA /cds=(585,3791) /gb=NM_130466 /gi=26080339 /ug=Hs.17639 /len=5731	NM_130466	Hs.17639	NP_569733
1836	0.001596	hypothetical protein FLJ23445 (FLJ23445), mRNA /cds=(44,658) /gb=NM_025075 /gi=13376622 /ug=Hs.288151 /len=963	NM_025075	Hs.288151	NP_079351
1844	0.001033	cDNA FLJ32247 fis, clone PROST1000120. /gb=AK056809 /gi=16552317 /ug=Hs.293663 /len=3019	AK056809	Hs.293663	
1854	0.001737	clone IMAGE:3611719, mRNA, partial cds /cds=(1,2592) /gb=BC003542 /gi=13097656 /ug=Hs.244482 /len=3234	BC003542	Hs.244482	
1858	0.00448	cDNA FLJ41000 fis, clone UTERU2016761, highly similar to ES/130 mRNA. /gb=AK098319 /gi=21758311 /ug=Hs.356310 /len=2196	AK098319	Hs.356310	
1860	0.0261	hypothetical protein FLJ20559 (FLJ20559), mRNA /cds=(211,810) /gb=NM_017881 /gi=8923529 /ug=Hs.98135 /len=1172	NM_017881	Hs.98135	NP_060351

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1861	0.031117	hypothetical protein FLJ21841 (FLJ21841), mRNA /cds=(184,1476) /gb=NM_024609 /gi=13375818 /ug=Hs.29076 /len=2327	NM_024609	Hs.29076	NP_078885
1872	0.027691	suppressor of Ty 16 (S. cerevisiae) (SUPT16H), mRNA /cds=(340,3483) /gb=NM_007192 /gi=19924176 /ug=Hs.14963 /len=4696	NM_007192	Hs.14963	NP_009123
1873	0.015924	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30 (FAU), mRNA /cds=(106,507) /gb=NM_001997 /gi=17981709 /ug=Hs.177415 /len=574	NM_001997	Hs.177415	NP_001988
1882	0.005674	HSPC023 protein (HSPC023), mRNA /cds=(10,309) /gb=NM_014047 /gi=7661741 /ug=Hs.420065 /len=616	NM_014047	Hs.420065	NP_054766
1896	0.039034	ATP synthase, H transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 (ATP5G2), mRNA /cds=(60,485) /gb=NM_005176 /gi=6671590 /ug=Hs.89399 /len=746	NM_005176	Hs.89399	NP_005167
1897	0.024587	Csa-19	U12404		NP_009035
1918	0.001465	voltage-dependent anion channel 3 (VDAC3), mRNA /cds=(100,951) /gb=NM_005662 /gi=25188178 /ug=Hs.7381 /len=1414	NM_005662	Hs.7381	NP_005653
1926	0.011469	KIAA0738 gene product (KIAA0738), mRNA /cds=(134,2899) /gb=NM_014719 /gi=7662275 /ug=Hs.406492 /len=4076	NM_014719	Hs.406492	NP_055534
1932	0.041254	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2 (SMARCD2), mRNA /cds=(423,1850) /gb=NM_003077 /gi=21264350 /ug=Hs.250581 /len=2704	NM_003077	Hs.250581	NP_003068
1970	0.00223	Yeast centromere vector pRS315 with LEU2 marker, complete sequence	U03441		
1976	0.016974	likely ortholog of mouse exocyst component protein 70 kDa (S. cerevisiae) Exo70: exocyst component protein 70 kDa (S. cerevisiae) (EXO70), mRNA /cds=(4,1965) /gb=NM_015219 /gi=24308034 /ug=Hs.325530 /len=4596	NM_015219	Hs.325530	NP_056034
1987	0.008133	hypothetical protein MGC8721 (MGC8721), mRNA /cds=(17,1036) /gb=NM_016127 /gi=18252054 /ug=Hs.279921 /len=1840	NM_016127	Hs.279921	NP_057211

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2005	4.48E-04	class I histone deacetylase (HDAC8)	AF230097		NP_060956
2012	0.008722	polyhomeotic-like 2 (Drosophila) (PHC2), mRNA /cds=(9,1310) /gb=NM_004427 /gi=4758241 /ug=Hs.165263 /len=2555	NM_004427	Hs.165263	NP_004418
2033	0.003079	calmodulin 1 (phosphorylase kinase, delta) (CALM1), mRNA /cds=(200,649) /gb=NM_006888 /gi=5901911 /ug=Hs.282410 /len=1526	NM_006888	Hs.282410	NP_008819
2041	0.008722	ribosomal protein L32 (RPL32), mRNA /cds=(51,458) /gb=NM_000994 /gi=15812220 /ug=Hs.169793 /len=521	NM_000994	Hs.169793	NP_000985
2044	0.03489	CGI-31 protein (CGI-31), mRNA /cds=(50,940) /gb=NM_015959 /gi=7705725 /ug=Hs.279861 /len=1669	NM_015959	Hs.279861	NP_057043
2047	0.010015	p8 protein (candidate of metastasis 1) (P8), mRNA /cds=(103,351) /gb=NM_012385 /gi=6912569 /ug=Hs.424279 /len=719	NM_012385	Hs.424279	NP_036517
2048	0.009349	mRNA for KIAA0701 protein, partial cds. /cds=(1,4065) /gb=AB014601 /gi=20521136 /ug=Hs.153293 /len=4625	AB014601	Hs.153293	
2054	0.006566	mRNA; cDNA DKFZp586J1922 (from clone DKFZp586J1922) /gb=AL110203 /gi=5817122 /ug=Hs.138411 /len=2060	AL110203	Hs.138411	
2070	0.029363	myotubular myopathy 1 (MTM1), mRNA /cds=(55,1866) /gb=NM_000252 /gi=4557895 /ug=Hs.75302 /len=3411	NM_000252	Hs.75302	NP_000243
2071	0.048543	mRNA for KIAA0194 gene, partial cds. /cds=(1,4310) /gb=D83778 /gi=1228038 /ug=Hs.216958 /len=5245	D83778	Hs.216958	
2077	0.002054	musculus exoribonuclease 1 (Xrn1)	NM_011916		NP_036046
2083	0.018081	major histocompatibility complex, class I, B (HLA-B), mRNA /cds=(11,1099) /gb=NM_005514 /gi=21327676 /ug=Hs.77961 /len=1310	NM_005514	Hs.77961	NP_005505
2088	0.003079	hypothetical protein LOC51257 (LOC51257), mRNA /cds=(352,1092) /gb=NM_016496 /gi=24475980 /ug=Hs.132744 /len=1614	NM_016496	Hs.132744	NP_057580
2128	0.021781	vacuolar protein sorting 35 (yeast) (VPS35), mRNA /cds=(48,2438) /gb=NM_018206 /gi=17999540 /ug=Hs.264190 /len=2707	NM_018206	Hs.264190	NP_060676
2151	0.003079	retinoblastoma-like 2 (p130) (RBL2), mRNA /cds=(70,3489) /gb=NM_005611 /gi=21361291 /ug=Hs.79362 /len=4853	NM_005611	Hs.79362	NP_005602

Genes C responding To Differentially Expressed Genes in Figure 12 - Hyp rtension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2163	0.012262	eukaryotic translation initiation factor 3, subunit 6 interacting protein (EIF3S6IP), mRNA /cds=(34,1728) /gb=NM_016091 /gi=7705432 /ug=Hs.119503 /len=1901	NM_016091	Hs.119503	NP_057175
2164	0.002054	KIAA1074 protein (KIAA1074); mRNA /cds=(151,5280) /gb=NM_014915 /gi=7662473 /ug=Hs.129218 /len=5360	NM_014915	Hs.129218	NP_055730
2166	0.010015	nephroblastoma overexpressed gene (NOV), mRNA /cds=(73,1146) /gb=NM_002514 /gi=19923725 /ug=Hs.235935 /len=2389	NM_002514	Hs.235935	NP_002505
2168	0.003079	LOC119392 (LOC119392), mRNA /cds=(53,751) /gb=NM_145247 /gi=21687029 /ug=Hs.93667 /len=1460	NM_145247	Hs.93667	NP_660290
2175	0.041254	clone IMAGE:4799018, mRNA /gb=BC045722 /gi=28277129 /ug=Hs.153527 /len=2587	BC045722	Hs.153527	
2178	0.043576	crystallin, zeta (quinone reductase)-like 1 (CRYZL1), transcript variant 3, mRNA /cds=(86,682) /gb=NM_145858 /gi=22202615 /ug=Hs.330208 /len=2099	NM_145858	Hs.330208	NP_665857
2191	0.009349	cDNA FLJ34376 fis, clone FEBRA2017780, weakly similar to RNA binding motif protein 9. /gb=AK091695 /gi=21750125 /ug=Hs.376650 /len=2397	AK091695	Hs.376650	
2192	0.013102	hypothetical protein KIAA0473 gene product	NM_014787		NP_055602
2197	0.007578	COX11 cytochrome c oxidase assembly protein (yeast) (COX11), nuclear gene encoding mitochondrial protein, mRNA /cds=(48,878) /gb=NM_004375 /gi=17921983 /ug=Hs.241515 /len=2717	NM_004375	Hs.241515	NP_004366
2199	0.043576	DnaJ (Hsp40) subfamily C, member 8 (DNAJC8), mRNA /cds=(8,802) /gb=NM_014280 /gi=7657610 /ug=Hs.433540 /len=1525	NM_014280	Hs.433540	NP_055095
2211	6.55E-04	L-isoaspartyl/D-aspartyl O-methyltransferase (PCMT1) gene, exon 1,	U49740		
2221	0.0261	clone MGC:43950 IMAGE:5276217, mRNA, complete cds /cds=(351,392) /gb=BC037901 /gi=23138800 /ug=Hs.262716 /len=2214	BC037901	Hs.262716	
2239	0.03489	hypothetical protein (KIAA1162)	AB032988		NP_066979
2256	0.03489	splicing factor 3a, subunit 3, 60kDa (SF3A3), mRNA /cds=(9,1514) /gb=NM_006802 /gi=5803166 /ug=Hs.77897 /len=2733	NM_006802	Hs.77897	NP_006793
2269	0.003603	PRO2822	AAF69654		

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2271	0.001596	transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein; A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>	AF196779		
2289	0.003332	SPARC-like 1 (mast9, hev1) (SPARCL1), mRNA /cds=(323,2317) /gb=NM_004684 /gi=21359870 /ug=Hs.75445 /len=2808	NM_004684	Hs.75445	NP_004675
2295	0.016974	non-metastatic cells 1, protein (NM23A) expressed in (NME1), mRNA /cds=(85,543) /gb=NM_000269 /gi=4557796 /ug=Hs.118638 /len=732	NM_000269	Hs.118638	NP_000260
2297	0.003332	zinc finger protein 2 (A1-5) (ZNF2), mRNA /cds=(855,1733) /gb=NM_021088 /gi=20304090 /ug=Hs.192285 /len=2630	NM_021088	Hs.192285	NP_066574
2303	0.023148	cDNA FLJ13446 fis, clone PLACE1002968. /gb=AK023508 /gi=10435460 /ug=Hs.201925 /len=1712	AK023508	Hs.201925	
2305	0.021781	KIAA0970 protein (KIAA0970), mRNA /cds=(335,2668) /gb=NM_014923 /gi=7662419 /ug=Hs.103329 /len=4863	NM_014923	Hs.103329	
2306	0.036914	S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental (S100A4), transcript variant 1, mRNA /cds=(70,375) /gb=NM_002961 /gi=9845514 /ug=Hs.81256 /len=512	NM_002961	Hs.81256	NP_062427
2307	0.01925	matrilin 3 (MATN3) precursor, mRNA /cds=(64,1524) /gb=NM_002381 /gi=13518040 /ug=Hs.278461 /len=2599	NM_002381	Hs.278461	NP_002372
2317	0.012262	mRNA for KIAA0570 protein, partial cds. /cds=(480,10718) /gb=AB011142 /gi=20521084 /ug=Hs.180948 /len=11269	AB011142	Hs.180948	
2324	0.018081	hypothetical protein KIAA0883	AB020690		NP_009188
2341	0.011469	eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa (EIF3S5), mRNA /cds=(7,1080) /gb=NM_003754 /gi=4503518 /ug=Hs.7811 /len=1231	NM_003754	Hs.7811	NP_003745
2348	0.031117	neuropilin-2 (a5)	AF022861		
2414	0.007578	metaxin 1 (MTX1), mRNA /cds=(1,954) /gb=NM_002455 /gi=4505280 /ug=Hs.247551 /len=1065	NM_002455	Hs.247551	NP_002446

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Prot in Accession No.
2445	0.014931	matrilin 1, cartilage matrix protein (MATN1), mRNA /cds=(490,1980) /gb=NM_002379 /gi=13518035 /ug=Hs.150366 /len=2414	NM_002379	Hs.150366	NP_002370
2457	0.029362	ATPase, Na /K transporting, alpha 2 () polypeptide (ATP1A2), mRNA /cds=(105,3167) /gb=NM_000702 /gi=4502270 /ug=Hs.34114 /len=5511	NM_000702	Hs.34114	NP_000693
2475	0.00189	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), transcript variant 1, nuclear gene encoding mitochondrial protein, mRNA /cds=(29,1675) /gb=NM_170740 /gi=25777720 /ug=Hs.5299 /len=5170	NM_170740	Hs.5299	NP_733936
2491	0.003332	clone IMAGE:5265791, mRNA /gb=BC035170 /gi=23958673 /ug=Hs.385807 /len=3000	BC035170	Hs.385807	
2510	0.046005	EST (xm35g05.x1 NCI_CGAP_GC6 cDNA clone IMAGE:2686232 3')	AW196683		NP_004958
2511	0.015924	ribosomal protein L35a (RPL35A), mRNA /cds=(74,406) /gb=NM_000996 /gi=16117790 /ug=Hs.288544 /len=511	NM_000996	Hs.288544	NP_000987
2525	0.032959	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
2539	1.18E-04	Similar to hypothetical protein DKFZp547I224, clone IMAGE:5271326, mRNA /gb=BC039372 /gi=25058800 /ug=Hs.439358 /len=2494	BC039372	Hs.439358	
2542	0.004203	leucyl-tRNA synthetase (LARS), mRNA /cds=(73,3603) /gb=NM_020117 /gi=24496788 /ug=Hs.6762 /len=4248	NM_020117	Hs.6762	NP_064502
2590	0.046131	enabled (Drosophila) (ENAH), mRNA /cds=(77,646) /gb=NM_018212 /gi=8922657 /ug=Hs.14838 /len=2943	NM_018212	Hs.14838	NP_060682
2607	0.014931	mitochondrion, complete genome	NC_001807		
2609	0.036914	cDNA FLJ14643 fis, clone NT2RP2001597, weakly similar to RYANODINE RECEPTOR, CARDIAC MUSCLE. /gb=AK027549 /gi=14042305 /ug=Hs.181161 /len=3586	AK027549	Hs.181161	
2625	0.001128	hypothetical protein (KIAA0714)	AB018257		
2626	0.048543	general transcription factor IIB (GTF2B), mRNA /cds=(39,989) /gb=NM_001514 /gi=13435384 /ug=Hs.258561 /len=1268	NM_001514	Hs.258561	NP_001505

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2633	0.036914	qb78b04.x1 Soares_fetal_heart_NbHH19W cDNA clone IMAGE:1706191 3', mRNA sequence /clone=IMAGE:1706191 /clone_end=3' /gb=AI144533 /gi=3666342 /ug=Hs.368824 /len=461	AI144533	Hs.368824	
2645	0.013102	cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA /cds=(90,281) /gb=NM_001867 /gi=18105039 /ug=Hs.430075 /len=448	NM_001867	Hs.430075	NP_001858
2678	0.015924	protein-L-isoaspartate (D-aspartate) O- methyltransferase (PCMT1), mRNA /cds=(74,757) /gb=NM_005389 /gi=4885538 /ug=Hs.79137 /len=1599	NM_005389	Hs.79137	NP_005380
2679	7.18E-04	goliath protein (GP), mRNA /cds=(428,1258) /gb=NM_018434 /gi=20127393 /ug=Hs.155718 /len=1445	NM_018434	Hs.155718	NP_060904
2684	6.55E-04	squalene epoxidase (SQLE), mRNA /cds=(215,1939) /gb=NM_003129 /gi=6806899 /ug=Hs.71465 /len=2277	NM_003129	Hs.71465	NP_003120
2696	0.032959	cartilage linking protein 1 (CRTL1), mRNA /cds=(316,1380) /gb=NM_001884 /gi=4503052 /ug=Hs.2799 /len=1492	NM_001884	Hs.2799	NP_001875
2708	0.020482	mRNA for KIAA1338 protein, partial cds. /cds=(1,4488) /gb=AB037759 /gi=7243056 /ug=Hs.261587 /len=4994	AB037759	Hs.261587	
2713	0.003332	caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 CAV1	AJ133269		
2718	0.048543	17-beta-hydroxysteroid dehydrogenase type VII isoform mRNA, complete cds. /cds=(79,414) /gb=AF165514 /gi=9294734 /ug=Hs.380900 /len=1272	AF165514	Hs.380900	NP_057455
2721	0.002625	NRF1 protein (NRF1)= non-functional folate binding protein	L24123		
2723	0.006106	hypothetical protein FLJ12552 (FLJ12552), mRNA /cds=(6,1106) /gb=NM_022832 /gi=12383077 /ug=Hs.109268 /len=2483	NM_022832	Hs.109268	NP_073743
2732	0.006566	Similar to RIKEN cDNA 4921510P06 gene, clone MGC:9752 IMAGE:3855177, mRNA, complete cds	BC009053		NP_055494
2736	0.020482	Down syndrome critical region gene 3 (DSCR3), mRNA /cds=(240,1133) /gb=NM_006052 /gi=5174424 /ug=Hs.26146 /len=3252	NM_006052	Hs.26146	NP_006043

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2743	0.012262	clone MGC:9947 IMAGE:3876105, mRNA, complete cds /cds=(51,2216) /gb=BC013590 /gi=15488925 /ug=Hs.2437 /len=2651	BC013590	Hs.2437	
2745	0.006106	calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	AF223391		
2751	0.015924	transmembrane 4 superfamily member tetraspan NET-2 (NET-2), mRNA /cds=(66,983) /gb=NM_012338 /gi=21264567 /ug=Hs.16529 /len=2267	NM_012338	Hs.16529	NP_036470
2778	0.032959	SET translocation (myeloid leukemia-associated) (SET), mRNA /cds=(4,837) /gb=NM_003011 /gi=4506890 /ug=Hs.145279 /len=2577	NM_003011	Hs.145279	NP_003002
2810	0.007578	ATP synthase, H transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), mRNA /cds=(255,683) /gb=NM_001689 /gi=4502300 /ug=Hs.429 /len=826	NM_001689	Hs.429	NP_001680
2815	0.015924	proteasome (prosome, macropain) subunit, alpha type, 6 (PSMA6), mRNA /cds=(110,850) /gb=NM_002791 /gi=23110943 /ug=Hs.410276 /len=1035	NM_002791	Hs.410276	NP_002782
2816	0.039034	CD109 (CD109), mRNA /cds=(113,4450) /gb=NM_133493 /gi=19424129 /ug=Hs.55964 /len=5883	NM_133493	Hs.55964	NP_598000
2821	8.48E-05	transcription factor forkhead-like 7 (FKHL7) gene, complete cds	AF048693		
2822	0.011469	Rho-related BTB domain containing 3 (RHOBTB3), mRNA /cds=(336,2171) /gb=NM_014899 /gi=7662355 /ug=Hs.10432 /len=4099	NM_014899	Hs.10432	NP_055714
2840	0.013991	KIAA0040 gene product (KIAA0040), mRNA /cds=(921,1382) /gb=NM_014656 /gi=7657258 /ug=Hs.158282 /len=4564	NM_014656	Hs.158282	NP_055471
2843	0.048543	UI-E-EJ0-ahj-n-19-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahj-n-19-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahj-n-19-0-UI /clone_end=5' /gb=BM701108 /gi=19014366 /ug=Hs.401941 /len=1923	BM701108	Hs.401941	
2848	0.008133	BJ-HCC-24 tumor antigen mRNA, complete cds /cds=(2,1240) /gb=AY121805 /gi=22002585 /ug=Hs.433489 /len=1488	AY121805	Hs.433489	
2850	0.00223	helicase II (RAD54L) mRNA, complete cds. /cds=(54,4979) /gb=U09820 /gi=606832 /ug=Hs.96264 /len=6115	U09820	Hs.96264	NP_612115

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2856	0.013991	proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA /cds=(86,811) /gb=NM_002790 /gi=23110941 /ug=Hs.76913 /len=1023	NM_002790	Hs.76913	NP_002781
2867	0.001465	mitogen-activated protein kinase kinase 1 interacting protein 1 (MAP2K1IP1), mRNA /cds=(250,624) /gb=NM_021970 /gi=21614526 /ug=Hs.6361 /len=1416	NM_021970	Hs.6361	NP_068805
2883	0.020482	thymosin, beta 10 (TMSB10), mRNA /cds=(66,200) /gb=NM_021103 /gi=10863894 /ug=Hs.76293 /len=453	NM_021103	Hs.76293	NP_066926
2885	0.021781	chromosome 1 specific transCRipt KIAA0491	AB007960		NP_057093
2887	0.031117	RNA binding motif protein 12 (RBM12), transcript variant 1, mRNA /cds=(275,3073) /gb=NM_006047 /gi=23510460 /ug=Hs.180895 /len=6650	NM_006047	Hs.180895	NP_690051
2891	0.023148	patched related protein translocated in renal cancer (TRC8), mRNA /cds=(215,2209) /gb=NM_007218 /gi=21314653 /ug=Hs.28285 /len=2481	NM_007218	Hs.28285	NP_009149
2894	0.039034	ab23g04.x5 Stratagene lung (#937210) cDNA clone IMAGE:841686 3' similar to Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;, mRNA sequence /clone=IMAGE:841686 /clone_end=3' /gb=AI791154 /gi=5338870 /ug=Hs.445939 /len=440	AI791154	Hs.445939	
2901	0.03489	A kinase (PRKA) anchor protein (yotiao) 9 (AKAP9), transcript variant 4, mRNA /cds=(223,5190) /gb=NM_147166 /gi=22538388 /ug=Hs.58103 /len=6058	NM_147166	Hs.58103	NP_671714
2912	0.01072	KIAA0690 protein (KIAA0690), mRNA /cds=(87,3980) /gb=NM_015179 /gi=15987120 /ug=Hs.60103 /len=4396	NM_015179	Hs.60103	NP_055994
2913	0.006106	mortality factor 4 like 1 (MORF4L1), mRNA /cds=(132,1103) /gb=NM_006791 /gi=5803101 /ug=Hs.6353 /len=1766	NM_006791	Hs.6353	NP_006782
2928	0.004536	ligase IV, DNA, ATP-dependent (LIG4), mRNA /cds=(274,3009) /gb=NM_002312 /gi=23199992 /ug=Hs.166091 /len=3325	NM_002312	Hs.166091	NP_002303
2932	0.041254	cyclin D binding myb-like transcription factor 1 (DMTF1), mRNA /cds=(276,2558) /gb=NM_021145 /gi=10863946 /ug=Hs.5671 /len=3767	NM_021145	Hs.5671	NP_066968

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigen Accession No.	Protein Accession No.
2938	0.006106	ribosomal protein L7a (RPL7A), mRNA /cds=(31,831) /gb=NM_000972 /gi=18390348 /ug=Hs.99858 /len=890	NM_000972	Hs.99858	NP_000963
2946	0.007578	CD164 antigen, sialomucin (CD164), mRNA /cds=(94,687) /gb=NM_006016 /gi=21361273 /ug=Hs.43910 /len=3038	NM_006016	Hs.43910	NP_006007
2947	0.001596	hemoglobin, alpha 2 (HBA2), mRNA /cds=(38,466) /gb=NM_000517 /gi=14043068 /ug=Hs.347939 /len=575	NM_000517	Hs.347939	NP_000508
2948	0.041254	endothelial differentiation-related factor 1 (EDF1), transcript variant alpha, mRNA /cds=(29,475) /gb=NM_003792 /gi=24497592 /ug=Hs.174050 /len=658	NM_003792	Hs.174050	NP_694880
2950	6.55E-04	cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419 /len=802	NM_001861	Hs.433419	NP_001852
2954	0.023148	muscleblind-like (Drosophila) (MBNL), mRNA /cds=(1415,2527) /gb=NM_021038 /gi=10518339 /ug=Hs.28578 /len=5940	NM_021038	Hs.28578	NP_066368
2961	0.013102	line-1 protein ORF2 (=p150)	B28096		
2962	0.007578	ORF2 contains a reverse transcriptase domain	AAB59368		
2963	0.001232	cDNA FLJ40109 fis, clone TESTI2007685. /gb=AK097428 /gi=21757181 /ug=Hs.377146 /len=2007	AK097428	Hs.377146	
2975	0.0261	actin related protein 2/3 complex, subunit 3, 21kDa (ARPC3), mRNA /cds=(94,630) /gb=NM_005719 /gi=23397667 /ug=Hs.293750 /len=912	NM_005719	Hs.293750	NP_005710
2976	0.008133	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_079425	Hs.77385	NP_524149
2984	0.043576	hypothetical protein FLJ10290 (FLJ10290), mRNA /cds=(78,1340) /gb=NM_018047 /gi=8922327 /ug=Hs.25516 /len=2297	NM_018047	Hs.25516	NP_060517
2985	0.006106	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D), transcript variant 1, mRNA /cds=(198,2141) /gb=NM_032378 /gi=25453473 /ug=Hs.334798 /len=2216	NM_032378	Hs.334798	NP_115754

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2988	0.016974	cDNA: FLJ22636 fis, clone HSI06658, highly similar to HSAJ4162 mRNA for putative lipoic acid synthetase. /gb=AK026289 /gi=10439102 /ug=Hs.9280 /len=1732	AK026289	Hs.9280	NP_006850
2989	4.06E-04	hypothetical protein DKFZp434B195 (DKFZP434B195), mRNA /cds=(514,1290) /gb=NM_031284 /gi=21361960 /ug=Hs.10748 /len=2262	NM_031284	Hs.10748	NP_112574
2991	0.009349	prothymosin, alpha (gene sequence 28) (PTMA), mRNA /cds=(182,514) /gb=NM_002823 /gi=21359859 /ug=Hs.250655 /len=1233	NM_002823	Hs.250655	NP_002814
2993	0.001596	integrin beta 4 binding protein (ITGB4BP), mRNA /cds=(71,808) /gb=NM_002212 /gi=4504770 /ug=Hs.406444 /len=1112	NM_002212	Hs.406444	NP_002203
2996	0.048543	ribosomal protein L12 (RPL12), mRNA /cds=(89,586) /gb=NM_000976 /gi=15431291 /ug=Hs.405042 /len=632	NM_000976	Hs.405042	NP_000967
3002	7.18E-04	high-mobility group phosphoprotein (HMGI-C) gene; exons 1-3, complete cds	L41044		
3011	0.007578	mitochondrion, complete genome	NC_001807		
3020	0.046005	hypothetical protein DJ667H12.2 (DJ667H12.2), mRNA /cds=(180,1250) /gb=NM_019605 /gi=19923818 /ug=Hs.21068 /len=2038	NM_019605	Hs.21068	NP_062551
3025	0.018081	FLJ30708 fis, clone FCBBF2001238 /cds=UNKNOWN /gb=AK055270 /gi=16549967 /ug=Hs.94812 /len=1965	AK055270	Hs.94812	
3026	0.002844	calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA /cds=(69,518) /gb=NM_001743 /gi=20428653 /ug=Hs.425808 /len=1128	NM_001743	Hs.425808	NP_001734
3032	0.007578	golgi-specific brefeldin A resistance factor 1 (GBF1), mRNA /cds=(241,5820) /gb=NM_004193 /gi=4758415 /ug=Hs.155499 /len=6376	NM_004193	Hs.155499	NP_004184
3034	0.00223	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SERPINB6), mRNA /cds=(75,1205) /gb=NM_004568 /gi=28077084 /ug=Hs.41072 /len=1361	NM_004568	Hs.41072	NP_004559
3040	5.42E-04	DKFZp434F1011 (from clone DKFZp434F1011) /cds=UNKNOWN /gb=AL157490 /gi=7018535 /ug=Hs.274589 /len=6634	AL157490	Hs.274589	

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3044	0.002054	hypothetical protein LOC51321 (LOC51321), mRNA /cds=(635,1195) /gb=NM_016627 /gi=7706167 /ug=Hs.268122 /len=1304	NM_016627	Hs.268122	NP_057711
3046	0.004536	kinesin family member 3B (KIF3B), mRNA /cds=(168,2411) /gb=NM_004798 /gi=4758645 /ug=Hs.301206 /len=4724	NM_004798	Hs.301206	NP_004789
3049	0.03489	retinol dehydrogenase 14 (all-trans and 9-cis) (RDH14), mRNA /cds=(64,1074) /gb=NM_020905 /gi=10190745 /ug=Hs.288880 /len=1538	NM_020905	Hs.288880	NP_065956
3057	0.041254	ferredoxin 1 (FDX1), nuclear gene encoding mitochondrial protein, mRNA /cds=(134,688) /gb=NM_004109 /gi=13677224 /ug=Hs.744 /len=1468	NM_004109	Hs.744	NP_004100
3059	0.029363	DKFZp434O071 (from clone DKFZp434O071)	AL080184		NP_057217
3061	0.007578	mRNA; cDNA DKFZp586F1418 (from clone DKFZp586F1418) /gb=AL833819 /gi=21739144 /ug=Hs.296356 /len=4355	AL833819	Hs.296356	
3062	0.00489	myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), mRNA /cds=(115,630) /gb=NM_006471 /gi=5453739 /ug=Hs.180224 /len=944	NM_006471	Hs.180224	NP_006462
3065	0.006566	KIAA0433 protein (KIAA0433), mRNA /cds=(510,4241) /gb=NM_015216 /gi=7662117 /ug=Hs.26179 /len=5814	NM_015216	Hs.26179	NP_056031
3070	0.001737	signal sequence receptor, beta (translocon-associated protein beta) (SSR2), mRNA /cds=(51,602) /gb=NM_003145 /gi=6552341 /ug=Hs.74564 /len=1093	NM_003145	Hs.74564	NP_003136
3071	2.73E-04	endothelin receptor type A (EDNRA), mRNA /cds=(485,1768) /gb=NM_001957 /gi=4503464 /ug=Hs.76252 /len=4105	NM_001957	Hs.76252	NP_001948
3072	0.036914	trichorhinophalangeal syndrome I (TRPS1), mRNA /cds=(639,4484) /gb=NM_014112 /gi=7657658 /ug=Hs.26102 /len=10011	NM_014112	Hs.26102	NP_054831
3077	0.01072	mRNA; cDNA DKFZp586E1120 (from clone DKFZp586E1120) /gb=AL049437 /gi=4500220 /ug=Hs.351178 /len=2141	AL049437	Hs.351178	

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3079	2.73E-04	ATP synthase, H transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=NM_006886 /gi=21327678 /ug=Hs.177530 /len=417	NM_006886	Hs.177530	NP_008817
3080	0.021781	extracellular link domain containing 1 (XLKD1), mRNA /cds=(91,1059) /gb=NM_006691 /gi=5729910 /ug=Hs.17917 /len=2313	NM_006691	Hs.17917	NP_006682
3085	0.002844	PEF protein with a long N-terminal hydrophobic domain (peflin) (PEF), mRNA /cds=(13,867) /gb=NM_012392 /gi=6912581 /ug=Hs.241531 /len=1641	NM_012392	Hs.241531	NP_036524
3090	0.003893	Similar to kinesin family member C1, clone MGC:1202 IMAGE:3506669, mRNA, complete cds /cds=(168,2189) /gb=BC000712 /gi=12653842 /ug=Hs.20830 /len=2400	BC000712	Hs.20830	NP_002254
3094	0.029363	SON DNA binding protein (SON), transcript variant e, mRNA /cds=(50,6376) /gb=NM_058183 /gi=21040317 /ug=Hs.92909 /len=8482	NM_058183	Hs.92909	NP_620305
3102	0.013991	deoxyribonuclease I-like 3 (DNASE1L3), mRNA /cds=(71,988) /gb=NM_004944 /gi=4826697 /ug=Hs.88646 /len=1079	NM_004944	Hs.88646	NP_004935
3107	0.039034	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMTS5), mRNA /cds=(123,2915) /gb=NM_007038 /gi=5901887 /ug=Hs.58324 /len=5533	NM_007038	Hs.58324	NP_008969
3108	0.002625	glycogen synthase 1 (muscle) (GYS1), mRNA /cds=(161,2374) /gb=NM_002103 /gi=4504232 /ug=Hs.772 /len=3531	NM_002103	Hs.772	NP_002094
3117	4.93E-04	mRNA for Sec24 protein (Sec24A isoform), partial /cds=(1,3237) /gb=AJ131244 /gi=3947687 /ug=Hs.211612 /len=5967	AJ131244	Hs.211612	
3124	0.010015	hypothetical protein LOC51315 (LOC51315), mRNA /cds=(395,1174) /gb=NM_016618 /gi=7706155 /ug=Hs.5721 /len=1774	NM_016618	Hs.5721	NP_057702
3131	0.016974	putative translation initiation factor (SUI1), mRNA /cds=(148,489) /gb=NM_005801 /gi=20070210 /ug=Hs.150580 /len=1324	NM_005801	Hs.150580	NP_005792

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3136	0.001232	splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(219,542) /gb=NM_006925 /gi=5902077 /ug=Hs.166975 /len=1865	NM_006925	Hs.166975	NP_008856
3137	0.002844	yp24c06.s1 Soares breast 3NbHBst cDNA clone IMAGE:188362 3' similar to gb:M10942_cds1 metallothionein-le gene mRNA sequence /clone=IMAGE:188362 /clone_end=3' /gb=H43642 /gi=919694 /ug=Hs.418241 /len=452	H43642	Hs.418241	
3138	0.012262	NCAG1 (NCAG1), mRNA /cds=(1477,5145) /gb=NM_032160 /gi=23943786 /ug=Hs.124673 /len=9528	NM_032160	Hs.124673	NP_115536
3142	0.008133	single-stranded DNA binding protein (SSBP1), mRNA /cds=(79,525) /gb=NM_003143 /gi=4507230 /ug=Hs.923 /len=628	NM_003143	Hs.923	NP_003134
3149	0.012262	thioredoxin domain-containing (TXNDC), mRNA /cds=(118,960) /gb=NM_030755 /gi=13559515 /ug=Hs.24766 /len=1112	NM_030755	Hs.24766	NP_110382
3151	2.47E-04	hypothetical protein FLJ37440 (FLJ37440), mRNA /cds=(272,1591) /gb=NM_153214 /gi=23397470 /ug=Hs.355577 /len=2299	NM_153214	Hs.355577	NP_694946
3156	0.004203	golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1 (GOLGB1), mRNA /cds=(127,9906) /gb=NM_004487 /gi=4758453 /ug=Hs.7844 /len=10300	NM_004487	Hs.7844	NP_004478
3162	0.01047	hypothetical protein FLJ22875 (FLJ22875), mRNA /cds=(152,634) /gb=NM_032231 /gi=15638951 /ug=Hs.406548 /len=1019	NM_032231	Hs.406548	NP_115607
3166	8.63E-04	hypothetical protein FLJ13855 (FLJ13855), mRNA /cds=(328,1068) /gb=NM_023079 /gi=20149671 /ug=Hs.168232 /len=3053	NM_023079	Hs.168232	NP_075567
3172	6.55E-04	myocyte-specific enhancer factor 2A (MEF2A) gene, last coding exon, and complete cds	U49020		
3173	0.004536	hypothetical protein FLJ11730 (FLJ11730), mRNA /cds=(33,608) /gb=NM_022756 /gi=20149668 /ug=Hs.17118 /len=1558	NM_022756	Hs.17118	NP_073593
3174	0.023148	lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA /cds=(69,476) /gb=NM_002305 /gi=6006015 /ug=Hs.382367 /len=526	NM_002305	Hs.382367	NP_002296

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hyp rtension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3189	0.001465	melanoma adhesion molecule (MCAM), mRNA /cds=(27,1967) /gb=NM_006500 /gi=5729917 /ug=Hs.211579 /len=3583	NM_006500	Hs.211579	NP_006491
3193	0.015924	phosphorylase, glycogen; brain (PYGB), nuclear gene encoding mitochondrial protein, mRNA /cds=(97,2628) /gb=NM_002862 /gi=21361369 /ug=Hs.75658 /len=4166	NM_002862	Hs.75658	NP_002853
3194	0.001033	ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=NM_004152 /gi=9845504 /ug=Hs.281960 /len=986	NM_004152	Hs.281960	NP_004143
3196	0.048543	DKFZp586E0524 (from clone DKFZp586E0524)	AL110153		NP_000974
3197	4.06E-04	NDRG family member 2 (NDRG2), mRNA /cds=(97,1170) /gb=NM_016250 /gi=10280619 /ug=Hs.243960 /len=2024	NM_016250	Hs.243960	NP_057334
3198	0.011469	cDNA: FLJ21691 fis, clone COL09555. /gb=AK025344 /gi=10437842 /ug=Hs.141003 /len=1824	AK025344	Hs.141003	
3201	0.012262	protein kinase C substrate 80K-H (PRKCSH), mRNA /cds=(137,1720) /gb=NM_002743 /gi=4506076 /ug=Hs.1432 /len=2056	NM_002743	Hs.1432	NP_002734
3204	0.01925	clone IMAGE:5263531, mRNA /gb=BC037740 /gi=22902216 /ug=Hs.18016 /len=5036	BC037740	Hs.18016	
3245	0.002625	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) (P4HB), mRNA /cds=(45,1571) /gb=NM_000918 /gi=20070124 /ug=Hs.410578 /len=2438	NM_000918	Hs.410578	NP_000909
3275	0.046005	KIAA0141 gene product (KIAA0141), mRNA /cds=(81,1628) /gb=NM_014773 /gi=7661939 /ug=Hs.63510 /len=3020	NM_014773	Hs.63510	NP_055588
3282	0.018081	YME1-like 1 (S. cerevisiae) (YME1L1), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA /cds=(183,2504) /gb=NM_139312 /gi=21327684 /ug=Hs.206521 /len=4036	NM_139312	Hs.206521	NP_647474
3294	0.048543	NCK adaptor protein 1 (NCK1), mRNA /cds=(117,1250) /gb=NM_006153 /gi=20070226 /ug=Hs.54589 /len=1947	NM_006153	Hs.54589	NP_006144
3316	0.036914	glutathione S-transferase M3 (brain) (GSTM3), mRNA /cds=(311,988) /gb=NM_000849 /gi=23065551 /ug=Hs.2006 /len=1572	NM_000849	Hs.2006	NP_000840

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3367	0.031117	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), mRNA /cds=(133,2466) /gb=NM_000176 /gi=4504132 /ug=Hs.75772 /len=4788	NM_000176	Hs.75772	NP_000167
3377	0.043576	cDNA: FLJ23538 fis, clone LNG08010, highly similar to BETA2 MEN1 region clone epsilon/beta mRNA. /gb=AK027191 /gi=10440260 /ug=Hs.240443 /len=1746	AK027191	Hs.240443	
3397	0.027691	chromosome 20 open reading frame 6 (C20orf6), mRNA /cds=(109,2664) /gb=NM_016649 /gi=22507381 /ug=Hs.88820 /len=3216	NM_016649	Hs.88820	NP_057733
3400	0.041254	KH domain containing, RNA binding, signal transduction associated 1 (KHDRBS1), mRNA /cds=(107,1438) /gb=NM_006559 /gi=5730026 /ug=Hs.119537 /len=2685	NM_006559	Hs.119537	NP_006550
3402	0.029363	basic transcription factor 3 (BTF3), mRNA /cds=(240,728) /gb=NM_001207 /gi=20070129 /ug=Hs.101025 /len=952	NM_001207	Hs.101025	NP_001198
3407	0.023148	BCL2/adenovirus E1B 19kD-interacting protein 3-like (BNIP3L)	XM_048077		
3413	0.046005	myoglobin (MB), mRNA /cds=(71,535) /gb=NM_005368 /gi=4885476 /ug=Hs.118836 /len=1066	NM_005368	Hs.118836	NP_005359
3431	0.020482	spermine synthase gene	AJ009633		
3440	0.03489	TERF1 (TRF1)-interacting nuclear factor 2 (TINF2), mRNA /cds=(263,1327) /gb=NM_012461 /gi=6912715 /ug=Hs.7797 /len=2095	NM_012461	Hs.7797	NP_036593
3441	0.024587	translocase of inner mitochondrial membrane 8 B (yeast) (TIMM8B), mRNA /cds=(13,264) /gb=NM_012459 /gi=6912711 /ug=Hs.279915 /len=423	NM_012459	Hs.279915	NP_036591
3443	0.007578	guanylate kinase 1 (GUK1), mRNA /cds=(225,818) /gb=NM_000858 /gi=20127414 /ug=Hs.3764 /len=1082	NM_000858	Hs.3764	NP_000849
3444	0.006566	laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=NM_002295 /gi=9845501 /ug=Hs.181357 /len=1039	NM_002295	Hs.181357	NP_002286
3456	2.47E-04	ionized calcium binding adapter molecule 2 (IBA2), mRNA /cds=(89,541) /gb=NM_031426 /gi=13899240 /ug=Hs.4944 /len=3381	NM_031426	Hs.4944	NP_113614

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3461	0.01072	ribosomal protein S3 (RPS3), mRNA /cds=(19,750) /gb=NM_001005 /gi=15718686 /ug=Hs.414990 /len=843	NM_001005	Hs.414990	NP_000996
3463	0.023148	mastermind-like 1 (Drosophila) (MAML1), mRNA /cds=(264,3314) /gb=NM_014757 /gi=13376996 /ug=Hs.76986 /len=5717	NM_014757	Hs.76986	NP_055572
3464	0.012262	matrilin 3 (MATN3) precursor, mRNA /cds=(64,1524) /gb=NM_002381 /gi=13518040 /ug=Hs.278461 /len=2599	NM_002381	Hs.278461	NP_002372
3470	0.039034	hypothetical protein FLJ10300 (FLJ10300), mRNA /cds=(1710,3359) /gb=NM_018051 /gi=21361686 /ug=Hs.42233 /len=3785	NM_018051	Hs.42233	NP_060521
3472	0.01925	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
3477	0.046005	vacuolar protein sorting 16 (yeast) (VPS16), transcript variant 1, mRNA /cds=(49,2568) /gb=NM_022575 /gi=17978478 /ug=Hs.302441 /len=2769	NM_022575	Hs.302441	NP_536339
3483	0.048543	signal sequence receptor, beta (translocon-associated protein beta) (SSR2), mRNA /cds=(51,602) /gb=NM_003145 /gi=6552341 /ug=Hs.74564 /len=1093	NM_003145	Hs.74564	NP_003136
3492	0.00527	UI-H-BI2-ags-a-03-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2725156 3', mRNA sequence /clone=IMAGE:2725156 /clone_end=3' /gb=AW292521 /gi=6699157 /ug=Hs.227074 /len=685	AW292521	Hs.227074	
3500	0.004536	ASC-1 complex subunit P100 (FLJ21588), mRNA /cds=(115,2388) /gb=NM_032204 /gi=20270252 /ug=Hs.334686 /len=2808	NM_032204	Hs.334686	NP_115580
3511	0.001033	xf26f10.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2619211 3', mRNA sequence /clone=IMAGE:2619211 /clone_end=3' /gb=AW130007 /gi=6131612 /ug=Hs.389726 /len=423	AW130007	Hs.389726	
3513	0.041254	chromosome 1 open reading frame 29 (C1orf29), mRNA /cds=(242,1483) /gb=NM_006820 /gi=5803026 /ug=Hs.75470 /len=2058	NM_006820	Hs.75470	NP_006811

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3521	0.039034	ubiquitin-like, containing PHD and RING finger domains 2 (URF2), transcript variant 1, mRNA /cds=(341,1852) /gb=NM_152306 /gi=23312361 /ug=Hs.348602 /len=3720	NM_152306	Hs.348602	NP_690856
3533	0.046005	nascent-polypeptide-associated complex alpha polypeptide (NACA), mRNA /cds=(26,673) /gb=NM_005594 /gi=5031930 /ug=Hs.32916 /len=797	NM_005594	Hs.32916	NP_005585
3538	0.027691	insulin-like growth factor binding protein 6 (IGFBP6), mRNA /cds=(54,776) /gb=NM_002178 /gi=11321592 /ug=Hs.274313 /len=952	NM_002178	Hs.274313	NP_002169
3539	0.007578	ubiquitin C (UBC), mRNA /cds=(136,2193) /gb=NM_021009 /gi=20149305 /ug=Hs.183704 /len=2309	NM_021009	Hs.183704	NP_066289
3540	0.001232	nucleoporin 155kDa (NUP155), transcript variant 1, mRNA /cds=(119,4294) /gb=NM_153485 /gi=24430148 /ug=Hs.23255 /len=4355	NM_153485	Hs.23255	NP_705618
3551	0.00527	RAB9A, member RAS oncogene family (RAB9A), mRNA /cds=(192,797) /gb=NM_004251 /gi=20070189 /ug=Hs.330994 /len=1106	NM_004251	Hs.330994	NP_004242
3576	0.007056	osteoglycin (osteoinductive factor, mimecan) (OGN), transcript variant 1, mRNA /cds=(422,1318) /gb=NM_033014 /gi=14916497 /ug=Hs.109439 /len=2976	NM_033014	Hs.109439	NP_148935
3606	0.018081	nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs) (NOLA3), mRNA /cds=(98,292) /gb=NM_018648 /gi=15011920 /ug=Hs.14317 /len=556	NM_018648	Hs.14317	NP_061118
3613	0.041254	ataxin 2 related protein (A2LP), transcript variant A, mRNA /cds=(169,3396) /gb=NM_007245 /gi=27262646 /ug=Hs.43509 /len=4386	NM_007245	Hs.43509	NP_680782
3619	6.03E-05	cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419 /len=802	NM_001861	Hs.433419	NP_001852
3623	0.016974	cDNA FLJ14089 fis, clone MAMMA1000257. /gb=AK024151 /gi=10436462 /ug=Hs.306668 /len=1730	AK024151	Hs.306668	

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3625	0.015924	UI-E-CQ1-aev-g-12-0-UI.s1 UI-E-CQ1 cDNA clone UI-E-CQ1-aev-g-12-0-UI 3', mRNA sequence /clone=UI-E-CQ1-aev-g-12-0-UI /clone_end=3' /gb=BM666437 /gi=18974127 /ug=Hs.279806 /len=1103	BM666437	Hs.279806	
3640	0.012262	PTD015 protein (PTD015), mRNA /cds=(148,504) /gb=NM_014040 /gi=7662642 /ug=Hs.95870 /len=620	NM_014040	Hs.95870	NP_054759
3641	0.006106	hypothetical protein CL25084 (CL25084), mRNA /cds=(132,1583) /gb=NM_015701 /gi=20070263 /ug=Hs.7100 /len=2412	NM_015701	Hs.7100	NP_056516
3642	0.002625	chromosome 1 open reading frame 22 (C1orf22), mRNA /cds=(54,2723) /gb=NM_025191 /gi=19923618 /ug=Hs.279951 /len=6298	NM_025191	Hs.279951	NP_079467
3645	0.0261	hypothetical protein MGC14697 (MGC14697), mRNA /cds=(264,440) /gb=NM_032747 /gi=14249375 /ug=Hs.171625 /len=581	NM_032747	Hs.171625	NP_116136
3652	0.001128	cDNA: FLJ22636 fis, clone HSI06658, highly similar to HSAJ4162 mRNA for putative lipoic acid synthetase. /gb=AK026289 /gi=10439102 /ug=Hs.9280 /len=1732	AK026289	Hs.9280	NP_006850
3662	0.01925	hypothetical protein FLJ10700 (FLJ10700), mRNA /cds=(184,1872) /gb=NM_018182 /gi=8922595 /ug=Hs.295909 /len=3434	NM_018182	Hs.295909	NP_060652
3666	0.023148	DAZ associated protein 2 (DAZAP2), mRNA /cds=(70,576) /gb=NM_014764 /gi=7661885 /ug=Hs.75416 /len=1897	NM_014764	Hs.75416	NP_055579
3677	0.023148	major histocompatibility complex, class I, B (HLA-B), mRNA /cds=(11,1099) /gb=NM_005514 /gi=21327676 /ug=Hs.77961 /len=1310	NM_005514	Hs.77961	NP_005505
3683	0.007578	thioredoxin reductase TR2 mRNA, partial cds /cds=(1,1740) /gb=AF171055 /gi=5764542 /ug=Hs.20030 /len=2593	AF171055	Hs.20030	
3685	0.018081	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 (SMARCE1), mRNA /cds=(122,1357) /gb=NM_003079 /gi=21264354 /ug=Hs.332848 /len=1576	NM_003079	Hs.332848	NP_003070

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3690	0.006566	IK cytokine, down-regulator of HLA II (IK), mRNA /cds=(112,1785) /gb=NM_006083 /gi=11038650 /ug=Hs.8024 /len=1785	NM_006083	Hs.8024	NP_006074
3705	0.00527	hypothetical protein FLJ10856 (FLJ10856), mRNA /cds=(148,1233) /gb=NM_018247 /gi=8922719 /ug=Hs.108530 /len=3720	NM_018247	Hs.108530	NP_060717
3708	0.046005	mRNA; cDNA DKFZp667D095 (from clone DKFZp667D095) /gb=AL512749 /gi=12224966 /ug=Hs.432978 /len=1396	AL512749	Hs.432978	
3716	0.0261	FLJ21563 fis, clone COL06445 (AK025216.1).	AK025216	Hs.24341	NP_056287
3730	0.023148	folliculin (FST), transcript variant FST317, mRNA /cds=(28,981) /gb=NM_006350 /gi=7242223 /ug=Hs.9914 /len=1386	NM_006350	Hs.9914	NP_037541
3733	0.041254	MAGEF1 protein (MAGEF1), mRNA /cds=(177,1103) /gb=NM_022149 /gi=11545891 /ug=Hs.306123 /len=1615	NM_022149	Hs.306123	NP_071432
3756	0.036914	Ste20-related serine/threonine kinase (SLK), mRNA /cds=(512,3970) /gb=NM_014720 /gi=7661993 /ug=Hs.105751 /len=5988	NM_014720	Hs.105751	NP_055535
3762	0.036914	heat shock 70kDa protein 8 (HSPA8), transcript variant 1, mRNA /cds=(79,2019) /gb=NM_006597 /gi=24234684 /ug=Hs.180414 /len=2276	NM_006597	Hs.180414	NP_694881
3768	0.005674	Mov10, Moloney leukemia virus 10, (mouse) (MOV10), mRNA /cds=(71,3082) /gb=NM_020963 /gi=14211539 /ug=Hs.20725 /len=3328	NM_020963	Hs.20725	NP_066014
3769	4.06E-04	signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3), transcript variant 1, mRNA /cds=(241,2553) /gb=NM_139276 /gi=21618339 /ug=Hs.321677 /len=3455	NM_139276	Hs.321677	NP_644805
3783	0.016974	Tat-SF1	U76992		NP_055315
3794	0.03489	coatamer protein complex, subunit alpha (COPA), mRNA /cds=(467,4141) /gb=NM_004371 /gi=6996002 /ug=Hs.75887 /len=5064	NM_004371	Hs.75887	NP_004362
3796	5.42E-04	immunoglobulin light chain	D87000		
3798	0.020482	chromodomain helicase DNA binding protein 4 (CHD4), mRNA /cds=(90,5828) /gb=NM_001273 /gi=4557452 /ug=Hs.74441 /len=6417	NM_001273	Hs.74441	NP_001264

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3800	0.016974	ribosomal protein, large, P0 (RPLP0), transcript variant 2, mRNA /cds=(111,1064) /gb=NM_053275 /gi=16933545 /ug=Hs.406511 /len=1148	NM_053275	Hs.406511	NP_444505
3801	0.003893	ribosomal protein S7 (RPS7), mRNA /cds=(91,675) /gb=NM_001011 /gi=15431308 /ug=Hs.301547 /len=729	NM_001011	Hs.301547	NP_001002
3802	0.001033	cartilage associated protein (CRTAP), mRNA /cds=(12,1217) /gb=NM_006371 /gi=21536278 /ug=Hs.155481 /len=2307	NM_006371	Hs.155481	NP_006362
3806	0.036914	period 1 (Drosophila) (PER1), mRNA /cds=(188,4060) /gb=NM_002616 /gi=4505712 /ug=Hs.68398 /len=4656	NM_002616	Hs.68398	NP_002607
3808	0.039034	MN/CA9	Z54349		
3826	0.036914	gene for neural cell adhesion molecule 3' region exon f; used in NCAM-140 6.7 kb and NCAM-180 7.4 kb transcripts	X07200		
3827	0.00527	helicase C-terminal domain- and SNF2 N-terminal domain-containing protein (CHD6-pending), mRNA /cds=(185,8326) /gb=NM_032221 /gi=21362041 /ug=Hs.45207 /len=8326	NM_032221	Hs.45207	NP_115597
3830	0.046005	eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=NM_001959 /gi=16519564 /ug=Hs.421608 /len=961	NM_001959	Hs.421608	NP_066944
3845	0.003893	nuclear distribution gene C (A. nidulans) (NUDC), mRNA /cds=(91,1086) /gb=NM_006600 /gi=5729952 /ug=Hs.263812 /len=1333	NM_006600	Hs.263812	NP_006591
3848	0.03489	PRP4 pre-mRNA processing factor 4 (yeast) (PRPF4), mRNA /cds=(60,1628) /gb=NM_004697 /gi=24431949 /ug=Hs.374973 /len=2765	NM_004697	Hs.374973	NP_004688
3849	0.020482	enigma (LIM domain protein) (ENIGMA), mRNA /cds=(67,1440) /gb=NM_005451 /gi=11496884 /ug=Hs.102948 /len=1706	NM_005451	Hs.102948	NP_005442
3866	0.016974	protocadherin gamma subfamily C, 5 (PCDHGC5), transcript variant 1, mRNA /cds=(1,2835) /gb=NM_018929 /gi=14277683 /ug=Hs.335001 /len=4641	NM_018929	Hs.335001	NP_115783
3872	0.001465	6-phosphogluconolactonase (PGLS), mRNA /cds=(18,794) /gb=NM_012088 /gi=6912585 /ug=Hs.100071 /len=1010	NM_012088	Hs.100071	NP_036220
3873	0.046005	proteasome (prosome, macropain) 26S subunit, ATPase, 1 (PSMC1), mRNA /cds=(49,1371) /gb=NM_002802 /gi=24430150 /ug=Hs.4745 /len=1586	NM_002802	Hs.4745	NP_002793

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3903	0.043934	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 (CHST1), mRNA /cds=(367,1602) /gb=NM_003654 /gi=4502840 /ug=Hs.104576 /len=2415	NM_003654	Hs.104576	NP_003645
3907	0.041254	Ig superfamily protein (Z39IG), mRNA /cds=(46,1245) /gb=NM_007268 /gi=6005957 /ug=Hs.8904 /len=1787	NM_007268	Hs.8904	NP_009199
3913	0.012262	hairy and enhancer of split 1, (Drosophila) (HES1), mRNA /cds=(237,1079) /gb=NM_005524 /gi=8400709 /ug=Hs.250666 /len=1471	NM_005524	Hs.250666	NP_005515
3916	0.013991	integral inner nuclear membrane protein (MAN1), mRNA /cds=(7,2742) /gb=NM_014319 /gi=7706606 /ug=Hs.7256 /len=4703	NM_014319	Hs.7256	NP_055134
3925	0.001033	similar to RIKEN cDNA 1110059E24, clone IMAGE:5218126, mRNA /gb=BC028019 /gi=20380167 /ug=Hs.112993 /len=3343	BC028019	Hs.112993	
3933	0.006106	cDNA FLJ10266 fis, clone HEMBB1001024. /gb=AK001128 /gi=7022194 /ug=Hs.210297 /len=1244	AK001128	Hs.210297	
3938	0.039034	mitochondrion, complete genome	NC_001807		
3942	0.039034	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) (SPTAN1), mRNA /cds=(103,7521) /gb=NM_003127 /gi=4507190 /ug=Hs.77196 /len=7787	NM_003127	Hs.77196	NP_003118
3954	0.007056	esophageal cancer related gene 4 protein (ECRG4), mRNA /cds=(109,555) /gb=NM_032411 /gi=14165275 /ug=Hs.43125 /len=772	NM_032411	Hs.43125	NP_115787
3968	0.005674	protein tyrosine phosphatase type IVA, member 2 (PTP4A2), transcript variant 1, mRNA /cds=(1011,1514) /gb=NM_003479 /gi=18104974 /ug=Hs.82911 /len=3925	NM_003479	Hs.82911	NP_536317
3969	0.003893	likely ortholog of mouse phosducin-like 2 (PDCL2), mRNA /cds=(101,820) /gb=NM_024065 /gi=13129043 /ug=Hs.94576 /len=1044	NM_024065	Hs.94576	NP_076970
3970	0.011469	HSPC182 protein (HSPC182), mRNA /cds=(66,650) /gb=NM_014188 /gi=7661831 /ug=Hs.30026 /len=1059	NM_014188	Hs.30026	NP_054907
4012	0.03489	transcription termination factor, RNA polymerase I (TTF1), mRNA /cds=(45,2705) /gb=NM_007344 /gi=6678454 /ug=Hs.54780 /len=2847	NM_007344	Hs.54780	NP_031370

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4018	0.046005	major histocompatibility complex, class I, C (HLA-C), mRNA /cds=(16,1116) /gb=NM_002117 /gi=19557676 /ug=Hs.277477 /len=1549	NM_002117	Hs.277477	NP_002108
4019	0.014931	BCG-induced gene in monocytes, clone 103 (BIGM103), mRNA /cds=(478,1860) /gb=NM_022154 /gi=24586664 /ug=Hs.284205 /len=3246	NM_022154	Hs.284205	NP_071437
4023	0.036914	transforming growth factor, beta receptor III (betaglycan, 300kDa) (TGFB3), mRNA /cds=(349,2898) /gb=NM_003243 /gi=4507470 /ug=Hs.342874 /len=4208	NM_003243	Hs.342874	NP_003234
4026	0.041254	ribosomal protein L38 (RPL38), mRNA /cds=(107,319) /gb=NM_000999 /gi=16306562 /ug=Hs.425668 /len=368	NM_000999	Hs.425668	NP_000990
4074	0.024587	KIAA1018 protein, (KIAA1018), mRNA /cds=(242,3295) /gb=NM_014967 /gi=7662449 /ug=Hs.5400 /len=4839	NM_014967	Hs.5400	NP_055782
4078	0.029363	retinoblastoma binding protein 8 (RBBP8), mRNA /cds=(299,2992) /gb=NM_002894 /gi=4506440 /ug=Hs.29287 /len=3246	NM_002894	Hs.29287	NP_002885
4092	0.036914	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) (NDUFS3), mRNA /cds=(13,807) /gb=NM_004551 /gi=4758787 /ug=Hs.429506 /len=899	NM_004551	Hs.429506	NP_004542
4093	0.013991	coated vesicle membrane protein (RNP24), mRNA /cds=(24,629) /gb=NM_006815 /gi=21314646 /ug=Hs.75914 /len=2060	NM_006815	Hs.75914	NP_006806
4117	0.012262	RNA-directed DNA polymerase (EC	S21976		
4119	6.55E-04	reverse transcriptase homolog - human retrotransposon L1	I38588		
4124	0.046005	prothrombin (F2) gene (Alu and KpnI repeats)	M17262		
4130	0.027691	CGI-130 protein (CGI-130), mRNA /cds=(64,576) /gb=NM_016063 /gi=7705623 /ug=Hs.32826 /len=1372	NM_016063	Hs.32826	NP_057147
4133	0.005674	vimentin (VIM), mRNA /cds=(123,1523) /gb=NM_003380 /gi=4507894 /ug=Hs.297753 /len=1851	NM_003380	Hs.297753	NP_000995
4142	0.029363	chromosome 14 open reading frame 92 (C14orf92), mRNA /cds=(33,1898) /gb=NM_014828 /gi=7662273 /ug=Hs.194035 /len=4174	NM_014828	Hs.194035	NP_055643

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4146	0.043576	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SERPINB6), mRNA /cds=(75,1205) /gb=NM_004568 /gi=28077084 /ug=Hs.41072 /len=1361	NM_004568	Hs.41072	NP_004559
4169	0.008722	ribosomal protein S16	M60854		NP_001011
4170	0.003893	selenophosphate synthetase 2 (SPS2), mRNA /cds=(177,1523) /gb=NM_012248 /gi=24797146 /ug=Hs.118725 /len=2291	NM_012248	Hs.118725	NP_036380
4174	0.008133	soluble 29kDa NSF attachment protein (SNAP29) gene, complete cds	AF278704		
4178	0.004203	hypothetical protein (KIAA0536)	AB011108		NP_789770
4179	0.036914	CD109 (CD109), mRNA /cds=(113,4450) /gb=NM_133493 /gi=19424129 /ug=Hs.55964 /len=5883	NM_133493	Hs.55964	NP_598000
4181	0.027691	KIAA0663 gene product (KIAA0663), mRNA /cds=(214,2646) /gb=NM_014827 /gi=7662231 /ug=Hs.17969 /len=4365	NM_014827	Hs.17969	NP_055642
4185	0.021781	APR-1 protein (MAGEH1), mRNA /cds=(271,930) /gb=NM_014061 /gi=18105051 /ug=Hs.279819 /len=1475	NM_014061	Hs.279819	NP_054780
4189	0.01072	fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4), transcript variant 2, mRNA /cds=(507,2642) /gb=NM_022977 /gi=12669908 /ug=Hs.81452 /len=5356	NM_022977	Hs.81452	NP_075266
4192	0.029363	ribosomal 28S RNA	M11167		
4194	0.031117	peptidase D (PEPD), mRNA /cds=(17,1498) /gb=NM_000285 /gi=4557834 /ug=Hs.73947 /len=1888	NM_000285	Hs.73947	NP_000276
4201	0.024587	cytochrome c oxidase subunit VIb (COX6B), nuclear gene encoding mitochondrial protein, mRNA /cds=(163,423) /gb=NM_001863 /gi=17999530 /ug=Hs.431668 /len=578	NM_001863	Hs.431668	NP_001854
4206	0.01072	ring finger protein 4 (RNF4), mRNA /cds=(271,843) /gb=NM_002938 /gi=4506560 /ug=Hs.66394 /len=2918	NM_002938	Hs.66394	NP_002929
4210	0.00489	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa (NDUFA1), nuclear gene encoding mitochondrial protein, mRNA /cds=(143,355) /gb=NM_004541 /gi=13699820 /ug=Hs.74823 /len=479	NM_004541	Hs.74823	NP_004532
4220	0.00223	ribosomal protein S2 (RPS2), mRNA /cds=(12,893) /gb=NM_002952 /gi=15055538 /ug=Hs.356360 /len=978	NM_002952	Hs.356360	NP_002943

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4221	0.0261	ras inhibitor	M37190		NP_061866
4234	0.010015	ribosomal protein S4, Y-linked (RPS4Y), mRNA /cds=(13,804) /gb=NM_001008 /gi=17981706 /ug=Hs.180911 /len=931	NM_001008	Hs.180911	NP_000999
4246	0.009098	hypothetical protein MGC10471 (MGC10471), mRNA /cds=(227,1417) /gb=NM_030818 /gi=13540613 /ug=Hs.24998 /len=1688	NM_030818	Hs.24998	NP_110445
4261	0.010015	epithelial membrane protein 3 (EMP3), mRNA /cds=(242,733) /gb=NM_001425 /gi=4503562 /ug=Hs.9999 /len=817	NM_001425	Hs.9999	NP_001416
4263	0.036914	testis expressed gene 292 (FLJ14728), mRNA /cds=(49,2109) /gb=NM_032830 /gi=14249535 /ug=Hs.151001 /len=2192	NM_032830	Hs.151001	NP_116219
4294	0.006106	hypothetical protein FLJ20729 (FLJ20729), mRNA /cds=(135,1547) /gb=NM_017953 /gi=20149642 /ug=Hs.5111 /len=2821	NM_017953	Hs.5111	NP_060423
4296	0.023148	splicing factor 3b, subunit 2, 145kD, clone IMAGE:2822659, mRNA, partial cds /cds=(1,2696) /gb=BC000401 /gi=12653264 /ug=Hs.406423 /len=2873	BC000401	Hs.406423	
4307	5.42E-04	HT015 protein (HT015)	AF223466		NP_061049
4317	0.036914	accessory protein BAP31 (DXS1357E), mRNA /cds=(137,877) /gb=NM_005745 /gi=10047078 /ug=Hs.291904 /len=1314	NM_005745	Hs.291904	NP_005736
4347	7.88E-04	flap structure-specific endonuclease 1 (FEN1), mRNA /cds=(373,1515) /gb=NM_004111 /gi=19718776 /ug=Hs.4756 /len=2265	NM_004111	Hs.4756	NP_004102
4351	0.032959	KIP gene	AB021866		
4362	0.001232	AD024 protein (AD024), mRNA /cds=(131,805) /gb=NM_020675 /gi=21314698 /ug=Hs.21137 /len=1376	NM_020675	Hs.21137	NP_065726
4369	0.03489	ribosomal protein L36 (RPL36), transcript variant 2, mRNA /cds=(153,470) /gb=NM_015414 /gi=16117793 /ug=Hs.433411 /len=545	NM_015414	Hs.433411	NP_378669
4383	0.03489	ribosomal protein S26 (RPS26), mRNA /cds=(26,373) /gb=NM_001029 /gi=15011935 /ug=Hs.299465 /len=459	NM_001029	Hs.299465	NP_001020
4390	0.001596	ataxia telangiectasia and Rad3 related (ATR), mRNA /cds=(106,8040) /gb=NM_001184 /gi=20143978 /ug=Hs.77613 /len=8265	NM_001184	Hs.77613	NP_001175
4393	0.002625	KIAA1316 protein, partial cds /cds=UNKNOWN /gb=AB037737 /gi=7243012 /ug=Hs.24255 /len=5477	AB037737	Hs.24255	

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4394	0.011469	Likely ortholog of mouse tumor necrosis-alpha-induced adipose-related protein, cDNA FLJ14901 fis, clone PLACE1005409 (AK027807.1)	AK027807	Hs.44208	NP_078912
4401	0.01925	T-box 15 (TBX15), mRNA /cds=(230,1093) /gb=NM_152380 /gi=23943887 /ug=Hs.164680 /len=2782	NM_152380	Hs.164680	NP_689593
4405	0.041254	CGI-116 protein (CGI-116), mRNA /cds=(108,692) /gb=NM_016053 /gi=7705621 /ug=Hs.18885 /len=860	NM_016053	Hs.18885	NP_057137
4407	0.009349	15 kDa selenoprotein (SEP15), mRNA /cds=(5,493) /gb=NM_004261 /gi=20127464 /ug=Hs.90606 /len=1519	NM_004261	Hs.90606	NP_004252
4420	5.96E-04	Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3) (MJD), transcript variant 1, mRNA /cds=(59,1144) /gb=NM_004993 /gi=13518018 /ug=Hs.66521 /len=1900	NM_004993	Hs.66521	NP_109376
4424	2.01E-04	platelet glycoprotein IIB precursor	AAA60115		
4438	0.007578	trypsin-like serine protease (TLSP) gene	AF164623		
4448	0.007578	exostoses (multiple)-like 2 (EXTL2), mRNA /cds=(288,1280) /gb=NM_001439 /gi=14149608 /ug=Hs.61152 /len=2833	NM_001439	Hs.61152	NP_001430
4450	0.016974	glutathione S-transferase theta 2 (GSTT2) (GSTT1) genes	AF240786		
4464	1.81E-04	suCRase-isomaltase (SI)	M84646		
4466	0.008722	cDNA: FLJ21659 fis, clone COL08743. /gb=AK025312 /gi=10437802 /ug=Hs.248862 /len=2423	AK025312	Hs.248862	
4550	0.00242	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome) (HPRT1), mRNA /cds=(86,742) /gb=NM_000194 /gi=4504482 /ug=Hs.82314 /len=1331	NM_000194	Hs.82314	NP_000185
4553	0.018081	protein kinase (cAMP-dependent, catalytic) inhibitor beta (PKIB), mRNA /cds=(258,494) /gb=NM_032471 /gi=21359976 /ug=Hs.106106 /len=1209	NM_032471	Hs.106106	NP_115860
4560	0.006106	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 (ARHGEF6), mRNA /cds=(29,2359) /gb=NM_004840 /gi=22027524 /ug=Hs.79307 /len=4839	NM_004840	Hs.79307	NP_004831
4565	0.001596	Hypothetical protein(KIAA0469)	AB007938		NP_055666
4572	6.55E-04	neuroigin 3	AF217413		
4577	0.015924	biliverdin reductase A (BLVRA), mRNA /cds=(61,951) /gb=NM_000712 /gi=4502416 /ug=Hs.81029 /len=1070	NM_000712	Hs.81029	NP_000703

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4591	0.00489	KIAA0484	AB007953		
4616	0.021781	603054284F1 NIH_MGC_122 cDNA clone IMAGE:5203652 5', mRNA sequence /clone=IMAGE:5203652 /clone_end=5' /gb=BI767055 /gi=15758633 /ug=Hs.356004 /len=1067	BI767055	Hs.356004	
4624	1.63E-04	chromosome 11 open reading frame 17 (C11orf17), mRNA /cds=(77,709) /gb=NM_020642 /gi=21361869 /ug=Hs.131180 /len=1332	NM_020642	Hs.131180	NP_065693
4636	0.020482	thioredoxin (TXN), mRNA /cds=(64,381) /gb=NM_003329 /gi=4507744 /ug=Hs.432922 /len=501	NM_003329	Hs.432922	NP_003320
4637	0.021781	mitochondrion, complete genome	NC_001807		
4639	0.048543	ym45h08.s1 Soares infant brain 1NIB cDNA clone IMAGE:51273 3', mRNA sequence /clone=IMAGE:51273 /clone_end=3' /gb=H18675 /gi=884915 /ug=Hs.314777 /len=191	H18675	Hs.314777	
4643	2.01E-04	zinc finger protein (AF020591), mRNA /cds=(246,2393) /gb=NM_014480 /gi=7656870 /ug=Hs.142634 /len=3743	NM_014480	Hs.142634	NP_055295
4647	0.031117	S-phase kinase-associated protein 1A (p19A) (SKP1A), transcript variant 1, mRNA /cds=(140,622) /gb=NM_006930 /gi=25777710 /ug=Hs.171626 /len=2172	NM_006930	Hs.171626	NP_733779
4667	0.018081	histone deacetylase 2 (HDAC2), mRNA /cds=(205,1671) /gb=NM_001527 /gi=4557640 /ug=Hs.3352 /len=1985	NM_001527	Hs.3352	NP_001518
4680	0.03489	U4/U6-associated RNA splicing factor (HPRP3P), mRNA /cds=(73,2124) /gb=NM_004698 /gi=4758555 /ug=Hs.11776 /len=2344	NM_004698	Hs.11776	NP_004689
4683	0.036914	nucleotide binding protein 1 (MinD E. coli) (NUBP1), mRNA /cds=(5,967) /gb=NM_002484 /gi=4505336 /ug=Hs.81469 /len=1213	NM_002484	Hs.81469	NP_002475
4687	0.048543	CREBBP/EP300 inhibitory protein 1 (CRI1), mRNA /cds=(63,626) /gb=NM_014335 /gi=7656937 /ug=Hs.381137 /len=1719	NM_014335	Hs.381137	NP_055150
4698	0.01286	retinoic acid receptor, beta (RARβ), transcript variant 1, mRNA /cds=(469,1815) /gb=NM_000965 /gi=14916493 /ug=Hs.171495 /len=3119	NM_000965	Hs.171495	NP_057236
4699	0.031117	chromodomain protein, Y chromosome-like (CDYL), transcript variant 2, mRNA /cds=(336,1970) /gb=NM_170751 /gi=25777618 /ug=Hs.16081 /len=3474	NM_170751	Hs.16081	NP_736608

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	D scription	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4701	4.93E-04	ubiquitin-like 5 (UBL5), mRNA /cds=(66,287) /gb=NM_024292 /gi=13236509 /ug=Hs.13836 /len=413	NM_024292	Hs.13836	NP_077268
4702	0.046005	vascular cell adhesion molecule 1 (VCAM1), transcript variant 1, mRNA /cds=(121,2340) /gb=NM_001078 /gi=18201907 /ug=Hs.109225 /len=3119	NM_001078	Hs.109225	NP_542413
4704	0.01925	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa (NDUFAB1), mRNA /cds=(25,495) /gb=NM_005003 /gi=4826851 /ug=Hs.5556 /len=663	NM_005003	Hs.5556	NP_004994
4712	0.032959	vacuolar protein sorting 35 (yeast) (VPS35), mRNA /cds=(48,2438) /gb=NM_018206 /gi=17999540 /ug=Hs.264190 /len=2707	NM_018206	Hs.264190	NP_060676
4718	0.00527	3-oxoacid CoA transferase (OXCT), nuclear gene encoding mitochondrial protein, mRNA /cds=(99,1661) /gb=NM_000436 /gi=4557816 /ug=Hs.177584 /len=3337	NM_000436	Hs.177584	NP_000427
4720	0.048543	heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA /cds=(91,1992) /gb=NM_005826 /gi=14141188 /ug=Hs.15265 /len=2663	NM_005826	Hs.15265	NP_005817
4738	0.048543	hypothetical protein (KIAA1439)	AB037860		NP_005586
4740	0.004536	mRNA for KIAA0934 protein, partial cds. /cds=(1,4759) /gb=AB023151 /gi=20521699 /ug=Hs.227716 /len=6594	AB023151	Hs.227716	
4743	0.009349	KIAA0475 gene product (KIAA0475), mRNA /cds=(337,1566) /gb=NM_014864 /gi=7662149 /ug=Hs.5737 /len=5983	NM_014864	Hs.5737	NP_055679
4751	0.039034	hypothetical protein (HSPC117), mRNA /cds=(76,1593) /gb=NM_014306 /gi=7657014 /ug=Hs.10729 /len=2005	NM_014306	Hs.10729	NP_055121
4764	0.039034	mRNA for KIAA1025 protein, partial cds. /cds=(1,5755) /gb=AB028948 /gi=20521733 /ug=Hs.4084 /len=8444	AB028948	Hs.4084	
4774	0.014931	ribosomal protein S19 (RPS19), mRNA /cds=(70,507) /gb=NM_001022 /gi=14591914 /ug=Hs.298262 /len=569	NM_001022	Hs.298262	NP_001013
4778	0.007578	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994
4782	0.018081	CDC-like kinase1 (CLK1), mRNA /cds=(156,1610) /gb=NM_004071 /gi=4758007 /ug=Hs.2083 /len=1834	NM_004071	Hs.2083	NP_004062

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4785	0.039034	solute carrier family 38, member 2 (SLC38A2), mRNA /cds=(352,1872) /gb=NM_018976 /gi=21361601 /ug=Hs.298275 /len=4795	NM_018976	Hs.298275	NP_061849
4801	0.027691	growth hormone inducible transmembrane protein (GHITM), mRNA /cds=(130,1089) /gb=NM_014394 /gi=7657479 /ug=Hs.433957 /len=2374	NM_014394	Hs.433957	NP_055209
4805	0.021781	high-mobility group box 1 (HMGB1), mRNA /cds=(77,724) /gb=NM_002128 /gi=20149538 /ug=Hs.6727 /len=1207	NM_002128	Hs.6727	NP_002119
4807	0.03489	glypican 6 (GPC6), mRNA /cds=(616,2283) /gb=NM_005708 /gi=8051601 /ug=Hs.118407 /len=2760	NM_005708	Hs.118407	NP_005699
4810	0.029363	mRNA; cDNA DKFZp727I051 (from clone DKFZp727I051); partial cds /cds=(1,2099) /gb=AL117478 /gi=5911952 /ug=Hs.239370 /len=2480	AL117478	Hs.239370	NP_056412
4814	0.023628	ribosomal protein L10a (RPL10A), mRNA /cds=(16,669) /gb=NM_007104 /gi=15431287 /ug=Hs.425293 /len=700	NM_007104	Hs.425293	NP_009035
4815	0.013991	cDNA FLJ31247 fis, clone KIDNE2005296, weakly similar to ACTIN, CYTOPLASMIC 1. /gb=AK055809 /gi=16550632 /ug=Hs.170848 /len=2322	AK055809	Hs.170848	
4819	0.006566	ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500	NM_000991	Hs.356371	NP_000982
4821	0.041254	eukaryotic translation termination factor 1 (ETF1), mRNA /cds=(136,1449) /gb=NM_004730 /gi=4759033 /ug=Hs.77324 /len=3653	NM_004730	Hs.77324	NP_004721
4833	0.007578	ATP synthase, H transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), mRNA /cds=(98,868) /gb=NM_001688 /gi=21361564 /ug=Hs.81634 /len=1230	NM_001688	Hs.81634	NP_001679
4839	0.007056	tubulin alpha 6 (TUBA6), mRNA /cds=(1,1350) /gb=NM_032704 /gi=14389308 /ug=Hs.406578 /len=1350	NM_032704	Hs.406578	NP_116093
4840	0.029363	mRNA for KIAA1137 protein, partial cds. /cds=(1,2804) /gb=AB032963 /gi=6329896 /ug=Hs.43577 /len=4990	AB032963	Hs.43577	
4861	5.42E-04	protein serine kinase H1 (PSKH1), mRNA /cds=(131,1405) /gb=NM_006742 /gi=27901802 /ug=Hs.150601 /len=3460	NM_006742	Hs.150601	NP_006733

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4862	0.004536	mRNA for FLJ00005 protein, partial cds. /cds=(1,338) /gb=AK000005 /gi=7209310 /ug=Hs.367690 /len=4706	AK000005	Hs.367690	
4863	0.003079	FLJ14819 fis, clone OVARC1000241, moderately similar to HYPOXIA-INDUCIBLE FACTOR 1 ALPHA	AK027725		NP_690009
4868	3.69E-04	MLL septin-like fusion (MSF), mRNA /cds=(258,1964) /gb=NM_006640 /gi=19923366 /ug=Hs.181002 /len=3929	NM_006640	Hs.181002	NP_006631
4876	0.006106	solute carrier family 17 (anion/sugar transporter), member 5 (SLC17A5), mRNA /cds=(125,1612) /gb=NM_012434 /gi=21314648 /ug=Hs.117865 /len=3329	NM_012434	Hs.117865	NP_036566
4877	0.003893	chromosome 20 open reading frame 31 (C20orf31), mRNA /cds=(83,1819) /gb=NM_018217 /gi=8922666 /ug=Hs.93871 /len=1885	NM_018217	Hs.93871	NP_060687
4886	0.011469	proteasome (prosome, macropain) subunit, beta type, 4 (PSMB4), mRNA /cds=(24,818) /gb=NM_002796 /gi=22538466 /ug=Hs.89545 /len=925	NM_002796	Hs.89545	NP_002787
4893	0.006566	growth arrest and DNA-damage-inducible, beta (GADD45B), mRNA /cds=(101,586) /gb=NM_015675 /gi=9945331 /ug=Hs.110571 /len=1121	NM_015675	Hs.110571	NP_056490
4898	0.016974	cDNA FLJ12024 fis, clone HEMBB1001797. /gb=AK022086 /gi=10433407 /ug=Hs.8958 /len=1672	AK022086	Hs.8958	
4900	0.011469	hypothetical protein FLJ10702 (FLJ10702), mRNA /cds=(175,735) /gb=NM_018184 /gi=8922600 /ug=Hs.104222 /len=2944	NM_018184	Hs.104222	NP_060654
4904	0.014931	tj44d11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone IMAGE:2144373 3' similar to gb:Y00716 COMPLEMENT FACTOR H PRECURSOR mRNA sequence /clone=IMAGE:2144373 /clone_end=3' /gb=AI470482 /gi=4332572 /ug=Hs.387691 /len=384	AI470482	Hs.387691	
4905	0.0261	cytoskeleton associated protein 2 (CKAP2), mRNA /cds=(97,2145) /gb=NM_018204 /gi=19923520 /ug=Hs.24641 /len=3626	NM_018204	Hs.24641	NP_060674

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Acc ssion No.	Protein Accession No.
4912	0.00489	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit g (ATP5L); mRNA /cds=(60,371) /gb=NM_006476 /gi=21359881 /ug=Hs.107476 /len=580	NM_006476	Hs.107476	NP_006467
4919	0.013991	KIAA0436 mRNA, partial cds. /cds=(1,2070) /gb=AB007896 /gi=2662152 /ug=Hs.110 /len=4661	AB007896	Hs.110	
4921	8.63E-04	cDNA FLJ10423 fis, clone NT2RP1000259. /gb=AK001285 /gi=7022444 /ug=Hs.106909 /len=1837	AK001285	Hs.106909	
4928	0.016974	mitochondrion, complete genome	NC_001807		
4931	0.023148	testis enhanced gene transcript (TEGT), mRNA /cds=(41,754) /gb=NM_003217 /gi=4507432 /ug=Hs.74637 /len=2600	NM_003217	Hs.74637	NP_003208
4935	0.031117	clone TCCCTA00211 mRNA sequence /gb=AY007115 /gi=9956010 /ug=Hs.355779 /len=1505	AY007115	Hs.355779	
4936	0.003079	hypothetical protein FLJ20015 (FLJ20015), mRNA /cds=(32,523) /gb=NM_018996 /gi=9506648 /ug=Hs.375614 /len=1457	NM_018996	Hs.375614	NP_061869
4939	0.0261	UI-H-DH0-aui-p-19-0-UI.s1 NCI_CGAP_DH0 cDNA clone IMAGE:5871234 3', mRNA sequence /clone=IMAGE:5871234 /clone_end=3' /gb=BM994422 /gi=19719323 /ug=Hs.289721 /len=2081	BM994422	Hs.289721	
4943	0.005674	DKFZp434N1717 (from clone DKFZp434N1717)	AL133655		NP_473357
4944	0.005674	hypothetical protein FLJ20452 (FLJ20452), mRNA /cds=(15,614) /gb=NM_017828 /gi=21361660 /ug=Hs.351327 /len=1948	NM_017828	Hs.351327	NP_060298
4945	0.018081	eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa (EIF3S5), mRNA /cds=(7,1080) /gb=NM_003754 /gi=4503518 /ug=Hs.7811 /len=1231	NM_003754	Hs.7811	NP_003745
4946	0.013991	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_079425	Hs.77385	NP_524149
4948	0.016974	ovarian carcinoma immunoreactive antigen (OCIA), mRNA /cds=(168,905) /gb=NM_017830 /gi=8923426 /ug=Hs.132071 /len=1434	NM_017830	Hs.132071	NP_060300

Genes Corresponding To Differentially Expressed Genes in Figure 12 - Hypertension					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4949	2.23E-04	carboxypeptidase A3 (mast cell) (CPA3), mRNA /cds=(12,1265) /gb=NM_001870 /gi=4503000 /ug=Hs.646 /len=1633	NM_001870	Hs.646	NP_001861
4956	0.01072	hypothetical protein FLJ20671 (FLJ20671), mRNA /cds=(43,465) /gb=NM_017924 /gi=19923511 /ug=Hs.180201 /len=2855	NM_017924	Hs.180201	NP_060394
4962	0.031156	mRNA for KIAA1320 protein, partial cds. /cds=(2051,3754) /gb=AB037741 /gi=7243020 /ug=Hs.117414 /len=5321	AB037741	Hs.117414	
4963	0.013102	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,327) /gb=NM_001865 /gi=18105035 /ug=Hs.70312 /len=470	NM_001865	Hs.70312	NP_001856
4965	0.011469	microtubule-associated protein, RP/EB family, member 1 (MAPRE1), mRNA /cds=(65,871) /gb=NM_012325 /gi=6912493 /ug=Hs.234279 /len=2540	NM_012325	Hs.234279	NP_036457
4967	0.021781	ah42f05.s1 Soares_testis_NHT cDNA clone 1292193 3' similar to P54687 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, CYTOSOLIC ;, mRNA sequence /clone=1292193 /clone_end=3' /gb=AA705851 /gi=2715769 /ug=Hs.443872 /len=412	AA705851	Hs.443872	
4971	5.96E-04	muscle specific gene (M9), mRNA /cds=(172,828) /gb=NM_013234 /gi=10801344 /ug=Hs.283781 /len=911	NM_013234	Hs.283781	NP_037366
4975	0.00223	hypothetical protein MGC2747 (MGC2747), mRNA /cds=(93,248) /gb=NM_024104 /gi=13129111 /ug=Hs.194017 /len=1171	NM_024104	Hs.194017	NP_077009
4979	0.010015	ribosomal protein L6 (RPL6), mRNA /cds=(32,898) /gb=NM_000970 /gi=16753226 /ug=Hs.409045 /len=950	NM_000970	Hs.409045	NP_000961
4980	0.008133	Gene 33/Mig-6 (MIG-6), mRNA /cds=(213,1601) /gb=NM_018948 /gi=21314673 /ug=Hs.11169 /len=3099	NM_018948	Hs.11169	NP_061821
4988	0.005674	translocase of outer mitochondrial membrane 70 A (yeast) (TOMM70A), mRNA /cds=(92,1918) /gb=NM_014820 /gi=7662672 /ug=Hs.21198 /len=4017	NM_014820	Hs.21198	NP_055635
4991	0.013102	DNA sequence(chromosome 21q, section 38/105)	AP001694		